

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:30:32 ; Search time 16.3133 Seconds
(without alignments)
1028.511 Million cell updates/sec

Title: US-09-980-464-11_COPY_57_309

Perfect score: 1342
Sequence: 1 YEFLETGKGTGKVKKARE.....VNPTTRATLEDVASHWVWV 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1342	100.0	630	4	US-10-355-975A-38
2	1342	100.0	631	4	US-09-579-664B-11
3	1342	100.0	631	4	US-10-355-975A-11
4	649.5	48.4	729	2	US-08-677-298-2
5	649.5	48.4	729	4	US-09-523-849-33
6	647.5	48.2	722	4	US-09-984-890-4
7	647.5	48.2	722	4	US-10-274-194-4
8	647.5	48.2	745	4	US-09-523-849-36
9	646.5	48.2	713	4	US-09-538-092-1022
10	646.5	48.2	724	4	US-09-984-890-2
11	646.5	48.2	724	4	US-10-274-194-2
12	644	48.0	512	4	US-09-633-328B-2
13	642.5	47.9	722	4	US-08-817-832B-32
14	642.5	47.9	793	4	US-09-523-849-32
15	631	47.0	511	4	US-09-633-328B-4
16	629	46.9	779	4	US-08-817-832B-31
17	625	46.6	257	3	US-09-101-146-6
18	619.5	46.2	257	2	US-07-857-224B-25
19	619.5	46.2	633	3	US-08-557-006C-43
20	619.5	46.2	633	4	US-09-538-092-212
21	619.5	46.2	633	4	US-09-633-328B-3
22	619.5	46.2	633	4	US-09-824-735-3
23	618.5	46.1	345	3	US-09-101-146-1
24	615.5	45.9	1203	4	US-09-799-875-5
25	607.5	45.3	604	4	US-09-523-849-35
26	604	45.0	552	4	US-09-824-735-4
27	601	44.8	552	3	US-08-557-006C-40

28	600	44.7	552	4	US-09-538-092-1212	Sequence 1212, Ap
29	597.5	44.5	418	4	US-09-248-796A-18441	Sequence 18441, A
30	597.5	44.5	776	4	US-09-523-849-34	Sequence 34, Appl
31	562.5	41.9	778	4	US-10-116-326-2	Sequence 2, Appli
32	562.5	41.9	778	4	US-10-003-690-2	Sequence 2, Appli
33	556.5	41.5	668	4	US-09-930-181-2	Sequence 2, Appli
34	523	39.0	1064	4	US-09-538-092-154	Sequence 154, App
35	522	38.9	260	2	US-07-857-224B-28	Sequence 28, Appl
36	515.5	38.4	165	4	US-09-270-767-32886	Sequence 32886, A
37	513	38.2	260	2	US-07-857-224B-27	Sequence 27, Appl
38	507.5	37.8	703	4	US-10-116-326-6	Sequence 6, Appli
39	504.5	37.6	436	4	US-09-734-673-2	Sequence 2, Appli
40	504.5	37.6	436	4	US-09-523-849-2	Sequence 2, Appli
41	502.5	37.4	446	4	US-09-824-735-2	Sequence 2, Appli
42	499	37.2	391	4	US-09-248-796A-18435	Sequence 18435, A
43	498	37.1	915	4	US-09-538-092-63	Sequence 63, Appl
44	493	36.7	360	4	US-09-248-796A-20497	Sequence 20497, A
45	485.5	36.2	603	4	US-09-930-181-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-10-355-975A-38
; Sequence 38, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-355-975A-38

Query Match	100.0%;	Score	1342;	DB	4;	Length	630;
Best Local Similarity	100.0%;	Pred. No.	7.7e-130;				
Matches	253;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	YEFLETGKGTGKVKKARESSGRLVAIKSRDKIKDEQDLLHRRREIEMSSLNPHI	60				
Db	57	YEFLETGKGTGKVKKARESSGRLVAIKSRDKIKDEQDLLHRRREIEMSSLNPHI	116				
Qy	61	IAIHEVFENSKKIVVMEYASRGDLVDYISERPLSRDARHPFRQIVSALHYCHQNGIV	120				
Db	117	IAIHEVFENSKKIVVMEYASRGDLVDYISERPLSRDARHPFRQIVSALHYCHQNGIV	176				
Qy	121	HRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPIVNGKPYVGPEVD	180				
Db	177	HRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPIVNGKPYVGPEVD	236				
Qy	181	SWISGLVLLYTLVHGTPFDGQDHKTLLVKQISNGAYREPPKPSDACGLIRLLMWNPTT	240				
Db	237	SWISGLVLLYTLVHGTPFDGQDHKTLLVKQISNGAYREPPKPSDACGLIRLLMWNPTT	296				
Qy	241	TLEDVASHWVWV 253					
Db	297	TLEDVASHWVWV 309					

RESULT 2
US-09-579-664B-11
; Sequence 11, Application US/09579664B

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; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-579-664B-11

Query Match 100.0%; Score 1342; DB 4; Length 631;
Best Local Similarity 100.0%; Pred. No. 7.7e-130;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFLETGKGTGKTKKARESSGRLVAIKSRKDKIKDEQDLLHIREIEMSSLNHPHI 60
DB 57 YFLETGKGTGKTKKARESSGRLVAIKSRKDKIKDEQDLLHIREIEMSSLNHPHI 116

QY 61 IAIHEVPENSSKIVVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 120
DB 117 IAIHEVPENSSKIVVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 176

QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIIVNGKPYVGPEVD 180
DB 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIIVNGKPYVGPEVD 236

QY 181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRLLMWNPTERRA 240
DB 237 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRLLMWNPTERRA 296

QY 241 TLEDVASHWVWVW 253
DB 297 TLEDVASHWVWVW 309

RESULT 3
US-10-355-975A-11
; Sequence 11, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-355-975A-11

Query Match 100.0%; Score 1342; DB 4; Length 631;
Best Local Similarity 100.0%; Pred. No. 7.7e-130;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFLETGKGTGKTKKARESSGRLVAIKSRKDKIKDEQDLLHIREIEMSSLNHPHI 60
DB 57 YFLETGKGTGKTKKARESSGRLVAIKSRKDKIKDEQDLLHIREIEMSSLNHPHI 116

QY 61 IAIHEVPENSSKIVVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 120
DB 117 IAIHEVPENSSKIVVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 176

QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIIVNGKPYVGPEVD 180
DB 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIIVNGKPYVGPEVD 236

QY 181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRLLMWNPTERRA 240
DB 237 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRLLMWNPTERRA 296

QY 241 TLEDVASHWVWVW 253
DB 297 TLEDVASHWVWVW 309

RESULT 4
US-08-677-298-2
; Sequence 2, Application US/08677298
; Patent No. 5863729
; GENERAL INFORMATION:
; APPLICANT: Pivnica-Worms, Helen
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAP-1
; TITLE OF INVENTION: KINASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/677,298
; FILING DATE: 09-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 9-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-677-298-2

Query Match 48.4%; Score 649.5; DB 2; Length 729;
Best Local Similarity 51.6%; Pred. No. 3.2e-58;
Matches 131; Conservative 42; Mismatches 78; Indels 3; Gaps 3;

QY 1 YFLETGKGTGKTKKARESSGRLVAIKSRKDKIKDEQDLLHIREIEMSSLNHPHI 59
DB 56 YRLTKITGKGNFAKRLARHILTGREVAIKIDKTL-NPTSLQKLFREVRIMKILNHPN 114

QY 60 IAIHEVPENSSKIVVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGI 119
DB 115 IVKLFEVETETKLYLIMEYASGGEVFDYVAHGRMKREARSKFRQIVSAVQYCHOKRI 174

QY 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIIVNGKPYVGPEV 179
DB 175 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIIVNGKPYVGPEV 234
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QY 239 RATLEDVASHWVN 252
Db 292 RGTLEQIMKDRWN 305

RESULT 8
US-09-523-849-36
; Sequence 36, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scacchi, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: GenBank Accession No. 6458561 gi749794
US-09-523-849-36

Query Match 48.2%; Score 647.5; DB 4; Length 745;
Best Local Similarity 51.2%; Pred. No. 5.3e-58;
Matches 130; Conservative 44; Mismatches 77; Indels 3; Gaps 3;

QY 1 YEFLETGKGTGKVKKARE-SSGRVVAIKSIRKDKIKDEQDLLHRRREIEIMSSLNHPH 59
Db 20 YRLKTTIGKGNFAKVLARHILTGREVAIKIDTQL-NSSSLQKLFREVRIMKVLNHPN 78
QY 60 IIAIHEVFENSISKIVIMEYASRGDLYDISERPRLSERDARHFFRQIVSALHYCHQNGI 119
Db 79 IVKLFVEVETKTLYLIMEYASGGEVDYLVAHGRMKEARAKFRQIVSAVQYCHQKFI 138
QY 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYGPEV 179
Db 139 VHRDLKAENLLLDADNMNIKIADFGSNEFTFGNKLDTFCGSPPYAAPFLFQGGKYDGPEV 198
QY 180 DWSLGLVLLYLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 238
Db 199 DVMSLGVILYTLVSGSLPFDGQNLKELRERVLRGKIRIPFYMSTDCENLLKFLILNPSK 258
QY 239 RATLEDVASHWVN 252
Db 259 RGTLEQIMKDRWN 272

RESULT 9
US-09-538-092-1022
; Sequence 1022, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1022
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022

Query Match 48.2%; Score 646.5; DB 4; Length 713;
Best Local Similarity 51.6%; Pred. No. 6.3e-58;
Matches 131; Conservative 41; Mismatches 79; Indels 3; Gaps 3;

QY 1 YEFLETGKGTGKVKKARE-SSGRVVAIKSIRKDKIKDEQDLLHRRREIEIMSSLNHPH 59
Db 56 YRLKTTIGKGNFAKVLARHILTGREVAIKIDTQL-NFTSLQKLFREVRIMKVLNHPN 114
QY 60 IIAIHEVFENSISKIVIMEYASRGDLYDISERPRLSERDARHFFRQIVSALHYCHQNGI 119
Db 115 IVKLFVEVETKTLYLIMEYASGGEVDYLVAHGRMKEARAKFRQIVSAVQYCHQKFI 174
QY 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYGPEV 179
Db 175 VHRDLKAENLLLDADNMNIKIADFGSNEFTFGNKLDTFCGSPPYAAPFLFQGGKYDGPEV 234
QY 180 DWSLGLVLLYLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 238
Db 235 DVMSLGVILYTLVSGSLPFDGQNLKELRERVLRGKIRIPFYMSTDCENLLKFLILNPIK 294
QY 239 RATLEDVASHWVN 252
Db 295 RGTLEQIMKDRWN 308

RESULT 10
US-09-984-890-2
; Sequence 2, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-890-2

Query Match 48.2%; Score 646.5; DB 4; Length 724;
Best Local Similarity 50.8%; Pred. No. 6.4e-58;
Matches 129; Conservative 45; Mismatches 77; Indels 3; Gaps 3;

QY 1 YEFLETGKGTGKVKKARE-SSGRVVAIKSIRKDKIKDEQDLLHRRREIEIMSSLNHPH 59
Db 53 YRLKTTIGKGNFAKVLARHILTGREVAIKIDTQL-NSSSLQKLFREVRIMKVLNHPN 111
QY 60 IIAIHEVFENSISKIVIMEYASRGDLYDISERPRLSERDARHFFRQIVSALHYCHQNGI 119
Db 112 IVKLFVEVETKTLYLIMEYASGGEVDYLVAHGRMKEARAKFRQIVSAVQYCHQKFI 171
QY 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYGPEV 179
Db 172 VHRDLKAENLLLDADNMNIKIADFGSNEFTFGNKLDTFCGSPPYAAPFLFQGGKYDGPEV 231
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Qy 180 DWSLSGLVLLVILVHCTWPFPGQDHKTLVKQISNCAIYREPPKPSDAC-GLIRWLLMNNPTR 238
Db 232 DVMSLGIYLYTSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSK 291
Qy 239 RATLEDVASHWVN 252
Db 292 RGTLEQIMKDRWN 305

RESULT 11
US-10-274-194-2
; Sequence 2, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-194-2

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Query Match.          48.0%; Score 644; DB 4; Length 512;
Best local similarity 50.8%; Pred. No. 7.1e-58;
Matches 128; Conservative 47; Mismatches 75; Indels 2; Gaps 2;

Qy      1 YEFLETGKTYGKVKKARE-SSGRLLVAIKSRKDKQBDLLHRRRETEIMSSLNHPH 59
      Db      20 YLKGKTLTGTSFGKVKIAEHVVTGCHKVAIKLNRRKIKWMEKEKVRREIKILRFLWHPH 79
Qy      60 IIAIHEVFENSSKIVIMVEYASRGDLYDYIISERPRLSERDARHFFRQIVSALHYCHONGI 119
      Db      80 IIRQYEVIEETSDIYVMVEYKSGELFDYIVEKGRLQEOEARNFQOIISGVEYCHRMV 139
Qy      120 VHRDLKLENTLLDANGNIKTIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPEV 179
      Db      140 VHRDLKPEINLLDLSNCNIIKIDFGLSNVRMDGHFLKTCGSPNAAPEVISGKLYAGPEV 199
Qy      180 DWSLGLVLLYILVHGTMFPDQDQHKTLVQISNGAYREPPK-PDSACGLIRWLLMVNPTR 238
      Db      200 DVWSCGVILYALLCGTLPPFDENIPNLFKIKGGIYTLPSHLSSEARDLIPRLMIVDPVK 259
Qy      239 RATLEDVASHHW 250
      Db      260 RITPEIRQHRW 271

RESULT 13
US-08-817-832B-32
; Sequence 32, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-832B-32

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US-09-633-328B-2

Db 112 IVKLFVETETKTLVMEYASGEVFDYLVAGHMKKEARAKFRQIVSAVQCHHKFI 171
Qy 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYVGPEV 179
Db 172 VHRDLKAENLLDDAMNIKIADFGSNEFTFGNKLDITFCGSPFYAAPFQGGKYDGPV 231
Qy 180 DWSLSGLVLLYLVHGTWPFQGDHKTLLVKQISNGAYREPPEKPSDAC-GLIRWLLMVNPT 238
Db 232 DVWSLSGLVLLYLVHGTWPFQGDHKTLLVKQISNGAYREPPEKPSDAC-GLIRWLLMVNPT 238
Qy 239 RATLEDVASHWVN 252
Db 292 RGSLEQIMKORWVN 305

RESULT 14
US-09-523-849-32
; Sequence 32, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scaccheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g2052189
US-09-523-849-32

Query Match 47.9%; Score 642.5; DB 4; Length 793;
Best Local Similarity 51.2%; Pred. No. 1.9e-57;
Matches 130; Conservative 43; Mismatches 78; Indels 3; Gaps 3;
Qy 1 YEFLETGKGTGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 60 YRLQKTIGKGNFAVKLARHVLTCREAVAKIIDKTQL-NPTSLQKLFREVRIMKILNPN 118
Qy 60 IIAIHEVFENSSKIVIMEYASRGDLYISERPRLSERDARHFRQIVSALHYCHONGI 119
Db 119 IVKLFVETETKTLVMEYASGEVFDYLVAGHMKKEARAKFRQIVSAVQCHQKCI 178
Qy 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYVGPEV 179
Db 179 VHRDLKAENLLDDAMNIKIADFGSNEFTFGNKLDITFCGSPFYAAPFQGGKYDGPV 238
Qy 180 DWSLSGLVLLYLVHGTWPFQGDHKTLLVKQISNGAYREPPEKPSDAC-GLIRWLLMVNPT 238
Db 239 DVWSLSGLVLLYLVHGTWPFQGDHKTLLVKQISNGAYREPPEKPSDAC-GLIRWLLMVNPT 238
Qy 239 RATLEDVASHWVN 252
Db 299 RGSLEQIMKORWVN 312

RESULT 15
US-09-633-328B-4
; Sequence 4, Application US/09633328B
; Patent No. 6777587
; GENERAL INFORMATION:

; APPLICANT: BISARO, DAVID A.
; TITLE OF INVENTION: METHOD OF ENHANCING PLANT RESISTANCE TO PATHOGENS
; FILE REFERENCE: 22727-04041
; CURRENT APPLICATION NUMBER: US/09/633,328B
; CURRENT FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/147,613
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 4
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Nicotiana benthamiana
US-09-633-328B-4

Query Match 47.0%; Score 631; DB 4; Length 511;
Best Local Similarity 49.6%; Pred. No. 1.6e-56;
Matches 125; Conservative 48; Mismatches 77; Indels 2; Gaps 2;
Qy 1 YEFLETGKGTGKVKKARES-SGRLVAIKSIRKDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 19 YKLGKTLIGSGFGKVKIAEHTLTGHKVAVKILNRRKIKNMEMEEKVRREIKILFLFVHPH 78
Qy 60 IIAIHEVFENSSKIVIMEYASRGDLYISERPRLSERDARHFRQIVSALHYCHONGI 119
Db 79 IIRLYEVVETPSDIYVMEYVYKSGELFDYIVVEKGRLOEDEARKEFQIISGVEYCHRNWV 138
Qy 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYVGPEV 179
Db 139 VHRDLKPENLLDSKNVXIADFGLSNIMRDGHFLKTCGSPNYAAPEVTSGLYAGPEV 198
Qy 180 DWSLSGLVLLYLVHGTWPFQGDHKTLLVKQISNGAYREPPEKPS-DACGLIRWLLMVNPT 238
Db 199 DVWSGCVILYALLCGLTLPFDENIPNLFKKIKGIMSLPSHLGAGARDLIPRMLIVDPMK 258
Qy 239 RATLEDVASHWV 250
Db 259 RMTIPEIRMHWP 270

Search completed: January 22, 2005, 06:44:55
Job time : 17.3133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:22:58 ; Search time 63.8224 Seconds
(without alignments)
1422.048 Million cell updates/sec

Title: US-09-980-464-11_COPY_57_309

Perfect score: 1342

Sequence: 1 YEFLETLGKGYGVKKARE.....VNPTTRATLEDVASHWVNVN 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1342	100.0	631	4 AAB50056	Aab50056 Murine Ly
2	1313	97.8	630	5 AAE19885	Aae19885 Rat SNF1/
3	1293	96.3	628	4 AAM93360	Aam93360 Human pol
4	1293	96.3	628	4 ABU53319	Abu53319 Human cel
5	1293	96.3	628	5 ABP69116	Abp69116 Human pol
6	1293	96.3	628	5 AAU79652	Aau79652 Human pro
7	1293	96.3	628	7 ADF76965	Adf76965 Novel hum
8	1293	96.3	628	8 ADL30886	Adl30886 Human pro
9	1293	96.3	628	8 ADL25362	Adl25362 Human SNA
10	1293	96.3	628	8 ADL14161	Adl14161 Novel hum
11	1293	96.3	628	8 ADL20172	Ado20172 Human PRO
12	1293	96.3	672	8 ADJ96620	Adj96620 Human cal
13	1286	95.8	594	5 AAE16266	Aae16266 Human kin
14	1279.5	95.3	611	6 ABP96085	Abp96085 Human pro
15	1268.5	94.5	629	4 AAB65632	Aab65632 Novel pro
16	1268.5	94.5	629	8 ADL29239	Adl29239 Human MAR
17	1128.5	84.1	660	7 ADN95766	Adn95766 Human BEC
18	1128.5	84.1	661	4 AAE07847	Aae07847 Human pro
19	1128.5	84.1	661	4 AAE07846	Aae07846 Human pro
20	1128.5	84.1	661	7 ADE38421	Ade38421 Human pro
21	1128.5	84.1	661	8 ADJ75331	Adj75331 Marker ge
22	1128.5	84.1	661	8 ADL25353	Adl25353 Human ARK
23	1128.5	84.1	661	8 ADQ19734	Adq19734 Human sof
24	1085	80.8	534	4 AAB71959	Aab71959 Human TGF
25	822.5	61.3	434	4 ABB67451	Abb67451 Drosophil

ALIGNMENTS

RESULT 1
AAB50056
ID AAB50056 standard; protein; 631 AA.

XX AAB50056;

DT 19-MAR-2001 (first entry)

DE Murine Lymph node Stromal cell kinase 1.

XX Murine; Lymph node Stromal cell kinase; MLCK-1; autoimmune disorder;

KW wound healing; periodontal disease; inflammatory disease; tumour;

KW infection; allergy.

OS Mus musculus.

XX WO200073468-A1.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-USO14696.

XX PR 28-MAY-1999; 99US-0136781P.

XX (IMMV) IMMUNEX CORP.

PI Bird TA, Virca GD, Martin U, Anderson DM;

DR WPI; 2001-061546/07.

XX N-PSDB; AAC90433.

PT Novel murine and human kinase nucleic acids useful for treating
inflammations, infections, tumors, allergies, autoimmune diseases, and
for stimulating or suppressing immune responses.

XX Claim 10; Page 94-96; 106pp; English.

CC The present sequence is Murine Lymph node Stromal cell kinase 1 (MLSK-1).
This protein is useful for treating a variety of disorders listed in the
disclosure of the specification, including autoimmune disorders, allergic
reactions, myeloid or lymphoid cell deficiencies, wound healing and
tissue repair and replacement, burns, incisions and ulcers, periodontal
disease, inflammatory diseases, tumours and bacterial, viral or fungal
infection

SQ Sequence 631 AA;

Query Match 100.0%; Score 1342; DB 4; Length 631;

Best Local Similarity 100.0%; Pred. No. 2.6e-138; Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEFLETGKGYGVKVAKRESSGRLVAIKSRKDKIKDEQDLHRRREIEMSLNHPHI 60
Db 57 YEFLETGKGYGVKVAKRESSGRLVAIKSRKDKIKDEQDLHRRREIEMSLNHPHI 116

Qy 61 IAIHEVFENSKKIVMEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHQNGIV 120
Db 117 IAIHEVFENSKKIVMEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHQNGIV 176

Qy 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLASPEIVNGKPYVGVPEVD 180
Db 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLASPEIVNGKPYVGVPEVD 236

Qy 181 SWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRRA 240
Db 237 SWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRRA 296

Qy 241 TLEDVASHWVNW 253
Db 297 TLEDVASHWVNW 309

RESULT 2
AAE19885
ID AAE19885 standard; protein; 630 AA.
XX AAE19885;
AC AAE19885;
XX AAE19885;
DT 18-JUN-2002 (first entry)
XX Rat SNF1/AMPK-Related Kinase (SNARK) protein.
XX Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes;
KW glucose deprivation; lipid metabolism; therapy; lipoprotein disorder;
KW hyperglycaemic; drug screening; hypoglycaemia.
XX Rattus sp.
XX

Key Location/Qualifiers
FT Binding-site 63..89
FT Domain 137..140
FT /note= "Protein kinase ATP-binding region signature"
FT /note= "Serine/threonine kinase catalytic domain"
FT Active-site 175..187
FT /note= "Serine/threonine protein kinase active-site"
FT Domain 297..300
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 335..338
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 381..384
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 422..425
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 468..471
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 517..520
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 601..604
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 608..611
FT /note= "Serine/threonine kinase catalytic domain"
XX WO200212456-A2.
XX 14-FEB-2002.
XX 02-AUG-2001; 2001WO-CA001109.
XX 03-AUG-2000; 2000US-0222650P.
PR 12-MAR-2001; 2001US-0274613P.
PR 28-MAR-2001; 2001CA-02340783.

XX PA (ONEO-) 1149336 ONTARIO INC.
XX Drucker DJ, Rosen CF, Lefebvre DL;
XX WPI; 2002-241747/29.
XX N-PSDB; AAD31710.
XX AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polynucleotides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.
XX Claim 1; Fig 2; 94pp; English.
XX The invention relates to an AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polynucleotides. SNARK (SNIF/AMP-activated protein kinase) is involved in stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK stimulates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted to have insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipoprotein production leading to increased levels of cholesterol or triglycerides. SNARK or its variants may be administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as diabetes. SNARK antibodies are used to modulate SNARK activity either in vivo for therapeutic purposes, or in vitro for drug screening and related investigational purposes. SNARK antagonists may be administered to increase fuel production, decrease glucose uptake and increase levels of blood glucose in a patient suffering from hypoglycaemia. The present sequence is rat SNARK protein Sequence 630 AA;
SQ

Query Match 97.8%; Score 1313; DB 5; Length 630;
Best Local Similarity 98.0%; Pred. No. 4.1e-135;
Matches 248; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEFLETGKGYGVKVAKRESSGRLVAIKSRKDKIKDEQDLHRRREIEMSLNHPHI 60
Db 57 YEFLETGKGYGVKVAKRESSGRLVAIKSRKDKIKDEQDLHRRREIEMSLNHPHI 116

Qy 61 IAIHEVFENSKKIVMEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHQNGIV 120
Db 117 IAIHEVFENSKKIVMEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHQNGIV 176

Qy 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLASPEIVNGKPYVGVPEVD 180
Db 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLASPEIVNGKPYVGVPEVD 236

Qy 181 SWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRRA 240
Db 237 SWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRRA 296

Qy 241 TLEDVASHWVNW 253
Db 297 TLEDVASHWVNW 309

RESULT 3
AAW93360
ID AAW93360 standard; protein; 628 AA.
XX AC AAW93360;
XX AAW93360;
DT 06-NOV-2001 (first entry)
XX Human polypeptide, SEQ ID NO: 2919.
DE Human; full length cDNA; cDNA synthesis; oligo-capping.
XX KW

```
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 95JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183785.
XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX DR N-PSDB; AAK94280.
XX PS 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX PS Claim 8; SEQ ID NO 2919; 1380pp + Sequence Listing; English.
XX CC The invention relates to primers for synthesizing full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX CC been determined. Primers for synthesizing the full length cDNA are useful
XX CC for clarifying the function of the protein encoded by the cDNA. The full
XX CC length clones were obtained by construction of full length enriched cDNA
XX CC libraries that were synthesised by the oligo-capping method. The primers
XX CC enable the production of the full length cDNA easily without any special
XX CC methods. The present sequence is a polypeptide encoded by a full length
XX CC human cDNA of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in CD-ROM
XX CC format directly from EPO
XX SQ Sequence 628 AA;

Query Match 96.3%; Score 1293; DB 4; Length 628;
Best Local Similarity 95.7%; Pred. No. 6.5e-133;
Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YEFLETGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIETMSSLNHPHI 60
Db 53 YEFLETGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIETMSSLNHPHI 112

Qy 61 IAIHEVFENS KIVIVMEYASRGDLVDYISERPRLSERDARHFRQIVSALHYCHONGIV 120
Db 113 IAIHEVFENS KIVIVMEYASRGDLVDYISERQQLSEREARHFRQIVSAVHYCHQNRVV 172

Qy 121 HRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
Db 173 HRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232

Qy 181 SWSGLGVLLYILVHGTMPPFDGQDHKTLVKQISNGAYREP PKPSDACGLIRLWLLMVPTRRA 240
Db 233 SWSGLGVLLYILVHGTMPPFDGHDHKLTVKQISNGAYREP PKPSDACGLIRLWLLMVPTRRA 292

Qy 241 TLEDVASHHWVNW 253
Db 293 TLEDVASHHWVNW 305

RESULT 4
ABU53319
ID ABU53319 standard; protein; 628 AA.
XX AC ABU53319;
XX DT 14-APR-2003 (first entry)
```

```
XX DE Human cell cycle-associated protein from DKFZphtes3_7f3.
XX KW Human; gene therapy; vaccine; disease treatment; detection.
XX OS Homo sapiens.
XX PN WO200112659-A2.
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-IB001496.
XX PR 18-AUG-1999; 99US-0149499P.
XX PR 28-SEP-1999; 99US-0156503P.
XX PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX PI Wiemann S;
XX PI WIPI; 2001-327840/34.
XX DR N-PSDB; ABX71420.
XX PS Nucleic acids having the sequences of clones isolated from libraries of
XX PT different human tissues, useful in recombinant DNA methodologies.
XX PS Claim 21; Page 943; 1095pp; English.
XX CC This invention describes novel polynucleotides and polypeptides isolated
XX CC from human cDNA libraries which can be used for gene therapy or in
XX CC vaccines. The polynucleotides of the invention and antibodies encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate polypeptide expression. The products of the
XX CC invention may also be used to identify modulators of expression and
XX CC activity and to down regulate expression and activity. The antibodies of
XX CC the invention may also be used as diagnostic agents for detecting the
XX CC presence of polypeptides in samples. This sequence represents a
XX CC polypeptide described in the disclosure of the invention
XX SQ Sequence 628 AA;

Query Match 96.3%; Score 1293; DB 4; Length 628;
Best Local Similarity 95.7%; Pred. No. 6.5e-133;
Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YEFLETGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIETMSSLNHPHI 60
Db 53 YEFLETGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIETMSSLNHPHI 112

Qy 61 IAIHEVFENS KIVIVMEYASRGDLVDYISERPRLSERDARHFRQIVSALHYCHONGIV 120
Db 113 IAIHEVFENS KIVIVMEYASRGDLVDYISERQQLSEREARHFRQIVSAVHYCHQNRVV 172

Qy 121 HRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
Db 173 HRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232

Qy 181 SWSGLGVLLYILVHGTMPPFDGQDHKTLVKQISNGAYREP PKPSDACGLIRLWLLMVPTRRA 240
Db 233 SWSGLGVLLYILVHGTMPPFDGHDHKLTVKQISNGAYREP PKPSDACGLIRLWLLMVPTRRA 292

Qy 241 TLEDVASHHWVNW 253
Db 293 TLEDVASHHWVNW 305

RESULT 5
ABP69116
ID ABP69116 standard; protein; 628 AA.
XX AC ABP69116;
XX DT 20-JAN-2003 (first entry)
```

XX DE Human polypeptide SEQ ID NO 1163.

XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;

XX KW cell-proliferative disorder; neurodegenerative disease; bacterial;

XX KW Parkinson's disease; Alzheimer's disease; autoimmune disease;

XX KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;

XX KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;

XX KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

XX KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;

XX KW antiarthritic.

XX OS Homo sapiens.

XX PN WO200270539-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US005095.

XX PR 05-MAR-2001; 2001US-00799451.

XX FA (HYSE-) HVSEQ INC.

XX PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;

XX PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

XX PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX DR WPI; 2002-759812/82.

XX DR N-PSDB; ABZ11333.

XX PT New polynucleotides comprising sequences assembled from expressed

XX PT sequence tags (ESTs), useful for treating cell-proliferative,

XX PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet

XX PT or coagulation disorders.

XX PS Claim 9; SEQ ID NO 1163; 1012pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (I) comprising a

XX CC nucleotide sequence selected from any of 948 sequences (ABZ11119-

XX CC ABZ12066) or their mature protein coding portion, active domain coding

XX CC protein or complementary sequences. The polynucleotides are useful for

XX CC identifying expressed genes or for physical mapping of human genome. The

XX CC encoded polypeptides (ABP68902-ABP6949) are useful as molecular weight

XX CC markers, as a food supplement, for generating antibodies, in medical

XX CC imaging, screening and diagnostic assays and for treating cell-

XX CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's

XX CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,

XX CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,

XX CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver

XX CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),

XX CC arthritis, etc. Note: The sequence data for this patent did not form part

XX CC of the printed specification, but was obtained in electronic format

XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 628 AA;

Query Match 96.3%; Score 1293; DB 5; Length 628;

Best Local Similarity 95.7%; Pred. No. 6.5e-133;

Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEFLETGKGYGVKVKARESSGRVAKSRKDKIKDEQDLHIREIETMSLNPHI 60

DB 53 YEFLETGKGYGVKVKARESSGRVAKSRKDKIKDEQDLHIREIETMSLNPHI 112

QY 61 IAIHEVFENSKTIVVMEYASRGDLVYISRRPLSRDARHFRQIVSAHYCHQNGIV 120

DB 113 IAIHEVFENSKTIVVMEYASRGDLVYISRRQQLSREARHFRQIVSAHYCHQNRV 172

QY 121 HRDLKLENILLDANGNKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYVGPEVD 180

DB 173 HRDLKLENILLDANGNKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYVGPEVD 232

QY 181 SWSLGVLLYILVHCTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRR 240

DB 233 SWSLGVLLYILVHCTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRR 292

QY 241 TLEDVASHWVWVW 253

DB 293 TLEDVASHWVWVW 305

RESULT 6

AAU79652

ID AAU79652 standard; protein; 628 AA.

XX AC AAU79652;

XX DT 02-JUL-2002 (first entry)

XX DE Human protein kinase 3700.

XX KW Human; protein kinase 3700; PK; protein phosphorylation; tumorigenesis;

XX KW cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma;

XX KW tissue repair; tissue regeneration; atherosclerosis; blood-brain barrier;

XX KW cell proliferation disorder; cell differentiation disorder; carcinoma;

XX KW haematopoietic neoplastic disorder; metastatic disorder; leukaemia;

XX KW cytostatic; antiatherosclerotic; enzyme.

XX OS Homo sapiens.

XX PN WO200224921-A2.

XX PD 28-MAR-2002.

XX PF 25-SEP-2001; 2001WO-US030115.

XX PR 25-SEP-2000; 2000US-0234922P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Curtis RAJ, Galvin KM;

XX WPI; 2002-352007/38.

XX N-PSDB; ABK14000.

XX PT Use of modulators of activity of 3700 protein for making medicament for

XX PT e.g., modulating protein phosphorylation or cell signaling, or for

XX PT treating or preventing cellular proliferative and/or differentiative

XX PT disorders.

XX PS Claim 19; Fig 1; 115pp; English.

XX CC The present invention relates to the isolation of a novel human protein

XX CC kinase designated 3700, and the polynucleotide sequence encoding it. The

XX CC invention also describes the use of a modulator of the activity of

XX CC protein kinase (PK) 3700 for making a medicament or pharmaceutical

XX CC composition for modulating the ability of a cell to phosphorylate an

XX CC amino acid residue of a substrate protein. Modulators of protein kinase

XX CC 3700 activity are useful for modulating protein phosphorylation, cell

XX CC signalling, tumorigenesis, mitogenesis, transcription of a gene,

XX CC angiogenesis, tissue repair, tissue regeneration, establishment or

XX CC progression of atherosclerosis, and signalling across the blood-brain

XX CC barrier. The polynucleotide and polypeptide molecules for protein kinase

XX CC 3700 may be used as diagnostic targets and therapeutic agents for

XX CC prognosticating, diagnosing, preventing, inhibiting, alleviating, or

XX CC curing PK-related disorders and cellular proliferative and/or

XX CC differentiative disorders (e.g. haematopoietic neoplastic disorders,

XX CC carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700

XX CC polynucleotide sequence can be used to express protein kinase 3700, to

XX CC detect a genetic alteration in a 3700 gene, in chromosome mapping, for

XX CC tissue typing, in forensic biology, and as surrogate markers. The present

XX CC sequence represents human protein kinase 3700

XX SQ Sequence 628 AA;

Query Match		96.3%; Score 1293; DB 5; Length 628;
Best Local Similarity		95.7%; Pred. No. 6.5e-133;
Matches 242; Conservative		6; Mismatches 5; Indels 0; Gaps 0;
QY	1 YEFLETGKGYGKVKKARESSGRLVAIKSRDKIKDEQDLHRRREIETMSSLNHPHI	60
DB	53 YEFLETGKGYGKVKKARESSGRLVAIKSRDKIKDEQDLHRRREIETMSSLNHPHI	112
QY	61 IAIHEVFENSKIVIVMEYASRGDLVDYISERPRLSERDARHFRQIVSALHYCHQNGIV	120
DB	113 IAIHEVFENSKIVIVMEYASRGDLVDYISERQQLSEREARHFRQIVSAVHYCHQNRVV	172
QY	121 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQTCGSPLYASPEIVNGKPYVGPEVD	180
DB	173 HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTCGSPLYASPEIVNGKPYTGPEVD	232
QY	181 SWSLGVLVLYLVHGTMPDFGDHKTLYKQISNGAYRBPBPKPSDACGLIRWLLMVPTRRA	240
DB	233 SWSLGVLVLYLVHGTMPDFGDHKLILVKQISNGAYRBPBPKPSDACGLIRWLLMVPTRRA	292
QY	241 TLEDVASHWVWVNW	253
DB	293 TLEDVASHWVWVNW	305
RESULT 7		
ADF76965		
ID	ADF76965 standard; protein; 628 AA.	
XX		
AC	ADF76965;	
XX		
XX	26-FEB-2004 (first entry)	
XX		
XX	Novel human secreted and transmembrane protein SeqID 640.	
XX	human; PRO; membrane bound protein; membrane bound receptor;	
KW	cell proliferation; cell migration; cell differentiation;	
KW	mitogenic factor; survival factor; cytotoxic factor;	
KW	differentiation factor; neuroepithel; hormone; cell receptor;	
KW	receptor-ligand interaction; cytostatic; chondrocyte; tumour.	
XX		
OS	Homo sapiens.	
XX		
XX	WO2003072035-A2.	
XX		
XX	04-SEP-2003.	
XX		
XX	21-FEB-2003; 2003WO-US005241.	
XX		
XX	22-FEB-2002; 2002US-0359461P.	
XX		
XX	(GETH) GENENTECH INC.	
XX	Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;	
PI	Williams PM, Wood WI, Wu TD;	
XX		
XX	WPI; 2003-721702/68.	
XX	N-PSDB; ADF76964.	
XX		
XX	New PRO polypeptides, useful for diagnosing and treating an immune	
PT	related disorder, e.g. systemic lupus erythematosus, rheumatoid	
PT	arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or	
PT	diabetes mellitus.	
XX		
XX	Claim 10; SEQ ID NO 640; 918pp; English.	
XX		
XX	This invention relates to novel nucleic acids encoding human PRO secreted	
CC	and transmembrane proteins. Extracellular proteins play important roles	
CC	in the formation, differentiation and maintenance of multicellular	
CC	organisms. The fate of many individual cells (for example proliferation,	
CC	migration or differentiation) is typically governed by information	
CC	received from other cells and the immediate environment. The information	
CC	is often transmitted by secreted polypeptides (for example mitogenic	
factors, survival factors, cytotoxic factors, differentiation factors,		
neuropeptides and hormones) which are received and interpreted by diverse		
cell receptors or membrane bound proteins. These membrane bound proteins		
and receptors may be of use as pharmaceutical and diagnostic agents, such		
as in the blocking of receptor-ligand interactions. The current invention		
provides the amino acid sequences of novel human membrane bound receptors		
and proteins, along with the cDNA sequences encoding them. The novel		
proteins of the invention may have cytostatic activities through the		
stimulation of chondrocytes. The nucleic acids of the invention may be		
useful for the manufacture of a medicament for diagnosing or treating a		
tumour in a mammal. In addition, they may be useful for measuring or		
detecting the expression of a tumour associated gene. The present		
sequence is the amino acid sequence of a human PRO protein of the		
invention.		
XX		
SQ	Sequence 628 AA;	
Query Match		
Best Local Similarity		
Matches 242; Conservative		
6; Mismatches 5; Indels 0; Gaps 0;		
QY	1 YEFLETGKGYGKVKKARESSGRLVAIKSRDKIKDEQDLHRRREIETMSSLNHPHI	60
DB	53 YEFLETGKGYGKVKKARESSGRLVAIKSRDKIKDEQDLHRRREIETMSSLNHPHI	112
QY	61 IAIHEVFENSKIVIVMEYASRGDLVDYISERPRLSERDARHFRQIVSALHYCHQNGIV	120
DB	113 IAIHEVFENSKIVIVMEYASRGDLVDYISERQQLSEREARHFRQIVSAVHYCHQNRVV	172
QY	121 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQTCGSPLYASPEIVNGKPYVGPEVD	180
DB	173 HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTCGSPLYASPEIVNGKPYTGPEVD	232
QY	181 SWSLGVLVLYLVHGTMPDFGDHKTLYKQISNGAYRBPBPKPSDACGLIRWLLMVPTRRA	240
DB	233 SWSLGVLVLYLVHGTMPDFGDHKLILVKQISNGAYRBPBPKPSDACGLIRWLLMVPTRRA	292
QY	241 TLEDVASHWVWVNW	253
DB	293 TLEDVASHWVWVNW	305
RESULT 8		
ADL30886		
ID	ADL30886 standard; protein; 628 AA.	
XX		
AC	ADL30886;	
XX		
XX	20-MAY-2004 (first entry)	
XX		
XX	Human protein encoded by a full length cDNA clone SeqID 2919.	
XX	human; medicine; signal transduction; glycoprotein; transcription;	
KW	oligo-capping method.	
XX		
OS	Homo sapiens.	
XX		
XX	EP1396543-A2.	
XX		
XX	10-MAR-2004.	
XX		
XX	07-JUL-2000; 2003EP-00025638.	
XX		
XX	08-JUL-1999; 99JP-00194486.	
PR	11-JAN-2000; 2000JP-00118774.	
PR	02-MAY-2000; 2000JP-00183865.	
PR	07-JUL-2000; 2000EP-00114089.	
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.	
XX		
XX	Ota T, Nishikawa T, Isogai T, Hayaishi K, Ishii S, Kawai Y;	
PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;	
XX		

DR WPI; 2004-204755/20.
 DR N-PSDB; ADL30885.
 XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
 PT length human cDNAs.
 XX Example 1; SEQ ID NO 2919; 1340pp; English.
 PS This invention relates to a novel primers useful for synthesizing full
 CC length cDNA molecules that encode human proteins. Specifically, it refers
 CC to secretory or membrane proteins that are potential therapeutic agents/
 CC target molecules in the field of medicine, and in particular genes
 CC encoding proteins that are associated with signal transduction,
 CC glycoproteins and transcription. The present invention describes a method
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'
 CC ends using the oligo-capping method. This polypeptide sequence is a full
 CC length human protein of the invention.
 XX
 SQ Sequence 628 AA;

Query Match 96.3%; Score 1293; DB 8; Length 628;
 Best Local Similarity 95.7%; Pred. No. 6.5e-133;
 Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEFLETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPHI 60
 DB 53 YEFLETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPHI 112
 QY 61 IAIHEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFRQIVSAHYCHONGIV 120
 DB 113 IAIHEVFENSSKIVIVMEYASRGDLVDYISERQOLSEREARHFRQIVSAHYCHONRV 172
 QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPVVGPEVD 180
 DB 173 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYTGPEVD 232
 QY 181 SWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAGLIRLLMVNPTERRA 240
 DB 233 SWSLGVLLYLIVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDAGLIRLLMVNPTERRA 292
 QY 241 TLEDVASHWWVNW 253
 DB 293 TLEDVASHWWVNW 305

RESULT 9
 ADL25362
 ID ADL25362 standard; protein; 628 AA.
 XX
 AC ADL25362;
 DT 03-JUN-2004 (first entry)
 XX
 DE Human SNARK, SEQ ID 12.
 XX
 KW Cytostatic; Neuroprotective; Nootropic; Muscular; Gene therapy;
 KW Adenosine Monophosphate activated Protein Kinase-related kinase 5;
 KW AMPK-related kinase 5; ARK5; KIAA0537; stress resistance; tumour;
 KW nervous disorder; muscle disorder; ataxia teleangiectasia; SNARK.
 XX
 OS Homo sapiens.
 XX
 XX WO2004019994-A1.
 XX
 XX 11-MAR-2004.
 XX
 XX 19-AUG-2003; 2003WO-JP010435.
 XX
 XX 27-AUG-2002; 2002JP-00247761.
 XX
 XX (NINA-) JAPAN AGENCY NAT INST HEALTH.
 XX (PHAR-) ORG PHARM SAFETY & RES.
 XX

PI Esumi H, Suzuki A;
 XX
 DR WPI; 2004-248195/23.
 XX
 PT Agent for imparting stress resistance to cells, comprises DNA encoding
 PT for adenosine monophosphate activated protein kinase-related kinase 5 for
 PT treatment of tumors, muscle and nervous disorders, and ataxia
 PT teleangiectasia.
 XX
 XX Example 1; SEQ ID NO 12; 143pp; Japanese.
 PS The present invention relates to human Adenosine Monophosphate activated
 CC Protein Kinase (AMPK)-related kinase 5 (ARK5/ KIAA0537) and its coding
 CC sequence, which are useful for imparting stress resistance to cells. ARK5
 CC is useful for treatment and prevention of tumours, nervous disorders,
 CC muscle disorders and ataxia teleangiectasia. The present sequence was
 CC used to illustrate the invention.
 XX
 SQ Sequence 628 AA;

Query Match 96.3%; Score 1293; DB 8; Length 628;
 Best Local Similarity 95.7%; Pred. No. 6.5e-133;
 Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEFLETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPHI 60
 DB 53 YEFLETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPHI 112
 QY 61 IAIHEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFRQIVSAHYCHONGIV 120
 DB 113 IAIHEVFENSSKIVIVMEYASRGDLVDYISERQOLSEREARHFRQIVSAHYCHONRV 172
 QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPVVGPEVD 180
 DB 173 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYTGPEVD 232
 QY 181 SWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAGLIRLLMVNPTERRA 240
 DB 233 SWSLGVLLYLIVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDAGLIRLLMVNPTERRA 292
 QY 241 TLEDVASHWWVNW 253
 DB 293 TLEDVASHWWVNW 305

RESULT 10
 ADL14161
 ID ADL14161 standard; protein; 628 AA.
 XX
 AC ADL14161;
 DT 17-JUN-2004 (first entry)
 XX
 DE Novel human gene 3700 encoded protein.
 XX
 KW cytotostatic; cardiant; hypotensive; antianginal; osteopathic;
 KW antiarthritic; antirheumatic; neuroprotective; antiinflammatory;
 KW antipsoriatic; antiaesthatic; cardiovascular; virucide; analgesic; CNS;
 KW angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective;
 KW nephrotropic; antithyroid; dermatological; immunomodulator;
 KW cell proliferation disorder; cell differentiation disorder;
 KW kidney disorder; renal disorder; lung disorder; ovarian disorder;
 KW prostate disorder; cervical disorder; spleen disorder; thymus disorder;
 KW thyroid disorder; testes disorder; haematopoietic disorder;
 KW pancreatic disorder; skeletal muscle disorder; skin disorder;
 KW dermal disorder; bone metabolism disorder; immune disorder;
 KW inflammatory disorder; cardiovascular disorder;
 KW endothelial cell disorder; liver disorder; erythroid disorder;
 KW metabolic disorder; neurological disorder;
 KW central nervous system disorder; angioecnic disorder; cancer; heart failure;
 KW blood vessel disorder; angioecnic disorder; cancer; heart failure;
 KW hypertension; angina; osteoarthritis; rheumatoid arthritis;

KW multiple sclerosis; Crohn's disease; psoriasis; asthma;
 KW cell proliferation; cell differentiation; cell growth; cell division;
 KW human.
 XX Homo sapiens.
 XX US2004058355-A1.
 XX 25-MAR-2004.
 XX 25-APR-2003; 2003US-004233543.
 XX 30-SEP-1998; 98US-00163821.
 XX 27-JAN-1999; 99US-0117580P.
 XX 25-MAR-1999; 99US-00276400.
 XX 30-JUL-1999; 99US-00365162.
 XX 09-SEP-1999; 99US-00392189.
 XX 05-OCT-1999; 99US-00412210.
 XX 23-NOV-1999; 99US-00448076.
 XX 29-FEB-2000; 2000US-0186061P.
 XX 28-APR-2000; 2000US-0200688P.
 XX 19-MAY-2000; 2000US-0205447P.
 XX 30-JUN-2000; 2000US-00608921.
 XX 31-JUL-2000; 2000US-0221925P.
 XX 25-SEP-2000; 2000US-0234922P.
 XX 25-SEP-2000; 2000US-0235035P.
 XX 08-NOV-2000; 2000US-0246669P.
 XX 09-NOV-2000; 2000US-00711216.
 XX 14-NOV-2000; 2000US-0248325P.
 XX 15-NOV-2000; 2000US-0248893P.
 XX 22-DEC-2000; 2000US-0257511P.
 XX 05-JAN-2001; 2001US-0260166P.
 XX 28-FEB-2001; 2001US-00797039.
 XX 27-APR-2001; 2001US-00845044.
 XX 20-JUL-2001; 2001US-00909743.
 XX 31-JUL-2001; 2001US-00920346.
 XX 13-AUG-2001; 2001US-00928531.
 XX 14-AUG-2001; 2001US-00929218.
 XX 15-AUG-2001; 2001US-0312539P.
 XX 25-SEP-2001; 2001US-00963159.
 XX 08-NOV-2001; 2001US-0008016.
 XX 13-NOV-2001; 2001US-00012055.
 XX 15-NOV-2001; 2001US-00003690.
 XX 30-JAN-2002; 2002US-00060763.
 XX 25-MAR-2002; 2002US-00105989.
 XX 12-APR-2002; 2002US-00121911.
 XX 12-AUG-2002; 2002US-00217168.
 XX 22-OCT-2002; 2002US-00278036.
 XX 02-JAN-2003; 2003US-00336489.
 XX 03-JAN-2003; 2003US-00336153.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA;
 PI Curtis RAJ, Olant PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;
 PI Silos-Santiago I, Bandaru R;
 XX MPI: 2004-268788/25.
 XX N-PSDB; ADL14160, ADL14162.
 XX New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,
 PT 26176, 26343, 56638, 18610, 33217, 21967, h1983, 38555 or 593
 PT nucleic acid molecules and proteins, useful for treating, e.g. cancer,
 PT heart failure and angina.
 XX Claim 4; SEQ ID NO 44; 139pp; English.
 XX The invention describes an isolated 21910, 56634, 55053, 2504, 15977,
 CC 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,
 CC 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising
 CC any one of 40 nucleotide sequences (i). The nucleic acid molecules and
 CC polypeptides are useful for diagnosing and treating a subject having a
 CC disorder, or a subject at risk of developing a disorder, which is

CC associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,
 CC 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,
 CC m1983, 38555 or 593 activity, such as cellular proliferative and/or
 CC differentiative disorders, brain disorders, platelet disorders, breast
 CC disorders, colon disorders, kidney (renal) disorders, lung disorders,
 CC ovarian disorders, prostate disorders, cervical disorders, spleen
 CC disorders, thymus disorders, thyroid disorders, testicular disorders,
 CC hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,
 CC skin (dermal) disorders, disorders associated with bone metabolism,
 CC immune, e.g. inflammatory disorders, cardiovascular disorders,
 CC endothelial cell disorders, liver disorders, viral diseases, pain
 CC disorders, metabolic disorders, neurological or central nervous system
 CC disorders, erythroid disorders, blood vessel disorders or angiogenic
 CC disorders (all claimed), e.g. cancer, heart failure, hypertension,
 CC angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's
 CC disease, psoriasis, or asthma. The nucleic acid molecules and
 CC polypeptides are also useful as modulating agents in regulating a variety
 CC of cellular process, e.g. cell proliferation, differentiation, growth and
 CC division. This is the amino acid sequence of a novel human protein of the
 CC invention. Note: The sequences given in the specification are also
 CC available in electronic format from
 CC ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355.
 XX
 XX SQ Sequence 628 AA;
 QY 1 YFLETLGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPHI 60
 DB 53 YFLETLGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPHI 112
 QY 61 IATHEVFENSSKIVVMEYASRGDLVDYISERPLSRDARHFRQTVSAHYCHQNGIV 120
 DB 113 IATHEVFENSSKIVVMEYASRGDLVDYISERQQLSREARHFRQTVSAHYCHQNRV 172
 QY 121 HRDLKLENIILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPVVGPEVD 180
 DB 173 HRDLKLENIILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPVVGPEVD 232
 QY 181 SWSLGVLLYILVHGTWPFQDQDKHTLVKQISNGAYREPPKPSDACGLIRLLMVPTRRA 240
 DB 233 SWSLGVLLYILVHGTWPFQDQDKHTLVKQISNGAYREPPKPSDACGLIRLLMVPTRRA 292
 QY 241 TLEDVASHWVWVNW 253
 DB 293 TLEDVASHWVWVNW 305
 RESULT 11
 ADO20172
 ID ADO20172 standard; protein; 628 AA.
 XX
 AC ADO20172;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #540.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX Homo sapiens.
 XX
 OS WO2004043361-A2.
 XX

PD 27-MAY-2004.
 XX 06-NOV-2003; 2003WO-US035268.
 XX 08-NOV-2002; 2002US-0425235P.
 XX (GETH) GENENTECH INC.
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX WPI; 2004-420067/39.
 DR N-PSDB; ADO20171.
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX Claim 7; SEQ ID NO 1080; 1731pp; English.
 PS The invention relates to human PRO polypeptides and the polynucleotides
 XX encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX Sequence 628 AA;
 SQ

Query Match 96.3%; Score 1293; DB 8; Length 628;
 Best Local Similarity 95.7%; Pred. No. 6.5e-133;
 Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEFLETIGKTYGKVKKARESSGRLVAIKSRKDKIKDEQDLHIREIEMSLNPHI 60
 DB 53 YEFLETIGKTYGKVKKARESSGRLVAIKSRKDKIKDEQDLHIREIEMSLNPHI 112
 QY 61 IAIHEVFENSSKIVIVMEYASRGDLYISERPLSERDARHFRQIVSAHYCHONGIV 120
 DB 113 IAIHEVFENSSKIVIVMEYASRGDLYISERQQLSREARHFRQIVSAHYCHONRVV 172
 QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFGSPLYASPEIVNGKPYVGPVD 180
 DB 173 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFGSPLYASPEIVNGKPYTGPVD 232
 QY 181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMNPTRRA 240
 DB 233 SWSLGVLLYILVHGTMPFDGHDHKLILVKQISNGAYREPPKPSDACGLIRWLLMNPTRRA 292
 QY 241 TLEDVASHWVNVN 253
 DB 293 TLEDVASHWVNVN 305

RESULT 12
 ADJ96620
 ID ADJ96620 standard; protein; 672 AA.
 XX
 AC ADJ96620;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human calcium/calmodulin-dependent protein kinase NuaK2 protein SeqID 77.
 XX kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
 KW PK; STK; Gene therapy; cancer; immune-related disease;
 KW

KW cardiovascular disease; brain; neuronal associated disease; metabolic;
 KW inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
 KW antiinflammatory; enzyme; calcium/calmodulin-dependent protein kinase;
 KW NuaK2.
 XX Homo sapiens.
 OS 72.
 XX WO2004006838-A2.
 PN 22-JAN-2004.
 XX 15-JUL-2003; 2003WO-US021730.
 PD 15-JUL-2002; 2002US-0395632P.
 XX (SUGE-) SUGEN INC.
 PA Whyte D, Manning G, Caenepeel S;
 PI WPI; 2004-122753/12.
 DR N-PSDB; ADJ96554.
 XX New nucleic acid molecule encoding a kinase polypeptide, useful for
 PT preparing a composition for treating diseases or disorders, e.g., cancer,
 PT or neurological, immunological or inflammatory disorders.
 XX Claim 1; SEQ ID NO 77; 366pp; English.
 PS This invention relates to a novel isolated, enriched or purified nucleic
 XX acid molecule that encodes a kinase polypeptide. Specifically, it relates
 CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
 CC as well as protein kinase-like enzymes. The present invention describes
 CC screening methods to identify agonists, antagonists and antibodies that
 CC can be used to modulate the activity or function of the mammalian kinase
 CC enzymes. As such, these compositions can be used for gene therapy
 CC purposes to treat diseases or disorders including cancer, immune-related
 CC diseases, cardiovascular disease, brain or neuronal associated disease,
 CC metabolic and inflammatory disorders. Accordingly, they exhibit
 CC cytostatic, neuroprotective, immunomodulator and antiinflammatory
 CC activities. This polypeptide sequence is a human kinase protein sequence
 CC of the invention.
 XX Sequence 672 AA;
 SQ

Query Match 96.3%; Score 1293; DB 8; Length 672;
 Best Local Similarity 95.7%; Pred. No. 7.2e-133;
 Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEFLETIGKTYGKVKKARESSGRLVAIKSRKDKIKDEQDLHIREIEMSLNPHI 60
 DB 97 YEFLETIGKTYGKVKKARESSGRLVAIKSRKDKIKDEQDLHIREIEMSLNPHI 156
 QY 61 IAIHEVFENSSKIVIVMEYASRGDLYISERPLSERDARHFRQIVSAHYCHONGIV 120
 DB 157 IAIHEVFENSSKIVIVMEYASRGDLYISERQQLSREARHFRQIVSAHYCHONRVV 216
 QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFGSPLYASPEIVNGKPYVGPVD 180
 DB 217 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFGSPLYASPEIVNGKPYTGPVD 276
 QY 181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMNPTRRA 240
 DB 277 SWSLGVLLYILVHGTMPFDGHDHKLILVKQISNGAYREPPKPSDACGLIRWLLMNPTRRA 336
 QY 241 TLEDVASHWVNVN 253
 DB 337 TLEDVASHWVNVN 349

RESULT 13
 AAE16266
 ID AAE16266 standard; protein; 594 AA.

XX AAE16266;
 XX 26-MAR-2002 (first entry)
 XX Human kinase PKIN-12 protein.
 XX Human; kinase; PKIN-12; cancer; leukaemia; adenocarcinoma; osteoporosis;
 KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
 KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
 KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
 KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
 KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
 KW rheumatoid arthritis; ulcerative colitis; cataract; angina pectoris;
 KW hepatitis; hypothyroidism; cerebral palsy; cirrhosis; Cushing's syndrome;
 KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
 KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
 KW fatty liver; Niemann-Pick's disease; gene therapy.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX Domain 19..269
 FT /note="Eukaryotic protein kinase domain"
 FT Domain 22..260
 FT /label= Protein_kinase_domain
 FT Domain 23..260
 FT /label= Protein_kinase_domain
 FT Domain 24..260
 FT /label= Protein_kinase_domain
 XX WO200196547-A2.
 XX 20-DEC-2001.
 XX 14-JUN-2001; 2001WO-US019444.
 XX 15-JUN-2000; 2000US-0212073P.
 PR 23-JUN-2000; 2000US-0213467P.
 PR 30-JUN-2000; 2000US-0215651P.
 PR 07-JUL-2000; 2000US-0216605P.
 PR 13-JUL-2000; 2000US-0218372P.
 PR 25-AUG-2000; 2000US-0228056P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
 PI Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DAM, Greenwald SR;
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
 PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
 PI Lo TP, Khan F, Recipon SA, Azimzai V, Policky JL, Ding L;
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
 XX WPI; 2002-090207/12.
 DR N-PSDB; AAD26459.
 XX New polypeptides, useful for diagnosing, treating or preventing disorders
 PT of growth and development, cardiovascular and lipid, and diseases such as
 PT cancer, comprise human kinase polypeptides.
 XX Claim 1; Page 152-153; 197pp; English.
 XX The invention relates to human kinase PKIN proteins and their
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for
 CC treating a disease or condition associated with decreased expression of
 CC PKIN and a composition comprising PKIN antagonist is useful for treating
 CC a disease or condition associated with overexpression of PKIN. The
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 CC hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
 CC of a test compound and in gene therapy. The present sequence is human
 XX PKIN-12 protein
 XX SQ Sequence 594 AA;
 Query Match 95.8%; Score 1286; DB 5; Length 594;
 Best Local Similarity 95.3%; Pred. No. 3.5e-132;
 Matches 241; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 YEFLETLGKTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRIREIEMSSLNHPHI 60
 Db 19 YEFLETLGKTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRIREIEMSSLNHPHI 78
 Qy 61 IAIHEVPENSSKIVIVMEYASRGDLVDYISERPLSRDARHPFRQIVSAHYCHQNGIV 120
 Db 79 IAIHEVPENSSKIVIVMEYASRGDLVDYISERQOLSEREARHPFRQIVSAHYCHQNRV 138
 Qy 121 HRDLKLENILLDANGNIKADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPEVD 180
 Db 139 HRDLKLENILLDANGNIKADFGLSNLYHOGKFLQTFCGSPLYASPEIVNGKPYGTGPEVD 198
 Qy 181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRLLMVPTRRA 240
 Db 199 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRLLMVPTRRA 258
 Qy 241 TLEDVASHWVWVW 253
 Db 259 TLEDVASHWVWVW 271
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 ABP96085
 ID ABP96085 standard; protein; 611 AA.
 XX AC ABP96085;
 XX 07-MAY-2003 (first entry)
 XX Human protein kinase SEQ ID NO:76.
 KW Human; protein kinase; enzyme; antiaesthatic; antiinflammatory;
 KW antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic;
 KW immunosuppressive; vulnery; gene therapy; COPD; asthma; migraine;
 KW chronic obstructive pulmonary disease; non-insulin dependent diabetes;
 KW Parkinson's disease; myocardial infarction; inflammatory bowel disease;
 KW autoimmune disorder; allograft rejection; graft versus host disease;
 KW cancer; leukaemia; wound granulation.
 XX Homo sapiens.
 XX WO2003000901-A2.
 XX 03-JAN-2003.
 XX 24-JUN-2002; 2002WO-IB002358.
 XX 26-JUN-2001; 2001US-0301098P.
 XX 06-NOV-2001; 2001US-0332870P.
 XX (DECO-) DECODE GENETICS EHF.
 XX Martinez RAM, Sigurdson GT;
 XX

```

DR WPI; 2003-201429/19.
XX N-PSDB; ABZ77163.
XX
PT New protein kinase genes and polypeptides, useful for diagnosing diseases
PT associated with a protein kinase, or in gene therapy for treating e.g.
PT Parkinson's disease, migraine, myocardial infarction, allograft rejection
PT or cancers.
XX
XX Claim 9; Page 87; 258pp; English.
XX
CC ABZ77126 to ABZ77165 encode the human protein kinases given in ABP96048
CC to ABP96087. The protein kinases have antiasthmatic, antiinflammatory,
CC antidiabetic, antiparkinsonian, antimigraine, cardiant, cytostatic,
CC immunosuppressive and vulnerary activities, and can be used in gene
CC therapy. A protein kinase therapeutic agent from the present invention,
CC particularly a protein kinase gene agonist or antagonist, can be used for
CC treating a disease or condition associated with a protein kinase in an
CC individual. These diseases include chronic obstructive pulmonary diseases
CC (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease,
CC migraine, myocardial infarction, inflammatory bowel disease, autoimmune
CC disorders (e.g. allograft rejection or graft vs. host disease), cancers
CC (e.g. leukaemias) or wound granulation
XX
XX Sequence 611 AA;
XX
Query Match 95.3%; Score 1279.5; DB 6; Length 611;
Best Local Similarity 93.1%; Pred. No. 1.9e-131;
Matches 242; Conservative 6; Mismatches 5; Indels 7; Gaps 1;
XX
QY 1 YFELETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRIREIEMSSLNHPHI 60
Db 53 YFELETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRIREIEMSSLNHPHI 112
QY 61 IATHEVFENSKIVIVMEYASRGDLVDYISERPLSERDARHFRQIVSAHYCHQNGIV 120
Db 113 IATHEVFENSKIVIVMEYASRGDLVDYISERQQLSEREARHFRQIVSAHYCHQNRVV 172
QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPIVNGKPVVGEVD 180
Db 173 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPIVNGKPYTGPEVD 232
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Db 233 SWSLGVLLYILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSAPAFCLPDACGLIRWLLM 292
QY 234 VNPTRATLEDVASHWWVNW 253
Db 293 VNPTRATLEDVASHWWVNW 312
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RESULT 15
AAB65632
ID AAB65632 standard; protein; 629 AA.
XX
AC AAB65632;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 159.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS Homo sapiens.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX

```

```

PF 26-MAY-2000; 2000WO-US014842.
XX
PR 28-MAY-1999; 99US-0136503P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudreanam S;
XX
XX WPI; 2001-032161/04.
DR N-PSDB; AAP44659.
XX
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX
XX Claim 10; Fig 1; 310pp; English.
XX
XX The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
XX Sequence 629 AA;
XX
Query Match 94.5%; Score 1268.5; DB 4; Length 629;
Best Local Similarity 94.5%; Pred. No. 3.3e-130;
Matches 240; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
XX
QY 1 YFELETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRIREIEMSSLNHPHI 60
Db 53 YFELETGKGTGKVKKARESSGRLVAIKSIRKDKIKDEQDLHRIREIEMSSLNHPHI 112
QY 61 IATHEVFENSKIVIVMEYASRGDLVDYISERPLSERDARHFRQIVSAHYCHQNGIV 120
Db 113 IATHEVFENSKIVIVMEYASRGDLVDYISERQQLSEREARHFRQIVSAHYCHQNRVV 172
QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPIVNGKPVVGEVD 180
Db 173 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPIVNGKPYTGPEVD 232
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Db 233 SWSLGVLLYILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDCLAGLIRWLLMVNPTRR 292
QY 240 ATLEDVASHWWVNW 253
Db 293 ATLEDVASHWWVNW 306
XX
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Job time : 64.8224 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:43:09 ; Search time 58.6708 Seconds
(without alignments)
1557.950 Million cell updates/sec

Title: US-09-980-464-11_COPY_57_309

Perfect score: 1342
Sequence: 1 YEFLETGKTYGKVKKARE.....VNPRRTATLEDVASHMVWVNW 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	1342	100.0	631	14	US-10-355-975-11
2	1325	98.7	251	16	US-10-343-514-103
3	1313	97.8	630	16	US-10-343-514-41
4	1296	96.6	251	16	US-10-343-514-50
5	1293	96.3	628	9	US-09-963-159-2
6	1293	96.3	628	15	US-10-423-543-44
7	1293	96.3	628	17	US-10-370-715B-640
8	1293	96.3	672	17	US-10-618-941-77
9	1286	95.8	594	15	US-10-311-034-12
10	1276	95.1	251	16	US-10-343-514-101
11	1273	94.9	640	16	US-10-322-281-23
12	1230	91.7	616	16	US-10-322-281-26
13	1128.5	84.1	661	9	US-09-780-949-2

14	1128.5	84.1	661	9	US-09-780-949-6	Sequence 6, Appli
15	1128.5	84.1	661	14	US-10-354-358-82	Sequence 82, Appl
16	1128.5	84.1	661	17	US-10-723-860-2553	Sequence 2553, Ap
17	1111.5	82.8	252	16	US-10-343-514-102	Sequence 102, App
18	814	60.7	530	9	US-09-836-392-20	Sequence 20, Appl
19	785.5	58.5	246	10	US-09-898-837A-29	Sequence 29, Appl
20	665.5	49.6	508	15	US-10-016-248-24	Sequence 24, Appl
21	665.5	49.6	639	15	US-10-016-248-71	Sequence 71, Appl
22	665.5	49.6	639	15	US-10-016-248-72	Sequence 72, Appl
23	665.5	49.6	688	15	US-10-276-645-8	Sequence 8, Appli
24	665.5	49.6	703	15	US-10-016-248-70	Sequence 70, Appl
25	665.5	49.6	752	9	US-09-835-081-2	Sequence 2, Appli
26	665.5	49.6	752	15	US-10-258-106-16	Sequence 16, Appl
27	665.5	49.6	752	15	US-10-276-645-7	Sequence 7, Appli
28	665.5	49.6	769	15	US-10-363-616-403	Sequence 403, App
29	665.5	49.6	825	15	US-10-425-114-54516	Sequence 54516, A
30	661.5	49.3	752	17	US-10-618-941-79	Sequence 79, Appl
31	660.5	49.2	639	15	US-10-016-248-73	Sequence 73, Appl
32	660.5	49.2	660	15	US-10-276-645-6	Sequence 6, Appli
33	660.5	49.2	688	14	US-10-161-565-28	Sequence 28, Appl
34	660.5	49.2	688	14	US-10-161-565-29	Sequence 29, Appl
35	660.5	49.2	724	15	US-10-276-645-5	Sequence 5, Appli
36	651.5	48.5	744	9	US-09-835-081-4	Sequence 4, Appli
37	649.5	48.4	729	14	US-10-142-356-11	Sequence 11, Appl
38	649.5	48.4	729	14	US-10-195-101-33	Sequence 33, Appl
39	649.5	48.4	729	14	US-10-161-565-26	Sequence 26, Appl
40	649.5	48.4	744	9	US-09-919-585-3	Sequence 3, Appli
41	647.5	48.2	691	9	US-09-919-585-6	Sequence 6, Appli
42	647.5	48.2	722	14	US-10-274-194-4	Sequence 4, Appli
43	647.5	48.2	722	16	US-10-760-407-4	Sequence 4, Appli
44	647.5	48.2	724	9	US-09-919-585-9	Sequence 9, Appli
45	647.5	48.2	745	14	US-10-195-101-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-10-355-975-11
; Sequence 11, Application US/103555975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/10/355,975
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975-11

Query Match 100.0%; Score 1342; DB 14; Length 631;
Best Local Similarity 100.0%; Pred. No. 9.4e-100;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 TLEDVASHWVNW 253
Db 297 TLEDVASHWVNW 309

RESULT 2

US-10-343-514-103
; Sequence 103, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; APPLICANT: LEBEVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 103
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-514-103

Query Match 98.7%; Score 1325; DB 16; Length 251;
Best Local Similarity 100.0%; Pred. No. 8e-99;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEFLETGKGTGKGVKKARESSGRLVAIKSRKDKIKDEQDLHHRREIETMSSLNHPHI 60
Db 1 YEFLETGKGTGKGVKKARESSGRLVAIKSRKDKIKDEQDLHHRREIETMSSLNHPHI 60
Qy 61 IAHEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 120
Db 61 IAHEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 120
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Qy 181 SWSLGVLLYILVHGTMPDGDHKTIVKQISNGAYREPPKPSDAGCLIRLLMVPNPTTRA 240
Db 181 SWSLGVLLYILVHGTMPDGDHKTIVKQISNGAYREPPKPSDAGCLIRLLMVPNPTTRA 240
Qy 241 TLEDVASHWVNW 251
Db 241 TLEDVASHWVNW 251

RESULT 3

US-10-343-514-41
; Sequence 41, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.

; APPLICANT: LEBEVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 41
; LENGTH: 630
; TYPE: PRT
; ORGANISM: RAT
US-10-343-514-41

Query Match 97.8%; Score 1313; DB 16; Length 630;
Best Local Similarity 98.0%; Pred. No. 2e-97;
Matches 248; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YEFLETGKGTGKGVKKARESSGRLVAIKSRKDKIKDEQDLHHRREIETMSSLNHPHI 60
Db 57 YEFLETGKGTGKGVKKARESSGRLVAIKSRKDKIKDEQDLHHRREIETMSSLNHPHI 116
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Db 117 IAHEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIV 176
Qy 121 HRDLKENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIYVNGKPYVGPEVD 180
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Db 237 SWSLGVLLYILVHGTMPDGDHKTIVKQISNGAYREPPKPSDAGCLIRLLMVPNPTTRA 296
Qy 241 TLEDVASHWVNW 253
Db 297 TLEDVASHWVNW 309

RESULT 4

US-10-343-514-50
; Sequence 50, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; APPLICANT: LEBEVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 50
; LENGTH: 251
; TYPE: PRT
; ORGANISM: RAT
US-10-343-514-50

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Db	61	IAIHEVPENSSKIVIMVEYASRGDLYDIISERPLNERDARHPFQIVSALHYCHONGIV	120	
Qy	121	HRDLKULENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPVYGVPEVD	180	
Db	121	HRDLKULENILLDASGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPVYGVPEVD	180	
Qy	181	SWSLGVLLYTLVHGTMFPDQODKHTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTERRA	240	
Db	181	SWSLGVLLYTLVHGTMFPDQODKHTLVKQISSNGAYREPCFSDACGLIRWLLMVNPTERRA	240	
Qy	241	TLEDVASHWWV	251	
Db	241	TLEDVASHWWV	251	

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RESULT 5
US-09-963-159-2
; Sequence 2, Application US/09963159
; Patent No. US20020077312A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-50U1
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-159-2

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Query Match	96.3%;	Score 1293;	DB 9;	Length 628;
Best Local Similarity	95.7%;	Pred. No. 8.4e-96;		
Matches 24;	Conservative 6;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	YEFLETIGKGTGYKVKKARESSGRLVAIKSRDKDKIQEODLLHRRREIETMSSLNHPHI	60	
Db	53	YEFLETIGKGTGYKVKKARESSGRLVAIKSRDKDKIQEODLMHRRREIETMSSLNHPHI	112	
Qy	61	IATHEVPENSSKIVIMVEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHONGIV	120	
Db	113	IATHEVPENSSKIVIMVEYASRGDLYDIYSERQQLSERAKHFRQIVSAVHYCHQNRVV	172	
Qy	121	HRDLKLENILLDANGNIKIADFGLSNLHYHGKFLQTCGSPLYASPEIVNGKPYVGPEVD	180	
Db	173	HRDLKLENILLDANGNIKIADFGLSNLHYHGKFLQTCGSPLYASPEIVNGKPYTGEVD	232	
Qy	181	SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMWNPTTRA	240	
Db	233	SWSLGVLLYILVHGTMPFDGHDHKLIVKQISNGAYREPPKPSDACGLIRWLLMWNPTTRA	292	
Qy	241	TLEDVASHHWVNVW	253	
Db	293	TLEDVASHHWVNVW	305	

RESULT 6

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US-10-423-543--44
; Sequence 44, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williamson, Mark J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
; TITLE OF INVENTION: AND US$S THEREFOR
; FILE REFERENCE: MPI03-0230MNM
; CURRENT APPLICATION NUMBER: US/10/423.543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-423-543--44

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	Query Match	96.3%	Score 1293;	DB 15;	Length 628;
	Best Local Similarity	95.7%;	Pred. No. 8.4e-96;		
	Matches 242;	Conservative	6;	Mismatches 5;	Indels 0; Gaps 0;
Qy	1	YFETLGKTYGKVKKARESSGRLLVAIKRKDKIKDEODLHIREIEMSSLNPHI	60		
Db	53	YFETLGKTYGKVKKARESSGRLLVAIKRKDKIKDEODLHIREIEMSSLNPHI	112		
Qy	61	IAIHEVPENSKIVIMVEYASRGDLYDIISERPLSERDARHPFRQTVSALHYCHONGIV	120		
Db	113	IAIHEVPENSKIVIMVEYASRGDLYDISERQQLSREARHFFPRQIVSAVHYCHQRNV	172		
Qy	121	HRDLKLNIILLDANGNIKIDFGLSNLHYHGKFLOTFCGSPLYASPIEVNGKPVGPEVD	180		
Db	173	HRDLKLNIILLDANGNIKIDFGLSNLHYHGKFLOTFCGSPLYASPIEVNGKPYTGPEVD	232		
Qy	181	SWSLGVLLYLTVHGTMPDFGDHKTLVKQISNGAYREPCKPSDACGLIRWLLMVNPTRRA	240		
Db	233	SWSLGVLLYLTVHGTMPDFGDHKILVKQISNGAYREPCKPSDACGLIRWLLMVNPTRRA	292		

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Qy 241 TLEDVASHWVNW 253
Db 293 TLEDVASHWVNW 305

RESULT 7
US-10-370-715B-640
; Sequence 640, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;   Patin Docket Preview
;   APPLICANT: BODARY, SARAH C.
;   APPLICANT: CLARK, HILLARY
;   APPLICANT: BRISDELL, HUNTE
;   APPLICANT: JACKMAN, JANET
;   APPLICANT: SCHOENFELD, JILL R.
;   APPLICANT: WILLIAMS, P. MICKY
;   APPLICANT: WOOD, WILLIAM I.
;   APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 640
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-370-715B-640

Query Match 96.3%; Score 1293; DB 17; Length 628;
Best Local Similarity 95.7%; Pred. No. 8.4e-96;
Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YEFLETGKGTGKGVKKARESSGRLVAIKSIRKDKIKDEQDLHIREIEIMSSLNHPHI 60
Db 53 YEFLETGKGTGKGVKKARESSGRLVAIKSIRKDKIKDEQDLHIREIEIMSSLNHPHI 112
Qy 61 IATHEVFENSKIVIVMEYASRGDLVDYISERPLSRDARHPFQIVSALHYCHONGIV 120
Db 113 IATHEVFENSKIVIVMEYASRGDLVDYISERQQLSREARHPFQIVSAVHYCHQNRV 172
Qy 121 HRDLKLENILLDANGNIKIADFGLSNLYHGKFLQTFGSGPLYSPIVNGKPYVGPEVD 180
Db 173 HRDLKLENILLDANGNIKIADFGLSNLYHGKFLQTFGSGPLYSPIVNGKPYTGPEVD 232
Qy 181 SWSLGVLLYILVHGTMPFDGQDHTLVKQISNGAYREPPKPSDACGLIRLLMVPTRRA 240
Db 233 SWSLGVLLYILVHGTMPFDGHDHKLVLKQISNGAYREPPKPSDACGLIRLLMVPTRRA 292
Qy 241 TLEDVASHWVNW 253
Db 293 TLEDVASHWVNW 305

RESULT 8
US-10-618-941-77
; Sequence 77, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
;   APPLICANT: WHYTE, DAVID
;   APPLICANT: MANNING, GERARD
;   APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 77

Qy 241 TLEDVASHWVNW 253
Db 337 TLEDVASHWVNW 349

RESULT 9
US-10-311-034-12
; Sequence 12, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
;   APPLICANT: INCYTE GENOMICS, INC.
;   APPLICANT: YUE, Henry
;   APPLICANT: LAL, Preeti
;   APPLICANT: BANDMAN, Olga
;   APPLICANT: BOROWSKY, Mark L.
;   APPLICANT: AU-YOUNG, Janice
;   APPLICANT: LU, Yan
;   APPLICANT: GANDHI, Ameen R.
;   APPLICANT: TRIBOULEY, Catherine M.
;   APPLICANT: CHAWLA, Narinder K.
;   APPLICANT: LU, Dyrung Aina M.
;   APPLICANT: GREENWALD, Sara R.
;   APPLICANT: RAMKUMAR, Jayalaxmi
;   APPLICANT: GRIFFIN, Jennifer A.
;   APPLICANT: KEARNEY, Liam
;   APPLICANT: BURFORD, Neil
;   APPLICANT: NGUYEN, Dannel B.
;   APPLICANT: TANG, Y. Tom
;   APPLICANT: BAUGHN, Mariah R.
;   APPLICANT: HE, Ann
;   APPLICANT: THORNTON, Michael
;   APPLICANT: HAFALIA, April
;   APPLICANT: ARVIZU, Chandra S.
;   APPLICANT: GURURAJAN, Rajagopal
;   APPLICANT: LO, Terence P.
;   APPLICANT: KHAH, Farrah A.
;   APPLICANT: RECIBON, Shirley A.
;   APPLICANT: AZIMZAI, Yalda
;   APPLICANT: POLICKY, Jennifer L.
;   APPLICANT: DING, Li
;   APPLICANT: GREYER, Megan
;   APPLICANT: ELLIOTT, Vicki S.
;   APPLICANT: THANGAVELU, Kavitha
;   APPLICANT: BATRA, Sajeew
;   APPLICANT: ISCON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
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; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-26

Query Match      91.7%; Score 1230; DB 16; Length 616;
Best Local Similarity 93.3%; Pred. No. 9.8e-91;
Matches 236; Conservative 6; Mismatches 5; Indels 6; Gaps 3;

Qy 1 YEFLETGKGYGVKVKARES-SGRLVAKSIRKDKIKDEQDLHIRREIEMSSLNHPHI 60
Db 53 YEFLETGKGYGVKVKARES-SGRLVAKSIRKDKIKDEQDLHIRREIEMSSLNHPHI 112
Qy 61 IAIHEVFENSKIVIMVEYASRGDLVDYISERPLSERDARHFRQIVSALHYCHONGIV 120
Db 113 IAIHEVFENSKIVIMVEYASRGDLVDYISQ--QLSE--ARHFRQIVSAVHYCHQNRV 168
Qy 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKELQTCGSPLYASPEIVNGKPYVGPEVD 180
Db 169 HRDLKLENILLDANGNIKIADFGLSNLYHKGKELQTCGSPLY--DELVNGKPYTGPEVD 226
Qy 181 SWSLGVLLYLILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAGCLIRWLLMVNPTRR 240
Db 227 SWSLGVLLYLILVHGTMPFDGHDHKLVLKQISNGAYREPPKPSDAGCLIRWLLMVNPTRR 286
Qy 241 TLEDVASHWWVNW 253
Db 287 TLEDVASHWWVNW 299

RESULT 13
US-09-780-949-2
; Sequence 2, Application US/09780949
; Patent No. US20020006618A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: Methods for Using 20893, a Human Protein
; FILE REFERENCE: 035800/209015
; CURRENT APPLICATION NUMBER: US/09/780,949
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,690
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 661
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-780-949-2

Query Match      84.1%; Score 1128.5; DB 9; Length 661;
Best Local Similarity 82.3%; Pred. No. 1.6e-82;
Matches 209; Conservative 24; Mismatches 20; Indels 1; Gaps 1;

Qy 1 YEFLETGKGYGVKVKARES-SGRLVAKSIRKDKIKDEQDLHIRREIEMSSLNHPH 59
Db 55 YELQETLGKGYGVKVKRATERFSGRVVAIKSIRKDKIKDEQDMVHIREIEMSSLNHPH 114
Qy 60 IAIHEVFENSKIVIMVEYASRGDLVDYISERPLSERDARHFRQIVSALHYCHONGI 119
Db 115 IISIVYEVFNKDKLVIIMEYASKGELYDIISERRLSERETRHFRQIVSAVHYCHNGV 174
Qy 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPEV 179
Db 175 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGREYRGPEV 234
Qy 180 DSWSLGVLLYLILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAGCLIRWLLMVNPTRR 239
Db 235 DSWALGVLLYTLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDARGLIRWLLMVNPD RR 294
Qy 240 ATLEDVASHWWVNW 253
Db 295 ATLEDIANHWWVNW 308

RESULT 14
US-09-780-949-6
; Sequence 6, Application US/09780949
; Patent No. US20020006618A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: Methods for Using 20893, a Human Protein
; FILE REFERENCE: 035800/209015
; CURRENT APPLICATION NUMBER: US/09/780,949
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,690
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 661
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-780-949-6

Query Match      84.1%; Score 1128.5; DB 9; Length 661;
Best Local Similarity 82.3%; Pred. No. 1.6e-82;
Matches 209; Conservative 24; Mismatches 20; Indels 1; Gaps 1;

Qy 1 YEFLETGKGYGVKVKARES-SGRLVAKSIRKDKIKDEQDLHIRREIEMSSLNHPH 59
Db 55 YELQETLGKGYGVKVKRATERFSGRVVAIKSIRKDKIKDEQDMVHIREIEMSSLNHPH 114
Qy 60 IAIHEVFENSKIVIMVEYASRGDLVDYISERPLSERDARHFRQIVSALHYCHONGI 119
Db 115 IISIVYEVFNKDKLVIIMEYASKGELYDIISERRLSERETRHFRQIVSAVHYCHNGV 174
Qy 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPEV 179
Db 175 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGREYRGPEV 234
Qy 180 DSWSLGVLLYLILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAGCLIRWLLMVNPTRR 239
Db 235 DSWALGVLLYTLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDARGLIRWLLMVNPD RR 294
Qy 240 ATLEDVASHWWVNW 253
Db 295 ATLEDIANHWWVNW 308

RESULT 15
US-10-354-358-82
; Sequence 82, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
US-10-354-358-82

Query Match      84.1%; Score 1128.5; DB 9; Length 661;
Best Local Similarity 82.3%; Pred. No. 1.6e-82;
Matches 209; Conservative 24; Mismatches 20; Indels 1; Gaps 1;

Qy 1 YEFLETGKGYGVKVKARES-SGRLVAKSIRKDKIKDEQDLHIRREIEMSSLNHPH 59
Db 55 YELQETLGKGYGVKVKRATERFSGRVVAIKSIRKDKIKDEQDMVHIREIEMSSLNHPH 114
Qy 60 IAIHEVFENSKIVIMVEYASRGDLVDYISERPLSERDARHFRQIVSALHYCHONGI 119
Db 115 IISIVYEVFNKDKLVIIMEYASKGELYDIISERRLSERETRHFRQIVSAVHYCHNGV 174
Qy 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPEV 179
Db 235 DSWALGVLLYTLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDARGLIRWLLMVNPD RR 294
Qy 240 ATLEDVASHWWVNW 253
Db 295 ATLEDIANHWWVNW 308
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 3011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MP102-020P1R0NM0M
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-354-358-82

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Query Match.	84.1%;	Score 1128.5;	DB 14;	Length 661;
Best Local Similarity	82.3%;	Pred. No. 1.6e-82;		
Matches 209;	Conservative 24;	Mismatches 20;	Indels 1;	Gaps 1;
QY	1	YEFLETIGKGYGVKKVARES-SGRLVAIKSRKDKIKDODLLHIRREIEIMSSLNHPH	59	
Db	55	YELQETLGKGYGVKKRATERFSGRVVAIKSRKDKIKDEQDMVHIRREIEIMSSLNHPH	114	
QY	60	IIAIEHFVENSKTVIYMEVYASRGDLDYIISERPLSRDARHPFROIIVSALHYCHONGI	119	
Db	115	IIISIEYFENKDKVIMYEYASKGELYDYISERRLSERETRFROIIVSAVHYCHNGV	174	
QY	120	VHRDLKLENTLLDANGNIKIADFGLSNLYHKGFLOTCGSPLYASPEIYNGRPYVGPEV	179	
Db	175	VHRDLKLENTLLDNCNIKIADFGLSNLYQDKFLQTCGSPLYASPEIYNGRPYRPEV	234	
QY	180	DSWSLGVLLYILVHGTFPFQDQDKHTLVKQISNGAYREPPKPSDACGLIRWLMVNPTRR	239	
Db	235	DSWALGVLLYLYVGTMPFQDFHKNLIRQISSGEYREPTQPSDARGIIRWLMVNPDRR	294	
QY	240	ATLEDVASHWVWVNW	253	
Db	295	ATTIEDIANHWVWVNW	308	

Search completed: January 22, 2005, 07:00:34
Job time : 59.6708 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:29:16 ; Search time 15.4548 Seconds
(without alignments)
1575.104 Million cell updates/sec

Title: US-09-980-464-11_COPY_57_309
Perfect score: 1342
Sequence: 1 YEFLETLGKTYGKVKKARE.....VNPTRRATLEDVASHWVNW 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : PIR_79:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	813.5	60.6	1558	2	T29253	hypothetical prote
2	647.5	48.2	745	2	G01025	serine/threonine p
3	646.5	48.2	713	2	S27966	probable serine/th
4	644	48.0	512	2	T52633	serine/threonine-s
5	641	47.8	504	2	T10449	probable serine/th
6	638.5	47.6	1398	2	T13741	hypothetical prote
7	637	47.5	512	1	JC1446	serine/threonine-s
8	631	47.0	511	1	A56009	serine/threonine-s
9	627.5	46.8	774	2	I48609	probable serine/th
10	621.5	46.3	1192	2	T18611	probable serine/th
11	621.5	46.3	1246	2	G83287	protein H39E23.1 [
12	621	46.3	472	2	B90100	SNF-related kinase
13	619.5	46.2	633	1	A26030	serine/threonine-s
14	618	46.1	504	2	T07415	probable serine/th
15	617.5	46.0	798	2	JC7500	glik protein - chic
16	616	45.9	562	2	T29858	hypothetical prote
17	614.5	45.8	602	2	S72513	FOA2 protein - yea
18	610	45.5	473	1	S59941	serine/threonine-s
19	604	45.0	552	1	S51025	[hydroxymethylglut
20	601	44.8	552	1	A53621	[hydroxymethylglut
21	599	44.6	512	2	T07788	probable serine/th
22	591.5	44.1	576	2	T41587	probable carbon ca
23	583.5	43.5	887	2	T20941	hypothetical prote
24	579.5	43.2	481	2	I49072	protein kinase - m
25	576.5	43.0	510	2	T04145	serine/threonine p
26	573	42.7	622	1	S44859	serine/threonine-s
27	567.5	42.3	502	1	A41361	serine/threonine-s
28	566.5	42.2	401	2	B90120	SNF1-related prote
29	561.5	41.8	513	1	S60303	serine/threonine-s

ALIGNMENTS

RESULT 1

КД00П1
Т29253

123233 hypothetical protein B0496.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text change 15-Oct-1999

C;Accession: T29253

R;Murray, J.; Le, T.T.

submitted to the EMBL Data Library, May 1996

A;Description: The sequence of *C. elegans* cosmid B0496.

A;Reference number: Z20596

A;Accession: T29253

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 1-1558 <MUR>

A;Cross-references: EMBL:U58749; PIDN:AAB00636.1; GSPDB:GN00022; CESP:B0496.3

A;Experimental source: strain Bristol N2; clone B0496

C;Genetics:

A;Gene: CESP:B0496.3

A;Map position: 4

A; Introns: 55/1; 100/3; 141/1; 226/3; 298/1; 468/3; 502/2; 609/3; 656/3; 795/3; 843/2; 9

Query Match	60.6%;	Score	813.5;	DB 2;	Length	1558;			
Best Local Similarity	61.7%;	Pred. No.	2.7e-27;						
Matches	156;	Conservative	33;	Mismatches	63;	Indels	1;	Gaps	1;
Qy	1	YFELETLGSGTGVKVKKARESS--GRLVAKSIRKDKIKOBDLLHTRREIEMSSLNHPH	59						
Db	75	FEITKLGSGTGVKSLAYDHRKFDREAVAVKLIKSAIESKADIVRIRREIRISALNHPN	134						
Qy	60	ITAIHEVFNSSKIVTVMEVASRGDLVDYISERPRLSERDARHFFQIVSALHYCHONGI	119						
Db	135	ITQIVFVNKOKIILVMEYSGGGLVDYVSRCSLPEAEARIRFQITSAVLVYCHKHRV	194						
Qy	120	VHRDLKENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYGVPEV	179						
Db	195	AHRDLKENILLDQNNNAKIADFGLSNYFADKNLLTTFCGSPLYASPEIINGTPTKGPV	254						
Qy	180	DSWSLGVLLYILVHGTMPPDGDQHKTLVKQISNGAYREPPKPSDACGLIRWLLMNPTRR	239						
Db	255	DOWSLGILLYTLVYSGMPDGRDFNRMVRQIKRGAYFETPTASTMLIRNMLRVNPERR	314						
Qy	240	ATLEDVASHWVN	252						
Db	315	ATIFDIASHWLN	327						

RESULT 2

REPUDI
G01025

serine/threonine protein kinase - human

C:Species: Homo sapiens (man)

C; Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text change 16-Aug-2004

C;Accession: G01025

R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A:Reference number: H00564
A:Accession: G01025
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <NAV>
A:Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C:Superfamily: protein kinase homology
F:18-271/Domain: protein kinase homology <KIN>

Query Match 48.2%; Score 647.5; DB 2; Length 745;
Best Local Similarity 51.2%; Pred. No. 1.3e-20;
Matches 130; Conservative 44; Mismatches 77; Indels 3; Gaps 3;

Qy 1 YFLETGKGTGYGVKKARE-SSGRLVAIKRKDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 20 YRLKTKTGKGNFAKVLARHILTCGEVAVKIIDTQL-NSSSLQKLFREVRIMKVLNHPN 78
Qy 60 IIAIHEVFENSCKIVIMVEYASRGDLYISERPRLSERDARHFRQIVSALHYCHONGI 119
Db 79 IVKLFEVETQKTLYLIMEYASGGEVDFYLVAGRMKEKARFQIVSAVQYCHOKFI 138
Qy 120 VHRDLKLENILLDANGNIKIADFGSLNLYHKGKFLQTFGSPLYASPEIVNGKPYGVPEV 179
Db 139 VHRDLKAENLLDADNMKIADFGSNEFTFGNKLDTFCGSPPYAAPLFGKKYDGPV 198
Qy 180 DSWSLGVLLYLVHGTWPPFDGQDHTLVKQISNGAYREPPKPSDAC-GLIRWLLMVPTR 238
Db 199 DVWSLGVILYLVSGSLPFDGQNLKELRERVLGRKYPFYMSTDCENLLKFLILNPSK 258
Qy 239 RATLEDVASHWVN 252
Db 259 RGTLEQIMKDRWIN 272

RESULT 3
S27966
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - human
N:Alternate names: protein p78
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
A:Accession: S27966
submitted to the EMBL Data Library, January 1992
R;Maheshwari, K.K.; Som, S.; Parsa, I.
A:Description: Sequence of a cDNA encoding 78kD marker protein lost in chemically induced
A:Reference number: S27966
A:Accession: S27966
A:Molecule type: mRNA
A:Residues: 1-713 <MAH>
A:Cross-references: UNIPROT:P27448; EMBL:M80359; NID:g189511; PIDN:AAA59991.1; PID:g1895
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:54-307/Domain: protein kinase homology <KIN>
F:62-70/Region: protein kinase ATP-binding motif

Query Match 48.2%; Score 646.5; DB 2; Length 713;
Best Local Similarity 51.6%; Pred. No. 1.4e-20;
Matches 131; Conservative 41; Mismatches 79; Indels 3; Gaps 3;

Qy 1 YFLETGKGTGYGVKKARE-SSGRLVAIKRKDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 56 YRLKTKTGKGNFAKVLARHILTCGEVAVKIIDTQL-NPTSLQKLFREVRIMKVLNHPN 114
Qy 60 IIAIHEVFENSCKIVIMVEYASRGDLYISERPRLSERDARHFRQIVSALHYCHONGI 119
Db 115 IVKLFEVETQKTLYLIMEYASGGEVDFYLVAGRMKEKARFQIVSAVQYCHOKRI 174
Qy 120 VHRDLKLENILLDANGNIKIADFGSLNLYHKGKFLQTFGSPLYASPEIVNGKPYGVPEV 179
Db 175 VHRDLKAENLLDADNMKIADFGSNEFTVGKGLDTFCGSPPYAAPLFGKKYDGPV 234
Qy 180 DSWSLGVLLYLVHGTWPPFDGQDHTLVKQISNGAYREPPKPSDAC-GLIRWLLMVPTR 238

Db 235 DVWSLGVILYLVSGSLPFDGQNLKELRERVLGRKYPFYMSTDCENLLKFLILNPIK 294
Qy 239 RATLEDVASHWVN 252
Db 295 RGTLEQIMKDRWIN 308

RESULT 4
T52633
serine/threonine-specific protein kinase (EC 2.7.1.1) AKIN11 [validated] - Arabidopsis th
N:Alternate names: SNF1 protein kinase omolog AKIN11
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
A:Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machida
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A:Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein kin
A:Reference number: Z25116; MUID:99238528; PMID:10220464
A:Accession: T52633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <BHA>
A:Cross-references: UNIPROT:P92958; EMBL:X99279; PIDN:CAA67671.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: AKIN11
C:Function:
A:Description: EC 2.7.1.1; serine/threonine-specific protein kinase AKIN11 [validated, M
complements SNF1 mutations in yeast
C:Superfamily: AMP-activated protein kinase; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 48.0%; Score 644; DB 2; Length 512;
Best Local Similarity 50.8%; Pred. No. 1.4e-20;
Matches 128; Conservative 47; Mismatches 75; Indels 2; Gaps 2;

Qy 1 YFLETGKGTGYGVKKARE-SSGRLVAIKRKDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 20 YLKGKTLGIGFQKVKIAEHVTVGHVAKILNRRKIKNMEEKVREIKIURLFMHPH 79
Qy 60 IIAIHEVFENSCKIVIMVEYASRGDLYISERPRLSERDARHFRQIVSALHYCHONGI 119
Db 80 IIRQYEVETTSDIYVMEYVKSGLFDYIVEKGRLEQDEARNFFQIIISGVEYCHRMV 139
Qy 120 VHRDLKLENILLDANGNIKIADFGSLNLYHKGKFLQTFGSPLYASPEIVNGKPYGVPEV 179
Db 140 VHRDLKPENLLDSRCNIKIADFGLSNVNRDGHFLKTSCTGSPNYAAPEVISGKLYAGPEV 199
Qy 180 DSWSLGVLLYLVHGTWPPFDGQDHTLVKQISNGAYREPPK-PSDACGLIRWLLMVPTR 238
Db 200 DVWSGVLVYALCGILPFDENIPNLFKKIKGGIYTLFSLHSSEARDLIPRLIIVDPVK 259
Qy 239 RATLEDVASHWVN 250
Db 260 RITIPIRQHRW 271

RESULT 5
T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - cucumber
N:Alternate names: SNF1-related protein kinase
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
A:Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z17020
A:Accession: T10449
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-504 <GUM>
A:Cross-references: UNIPROT:P93113; EMBL:Y10036

RESULT 8
A56009
serine/threonine-specific protein kinase (EC 2.7.1.1-) NPK5 - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C/Accession: A56009
R/Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A/Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cerevisiae
A/Reference number: A56009; MUID:94217693; PMID:8164654
A/Accession: A56009
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-511 <MUR>
A/Cross-references: UNIPROT:Q40544; GB:D26602; NID:G496384; PIDN:BAA05649.1; PID:G496385
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F:17-271/Domain: protein kinase homology <KIN>
F:25-33/Region: protein kinase ATP-binding motif
F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Asn, Asp) #status predicted
Query Match 47.0%; Score 631; DB 1; Length 511;
Best Local Similarity 49.6%; Pred. No. 4.78-20;
Matches 125; Conservative 48; Mismatches 77; Indels 2; Gaps 2;
Qy 1 YEFLETGKGYGVKKARE-SGRVVAIKSIRKDKIQEDLLHIREIEMSSLNHPH 59
Db 19 YLKGKTIGISFGVKVTAETHLTGHVAVKILNRKIKNMEMEKVREIKILFHPH 78
Qy 60 IIAIHEVFENSSKIVIVMEYASRGDLVDYISERPRLSERDARHPFRQIVSALHYCHQNGI 119
Db 79 IIRLYEVETPSDIYVMEYVYKSGELFDYIEVKRLQDEARKFFQIISGVEYCHRMV 138
Qy 120 VHRDLKLENTLLDANGNIKIADFGLSNLYHKGFLOFTFCGSPLYASPEIVNGKPYGPEV 179
Db 139 VHRDLKPENLDDSKNVKIADFGLSNIMRDGHFLKTS CGSPNVAAPAEVTSGLIYAGPEV 198
Qy 180 DWSLGLVLLYLIVHGTMPFDQDQDKHTLVKQISNGAYREPPKPS-DACGLIRWLLMVNPT 238
Db 199 DVWSCGVILYALLCGTLPFDDEINPFLFKIKGGWISLPSHLSAGARDLIPRLMIVDPMK 258
Qy 239 RATLEDVASHMW 250
Db 259 RWTPEIRMPHW 270
RESULT 9
I48609
probable serine/threonine-specific protein kinase (EC 2.7.1.1-) kem - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C/Accession: I48609; S31333
R/Ingilis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A/Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome 19.
A/Reference number: I48609; MUID:93364122; PMID:8358177
A/Accession: I48609
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-774 <INGI>
A/Cross-references: UNIPROT:Q05512; EMBL:X70764; NID:G57919; PIDN:CAA50040.1; PID:G57920
R/Ingilis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A/Description: A novel protein kinase with homologues in yeast maps to mouse chromosome
A/Reference number: S31333
A/Accession: S31333
A/Molecule type: mRNA
A/Residues: 1-698, 'K', 700-702, 'GRGLPTAAKASCTSGTCYCAGMAHQATRT', 731-774 <ING2>

A/Cross-references: EMBL:X70764

C/Genetics:

A/Gene: emk

C/Superfamily: protein kinase homology

C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:51-304/Domain: protein kinase homology <KIN>

F:59-67/Region: protein kinase ATP-binding motif

Query Match 46.8%; Score 627.5; DB 2; Length 774;

Best Local Similarity 50.0%; Pred. No. 8.9e-20;

Matches 127; Conservative 44; Mismatches 80; Indels 3; Gaps 3;

Qy 1 YEFLETGKGYGVKKARE-SGRVVAIKSIRKDKIQEDLLHIREIEMSSLNHPH 59

Db 53 YRLKLTIGKNFAKVKLARHILTGKEVAVKIIRKQTL-NSSSLQKLPRVIRIMKVLNHPN 111

Qy 60 IIAIHEVFENSSKIVIVMEYASRGDLVDYISERPRLSERDARHPFRQIVSALHYCHQNGI 119

Db 112 IVKLFEVETETKTLVLMVEYASGGEVFDYLVAHGRMKEKARAKFRQIVLHVQYCHQKFI 171

Qy 120 VHRDLKLENTLLDANGNIKIADFGLSNLYHKGFLOFTFCGSPLYASPEIVNGKPYGPEV 179

Db 172 VHRDLKAENLLDADNMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPPELFGKKIDGPEV 231

Qy 180 DWSLGLVLLYLIVHGTMPFDQDQDKHTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 238

Db 232 DVWSLGVILYTLVSGSLPFGQNLKELRERVLKGRIPFYMSTDCENLLKLFILNPSK 291

Qy 239 RATLEDVASHMWVN 252

Db 292 RGTLEQIMKDRWN 305

RESULT 10

T18611

probable serine/threonine-specific protein kinase (EC 2.7.1.1-), long splice form - Caenorhabditis elegans

N/Contains: probable serine/threonine kinase, short splice form

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18610; T23144; T23143

R/McMurray, A.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z18997

A/Accession: T18611

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1192 <WILI>

A/Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PIDN:CAB54179.1; GSPDB:GN00023; CESP:H39E23.1b

A/Experimental source: clone AH10

A/Accession: T18610

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-487, 536-1192 <WIL2>

A/Cross-references: EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b

A/Experimental source: clone AH10

R/McMurray, A.

submitted to the EMBL Data Library, June 1997

A/Reference number: Z19696

A/Accession: T23144

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1192 <WIL3>

A/Cross-references: EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a

A/Experimental source: clone H39E23

A/Accession: T23143

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-487, 536-1192 <WIL4>

A/Cross-references: EMBL:Z96102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b

A/Experimental source: clone H39E23

C/Genetics:

A/Gene: CESP:H39E23.1a; CESP:H39E23.1b

A/Map position: 5

A; Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 535/3; 487/3; 631/1; 825/2; 914/3; 992/3
C; Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #8
F; 1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splice form #1

Query Match 46.3%; Score 621.5; DB 2; Length 1192;
Best Local Similarity 48.0%; Pred. No. 2.2e-19;
Matches 122; Conservative 52; Mismatches 77; Indels 3; Gaps 3;

Qy 1 YFELETGKGTGKGVKKARE--SSGRLVAIKSRDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 170 YKLLKTIGKGNFAVKLAKHVITGHEVAIKIIDKTAL-NPSSLOKLFREVKIMKQLDHPN 228
Qy 60 IIAIHEVFENSSKIVIVMEYASRGDLVDYISERPRLSERDARHFQIVSALHYCHONGI 119
Db 229 IVKLYQVMEETEQTLLVLEYASGGEVFDYLVAGRMKEKEARAKFRQIVSAVQYLHAKNI 288
Qy 120 VHRDLKLENTLLDANGNIKTADFGSLNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPVEV 179
Db 289 IHRDLKAENLLDQDMNIKTADFGSNTFSLGNKLDITFCGSPPYAAPLFGSKKYDGPVEV 348
Qy 180 DWSLGLVLLYLVHGTMPFDGQDHKTIVKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 238
Db 349 DVMSLGVLLYLVSGSLPFDGQNLKELRVRVLRKRYRIPFMTDNCENLLKKFLVINPQR 408
Qy 239 RATLEDVASHWVN 252
Db 409 RSSLDNIMKDRWMN 422

RESULT 11
G89287
protein H39E23.1 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C; Accession: G89287
R; Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A; Reference number: A75000; MUID:99069613; PMID:9851916
A; Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C_elegans/Genome
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999
A; Accession: G89287
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1246 <STO>
A; Cross-references: GB:chr_V; PIDN: CAB09532.1; PID: g3878100; GSPDB: GN00023; CESP: H39E23.1
C; Genetics:
A; Map position: 5

Db 299 RSSLDNIMKDRWMN 312

RESULT 12
SNF-related kinase [imported] - Guillardia theta nucleomorph
C; Species: nucleomorph Guillardia theta
A; Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: B90100
R; Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reif, D.; et al.
Nature 410, 1091-1096, 2001
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:11323671; PMID:11323671
A; Accession: B90100
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-472 <DOU>
A; Cross-references: UNIPROT: Q98RL9; GB: AF165818; NID: g13794554; PIDN: AAK39929.1; GSPDB: G13794554
C; Genetics:
A; Gene: kin(snf1)
A; Map position: 1
A; Genome: nucleomorph
C; Superfamily: AMP-activated protein kinase; protein kinase homology
C; Keywords: nucleomorph

Query Match 46.3%; Score 621; DB 2; Length 472;
Best Local Similarity 48.0%; Pred. No. 1.2e-19;
Matches 122; Conservative 52; Mismatches 78; Indels 2; Gaps 2;

Qy 1 YFELETGKGTGKGVKKARE--SSGRLVAIKSRDKIKDEQDLHHRREIEIMSSLNHPH 59
Db 12 YLGLKTIGVSGFKVKGHELCGQKAVAILNKKIKNLKMEKVKREICILKLFMHHP 71
Qy 60 IIAIHEVFENSSKIVIVMEYASRGDLVDYISERPRLSERDARHFQIVSALHYCHONGI 119
Db 72 IIRLYEVIETPTDIFVVTEYITGSELFDYIVRGRNLNEDESRKPFQOMISGIEYCHNHV 131
Qy 120 VHRDLKLENTLLDANGNIKTADFGSLNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPVEV 179
Db 132 VHRDLKLENTLLDANGNIKTADFGSLNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPVEV 191
Qy 180 DWSLGLVLLYLVHGTMPFDGQDHKTIVKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 238
Db 192 DVMSLGVLLYLVSGSLPFDGQNLKELRVRVLRKRYRIPFMTDNCENLLKKFLVINPQR 251
Qy 239 RATLEDVASHWVN 252
Db 252 RITINEIRDPHPFN 265

RESULT 13
A26030
serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - yeast (Saccharomyces cerevisiae)
N; Alternate names: protein YDR477w
C; Species: Saccharomyces cerevisiae
C; Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jul-2004
C; Accession: A26030; S69644
R; Celis, J.B.; Carlson, M.
Science 233, 1175-1180, 1986
A; Title: A yeast gene that is essential for release from glucose repression encodes a protein kinase
A; Reference number: A26030; MUID: 86289463; PMID: 3526554
A; Accession: A26030
A; Molecule type: DNA
A; Residues: 1-633 <CEL>
A; Cross-references: UNIPROT: P06782; EMBL: M13971; NID: g172629; PIDN: AAA35058.1; PID: g172629
R; Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A; Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
A; Reference number: S69554
A; Accession: S69644
A; Molecule type: DNA
A; Residues: 1-633 <DIE>

	Query Match	46.1%	Score 618;	DB 2;	Length 504;
	Best Local Similarity	48.8%;	Pred. No.	1.6e-19;	
	Matches 123; Conservative	45;	Mismatches	82;	Indels 2; Gaps . 2
Oy	1 YEFLETGKGYGVKKVQARE--SSGRIVAITSRKDKIKDEODLLHRIEETIMSSLNPHF	59			
	: : : : : :	:	:	:	:
ph	17 VYVGKTIGHGSGVKVIKAHLITGHKVAKILNRRAKMTDPDVEEKLRKEI KICRLFLVFHPH	76			
	: : : : : :	:	:	:	:

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Query Match      46.0%; Score 617.5; DB 2; Length 798;
Best Local Similarity 48.6%; Pred. NO. 2.4e-19;
Matches 123; Conservative 47; Mismatches 80; Indels 3; Gaps 3
Qy      1 YEFLETLGKGTGYKVKYKKARESSGRL-VAIKIRKDKIKDEODLLHIRREIEMSSLNHPH 59
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      26 YDIERTLGKGNFAVVKLARHRVTQTQVAIKIIDKTRL-DPSNLEKIYREVQIMKLLNHPH 84
Db      26 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      60 IIAIHAEVFNSSKIYIVMEYASRGDLYDIYISERPLSGERDARHFFROIVSALHYCHQNGI 119
Db      60 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      85 IILQYQWETKMLYIVTEFAKNGEMFDHLTNSGHLSESEARKKFWIILSAVEYCHSHHI 149
Db      85 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      120 VHRDLKLENILDANGNIKIADFGLSUNLYHKGFLOTFPGSGPLVASPEIVNGKPYVGPEV 179
Db      120 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      145 VHRDLKTENLLLDANNIKIADFGFGFNFKSGEPLSTWCGSPPYAAPEVFEKGIEYEGPHL 204
Db      145 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      180 DWSLGVLYIIVHGTMPEPDGODHKTLLVKQISNGAYREPPKPSDAC-GLIRLLMLVNPTR 239
Db      180 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      205 DIWSLGVLYIIVCGSLPPDGNLPTLQKRVLEGRFRIYPYFWSDECETLIRRLMLVDPDK 266
Db      205 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      239 RATLEDVASHHWV 251
Db      239 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      265 RITISQIKQKWM 277
Db      265 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: January 22, 2005, 06:43:52
Job time : 16.4548 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:28:10 ; Search time 74.4118 Seconds
(without alignments)
1956.274 Million cell updates/sec

Title: US-09-980-464-11_COPY_57_309

Perfect score: 1342

Sequence: 1 YEFLETGLGKTYGKVKARE.....VNPRTRATLEDVASHVWVNW 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1342	100.0	631	2 Q8C1C0	Q8c1c0 mus musculus
2	1342	100.0	631	2 Q9DBV0	Q9dbv0 m mus muscu
3	1328	99.0	639	2 Q80ZW3	Q80zw3 mus musculus
4	1328	99.0	639	2 Q8BZM4	Q8bzm4 mus musculus
5	1293	96.3	628	2 Q9H093	Q9h093 homo sapien
6	1128.5	84.1	661	1 AKK5 HUMAN	Q60285 homo sapien
7	1128.5	84.1	698	2 BAA25463	Baa25463 homo sapi
8	1025	76.4	575	2 Q616D6	Q616d6 mus musculus
9	824.5	61.4	383	2 Q7QBH4	Q7qbh4 anopheles g
10	822.5	61.3	1180	2 Q7KSS0	Q7kss0 drosophila
11	822.5	61.3	1180	2 Q7YUL9	Q7yul9 drosophila
12	822.5	61.3	1180	2 AAS65135	Aas65135 drosophil
13	822.5	61.3	1427	2 Q9VH05	Q9vh05 drosophila
14	822.5	61.3	1427	2 AAF54517	Aaf54517 drosophil
15	813.5	60.6	1566	2 Q8WQG7	Q8wqg7 caenorhabdi
16	813.5	60.6	1607	2 Q9B1B1	Q9b1b1 caenorhabdi
17	665.5	49.6	752	1 MKK4 HUMAN	Q96134 homo sapien
18	665.5	49.6	752	2 Q8C1P4	Q8c1p4 mus musculus
19	660.5	49.2	752	2 Q8NG37	Q8ng37 homo sapien
20	652.5	48.6	725	2 Q804T2	Q804t2 xenopus lae
21	651.5	48.5	729	2 Q9JKE4	Q9jke4 mus musculus
22	651.5	48.5	744	2 Q9JKE5	Q9jke5 mus musculus
23	650	48.4	712	2 Q7QBH3	Q7qbh3 anopheles g
24	647.5	48.2	691	2 Q96RG0	Q96rg0 homo sapien
25	647.5	48.2	722	2 Q08679	Q08679 rattus norv
26	647.5	48.2	722	2 Q08679	Q08679 rattus norv
27	647.5	48.2	722	2 Q6PDR4	Q6pdr4 mus musculus
28	647.5	48.2	722	2 AAH58556	Aah58556 mus muscu
29	647.5	48.2	755	2 Q15524	Q15524 homo sapien
30	647.5	48.2	778	2 Q7KZ17	Q7kz17 homo sapien
31	647.5	48.2	778	2 Q96HB3	Q96hb3 homo sapien
				2 Aah08771	Aah08771 homo sapi

32 647.5 48.2 797 2 Q8VHF0 Q8vhf0 rattus norv
33 647.5 48.2 888 2 Q8BR95 Q8br95 mus musculus
34 644 48.0 512 2 P92958 P92958 arabidopsis
35 644 48.0 512 2 P92958 P92958 arabidopsis
36 643.5 48.0 722 2 Q802W0 Q802w0 brachydanio
37 642.5 47.9 792 2 Q6INT7 Q6int7 xenopus lae
38 642.5 47.9 792 2 AAH72186 Aah72186 xenopus l
39 642.5 47.9 793 2 Q08678 Q08678 rattus norv
40 642.5 47.9 795 2 Q8VHJ5 Q8vhj5 mus musculus
41 641.5 47.8 776 2 Q7ZYL7 Q7zyl7 xenopus lae
42 641.5 47.8 785 2 Q8QGV3 Q8qgv3 xenopus lae
43 641 47.8 504 2 P93113 P93113 cucumis sat
44 640.5 47.7 462 2 Q75271 Q75271 homo sapien
45 640.5 47.7 542 2 Q6V8Y5 Q6v8y5 physcomitre

ALIGNMENTS

RESULT 1
Q8C1C0 PRELIMINARY; PRT; 631 AA.
AC Q8C1C0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 1200013B22Rik protein.
GN Name=1200013B22Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Atschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.,
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC033302; AAH33302.1; -.
DR HSSP; P31751; IGZK.
DR MGD; MGI:1921387; 1200013B22Rik
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 631 AA; 69745 MW; C6C9042247D9174F CRC64;

Query Match 100.0%; Score 1342; DB 2; Length 631;
 Best Local Similarity 100.0%; Pred. No. 1.2e-97;
 Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEFLETGKGYGVKVKARESSGRLVAIKSRDKIKDEQDLLHRIEIEIMSSLNPHI 60
 Db 57 YEFLETGKGYGVKVKARESSGRLVAIKSRDKIKDEQDLLHRIEIEIMSSLNPHI 116
 Qy 61 IAIHEVFENSKIIVMEYASRGDLVDYISERPLSERDARHFRQIVSALHYCHQNGIV 120
 Db 117 IAIHEVFENSKIIVMEYASRGDLVDYISERPLSERDARHFRQIVSALHYCHQNGIV 176
 Qy 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQIOTFCGSPLYASPEIVNGKPYVGVPEVD 180
 Db 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGFQIOTFCGSPLYASPEIVNGKPYVGVPEVD 236
 Qy 181 SWSLGVLLYLLVHGTMPDGDQDHKTIVKQISNGAYRPPKPSDAGLIRLLMVPNTRRA 240
 Db 237 SWSLGVLLYLLVHGTMPDGDQDHKTIVKQISNGAYRPPKPSDAGLIRLLMVPNTRRA 296
 Qy 241 TLEDVASHWVWVNW 253
 Db 297 TLEDVASHWVWVNW 309

RESULT 2
 Q9DBV0 PRELIMINARY; PRT; 631 AA.
 ID Q9DBV0
 AC Q9DBV0
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
 DE clone:1200013B22 product:weakly similar to PROBABLE SERINE/THREONINE-
 DE PROTEIN KINASE KIAA0537 (EC 2.7.1.-) (Mus musculus adult male cecum
 DE cDNA, RIKEN full-length enriched library, clone:9130215K18
 DE product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE
 DE KIAA0537)
 GN Name=1200013B22Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;

RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RN Nature 420:563-573(2002).
 RL [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Taehiro H., Itoh A.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cecum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK004737; BAB23518.1; -
 DR EMBL; AK033672; BAC28421.1; -
 DR HSSP; P31751; 1GZK.
 DR MGI; MGI:1921387; 1200013B22Rik.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 631 AA; 69806 MW; DSIC042DE6CC174B CRC64;

Query Match 100.0%; Score 1342; DB 2; Length 631;
 Best Local Similarity 100.0%; Pred. No. 1.2e-97;
 Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEFLETGKGYGVKVKARESSGRLVAIKSIRKDKINDEQDLHIREIEMSSLNPHI 60
 DB 57 YEFLETGKGYGVKVKARESSGRLVAIKSIRKDKINDEQDLHIREIEMSSLNPHI 116
 QY 61 IATHEVENSKIVIVMEYASRGDLYDIISERPRLSERDARHFFRQIVSALH 120
 DB 117 IATHEVENSKIVIVMEYASRGDLYDIISERPRLSERDARHFFRQIVSALH 176
 QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPEIVNGKPYVGPEVD 180
 DB 177 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPEIVNGKPYVGPEVD 236
 QY 181 SWSLGLVLLYLVHGTMPFDGQDHKTLLVKQISNGAYRPPKPSDACGLIRLLMVNPTTRA 240
 DB 237 SWSLGLVLLYLVHGTMPFDGQDHKTLLVKQISNGAYRPPKPSDACGLIRLLMVNPTTRA 296
 QY 241 TLEDVASHHWVNW 253
 DB 297 TLEDVASHHWVNW 309

RESULT 3
 Q802W3 PRELIMINARY; PRT; 639 AA.

AC Q802W3
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 1200013B22Rik protein.
 GN Name=1200013B22Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Colling F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinska M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;

Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 EMBL; BC046833; AAH46833.1; --
 HSP; P31751; IGZK.
 DR MGD; MGI:1921387; 1200013B22Rik.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 639 AA; 70675 MW; FB9C40228F53872C CRC64;

Query Match 99.0%; Score 1328; DB 2; Length 639;
 Best Local Similarity 96.9%; Pred. No. 1.6e-96;
 Matches 253; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 YEFLETGKGYGVKVKARESSGRLVAIKSIRKDKINDEQDLHIREIEMSSLNPHI 60
 DB 57 YEFLETGKGYGVKVKARESSGRLVAIKSIRKDKINDEQDLHIREIEMSSLNPHI 116
 QY 61 IATHEVENSKIVIVMEYASRGDLYDIISERPRLSERDARHFFRQIVSALH 112
 DB 117 IATHEVENSKIVIVMEYASRGDLYDIISERPRLSERDARHFFRQIVSALH 176
 QY 113 YCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPEIVNGK 172
 DB 177 YCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLVASPEIVNGK 236
 QY 173 PYVGPEVDSWSLGLVLLYLVHGTMPFDGQDHKTLLVKQISNGAYRPPKPSDACGLIRLL 232
 DB 237 PYVGPEVDSWSLGLVLLYLVHGTMPFDGQDHKTLLVKQISNGAYRPPKPSDACGLIRLL 296
 QY 233 MVNPTTRATLEDVASHHWVNW 253
 DB 297 MVNPTTRATLEDVASHHWVNW 317

RESULT 4
 Q8B2N4 PRELIMINARY; PRT; 639 AA.

AC Q8B2N4
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male dienecephalon cDNA, RIKEN full-length enriched
 DE library, clone:9310154N24 product:weakly similar to PROBABLE
 DE SRINE/THRONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-).
 GN Name=1200013B22Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=2049374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hirozane T.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa K., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Iihikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK034082; BAC28575.1; -;
 DR HSP; P31751; IGZK.
 DR MGD; MG1:1921387; 1200013B22R1K.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 639 AA; 70632 MW; FB98EE915C95FA5D CRC64;

Query Match 99.0%; Score 1328; DB 2; Length 639;
 Best Local Similarity 96.9%; Pred. No. 1.6e-96;
 Matches 253; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 YEFLETGKGTGKVKVKARESSRLVAIKSIRKDKIKDQDILHRRREIEIMSSLNPHI 60
 DB 57 YEFLETGKGTGKVKVKARESSRLVAIKSIRKDKIKDQDILHRRREIEIMSSLNPHI 116
 QY 61 IAIHE-----VPENSSKIVIVMEYASRGDLVDYISERPRLSERDARHFRQIVSALH 112
 DB 117 IAIHEVGRSLVTVFENSSKIVIVMEYASRGDLVDYISERPRLSERDARHFRQIVSALH 176
 QY 113 YCHQNGIVHRDLKLENILLDANGNIKIAIDFGLSNLYHKGFLOTFGSGPLYASPEIVNGK 172
 DB 177 YCHQNGIVHRDLKLENILLDANGNIKIAIDFGLSNLYHKGFLOTFGSGPLYASPEIVNGK 236
 QY 173 PYVGPEVDSWLSGLVLLIYVHGTMPPDGDHDKTLVKQISNGAYREPDKPSDAGLLRWLL 232
 DB 237 PYVGPEVDSWLSGLVLLIYVHGTMPPDGDHDKTLVKQISNGAYREPDKPSDAGLLRWLL 296
 QY 233 MVNPTRRATLEDVASHWVNW 253
 DB 297 MVNPTRRATLEDVASHWVNW 317
 RESULT 5
 Q9H093 PRELIMINARY; PRT; 628 AA.
 AC Q9H093;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKF2p34J0337 (Hypothetical protein SNARK)
 DE (Hypothetical protein FLJ90349).
 GN Name=DKF2p34J0337; Synonym=SNARK;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Koehler K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feingold J., Helton E., Kettman M., Madao A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small U., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Oka T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwavanagi T., Ninomiya K.,
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AL136891; CAB6825.1; -;
 DR EMBL; BC017306; AAH17306.1; -;
 DR EMBL; AK074830; BAC11234.1; -;
 DR HSSP; P31751; IGZK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot.kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot.kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Hypothetical protein; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 628 AA; 69611 MW; F76F8B1BF94F4C87 CRC64;
 Query Match 96.3%; Score 1293; DB 2; Length 628;
 Best Local Similarity 95.7%; Pred. No. 9.3e-94;
 Matches 242; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YEFLETGKGYGVKKARESSGRVVAIKSRKDKIKDEQDLHRIEIMSSLNHPH 60
 DB 53 YEFLETGKGYGVKKARESSGRVVAIKSRKDKIKDEQDLHRIEIMSSLNHPH 112
 QY 61 IAIHEVFENSSKIVIMEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHQNGIV 120
 DB 113 IAIHEVFENSSKIVIMEYASRGDLYDIYSERQQLSREARHFRQIVSAVHYCHQNRV 172
 QY 121 HRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPEVD 180
 DB 173 HRDLKLENILLDANGNIKIADFGLSNLYHQKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232
 QY 181 SWSLGLVLLYLIVHGTMPDGDQDHTLVKQISNGAYREPPKPSDAGLIRLWLLMVPTRRA 240
 DB 233 SWSLGLVLLYLIVHGTMPDGDHDKILVKQISNGAYREPPKPSDAGLIRLWLLMVPTRRA 292
 QY 241 TLEDVASHWWVNW 253
 DB 293 TLEDVASHWWVNW 305
 RESULT 6
 ID ARKS HUMAN STANDARD; PRT; 661 AA.
 AC O60285;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE AMPK-related protein kinase 5 (EC 2.7.1.37).
 GN Name=ARK5; Synonyms=KIAA0537;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can
 code for large proteins in vitro.";
 DNA Res. 5:31-39(1998).
 (2)
 RP CHARACTERIZATION, AND MUTAGENESIS OF SER-600.
 RX MEDLINE=22393479; PubMed=12409306; DOI=10.1074/jbc.M206025200;
 RA Suzuki A., Kusakai G.-I., Kishimoto A., Lu J., Ogura T., Lavin M.F.,
 RA Esumi H.;
 RT "Identification of a novel protein kinase mediating Akt survival
 signaling to the ATM protein.";
 RL J. Biol. Chem. 278:48-53(2003).
 CC -!- FUNCTION: Involved in tolerance to glucose starvation.
 CC Phosphorylates ATM.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- ENZYME REGULATION: Activated by PKB/AKT1 during glucose
 starvation.
 CC -!- TISSUE SPECIFICITY: Expressed at high levels in heart and brain,
 and at lower levels in skeletal muscle, kidney, ovary, placenta,
 lung and liver.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; AB011109; BAA25463.1; -;
 DR HSSP; P31751; IGZK.
 DR MIW; 608130; -;
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR00719; Prot.kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot.kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Phosphorylation; Polymorphism;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 55 306
 FT NP_BIND 61 69 ATP (By similarity).
 FT ACT_SITE 178 178 Proton acceptor (By similarity).
 FT BINDING 84 84 ATP (By similarity).
 FT MOD_RES 600 600 Phosphoserine (by PKB/AKT1).
 FT VARIANT 543 543 P -> R (in dbSNP:3741883).
 FT FTID=VAR_017246.
 FT MUTAGEN 600 600 S->A: No phosphorylation.
 SQ SEQUENCE 661 AA; 74304 MW; 806F37D52CA4718F CRC64;
 Query Match 84.1%; Score 1128.5; DB 1; Length 661;
 Best Local Similarity 82.3%; Pred. No. 1e-80;
 Matches 209; Conservative 24; Mismatches 20; Indels 1; Gaps 1;
 QY 1 YEFLETGKGYGVKKARESSGRVVAIKSRKDKIKDEQDLHRIEIMSSLNHPH 59
 DB 55 YEFLETGKGYGVKKARESSGRVVAIKSRKDKIKDEQDLHRIEIMSSLNHPH 114
 QY 60 IAIHEVFENSSKIVIMEYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHQNGI 119
 DB 115 IISIEYFENKDKIIVIMEYASRGDLYDIYSERRLSERETRHFRQIVSAVHYCHQNGV 174
 QY 120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPEV 179
 DB 175 VHRDLKLENILLDANGNIKIADFGLSNLYKQKFLQTFCGSPLYASPEIVNGRYPGPEV 234
 QY 180 DSWSLGLVLLYLIVHGTMPDGDQDHTLVKQISNGAYREPPKPSDAGLIRLWLLMVPTRR 239
 DB 235 DSWALGLVLLYLIVGTMPDGDHDKILVKQISNGAYREPPKPSDAGLIRLWLLMVPDRR 294
 QY 240 ATLEDVASHWWVNW 253

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk K.S.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatic
RT genome perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003686; AAG65135.1; -
SQ SEQUENCE 1180 AA; 127743 MW; A88A012664046EC6 CRC64;

Query Match 61.3%; Score 822.5; DB 2; Length 1180;
Best Local Similarity 61.7%; Pred. No. 3.3e-56;
Matches 156; Conservative 44; Mismatches 52; Indels 1; Gaps 1;

Qy 1 YEFLETGKGYGVKKKA-RESSGRVLAISKDKIKQEDLLHIREIEMSLNHPH 59
Db 70 FDIITKLGQGYGVKQVGINKETQGEVAIKTKCKIEADLVIRREVOIMSSVHPN 129
Qy 60 IIAIHEVFENSSKIVIMEYASRGDLYDYISERPRLSERDARHPFRQIVSALHYCHONGI 119
Db 130 IIAIHEVFENREKVMWFEAAGELYDYLSERKVLTEEEARRIFRQVATVYCHHKI 189
Qy 120 VHRDLKLENILLDANGNIKIAIDFGLSNLYHKGKFLQTFCSPLYSPEIYNGKPYGVPEV 179
Db 190 CHRDLEKLENILLDEKNAKIADFGLSNVDFDQRLGTFCSPLYSPEIYNGKPYGVPEV 249
Qy 180 DWSISGLVLLYTLVHGTWPFQGDHKTIVKQISNGAYEPKPSDACGLIRWLLMVNTRR 239
Db 250 DCWSISGLVLLYTLVGSMPFGSNGPKRLVKQISQGDYEPKPSRASTLIRDMTLTVCPKRK 309

Qy 240 ATLEDVASHWVNV 252
Db 310 ASIEQICSHWVNV 322

RESULT 13
QyVH05
ID Q9VH05 PRELIMINARY; PRT; 1427 AA.
AC Q9VH05; Q9VH04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE CG11870-PA (TrEMBLrel. 26, Last annotation update)
OS ORFNames=CG11870;
GN *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Jbergway C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]

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RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaninker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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[6]
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DR InAct; Q9VH05; --
DR FlyBase; FBgn0037804; CG11870.
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DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IP0011009; Kinase like.
DR InterPro; IP000719; Prot_kinase.
DR InterPro; IP0002290; Ser_thr_kinase.
DR InterPro; IP0008271; Ser_thr_kinase.
DR Pfam; PF000069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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QY 240 ATLEDVASHHWN 252
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AC AAF54517;
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DT 01-APR-2004 (TREMBLrel. 27, Last sequence update)
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GN CG11870.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hestlin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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RA Yen R.F., Zaveri J.S., Zhao M., Zhang Q., Zhou Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
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RP SEQUENCE FROM N.A.
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RA Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Ashburner M., Myers S.E., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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RP SEQUENCE FROM N.A.
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
11866.113 Million cell updates/sec

Title: US-09-980-464-4_COPY_123_2015

Perfect score: 1893

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1773	93.7	1896	9 AY399041	AY399041 Mus muscu
5	1261	66.6	1887	9 AY399039	AY399039 Homo sapi
6	948.4	50.1	1887	9 AY399040	AY399040 Pan trogl
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ALIGNMENTS

RESULT 1	AK004737	2899 bp	linear	HTC 03-APR-2004
LOCUS	AK004737	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200013B22 product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.1-) [Homo sapiens], full insert sequence.	mrna	
DEFINITION	AK004737	GI:26334437		
ACCESSION	AK004737	HTC; CAP trapper.		
VERSION	AK004737.2	Mus musculus (house mouse)		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus			
ORGANISM	Mus musculus			
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci,P. and Hayashizaki,Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
REFERENCE	5			

AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL REFERENCE
Nature 420, 563-573 (2002)

AUTHORS
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
On Dec 10, 2002 this sequence version replaced gi:12836134. Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

FEATURES
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTNN 3'], cDNA was prepared by using tricholase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGATCCAGAGCTCAATTAAATTAATTAACCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOUR.

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94. 1989

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DB 394 ATACGAGGAGAGATTCAGATCATGTCTCACTCAACACACCCACATCATTTGCCATCCAT 453
QY 361 GAAAGTGTTCAGAAATAGCAGCAAGATTGTGATGTGTCAGTATGTCAGCGAGGCGAT 420
DB 454 GAAAGTGTTCAGAAATAGCAGCAAGATTGTGATGTGTCAGTATGTCAGCGAGGCGAT 513
QY 421 CTGTATGATTACATCAGTAGCGGCCACCGCTGAGTGAGCGGACCGCAGGCAATTTCTTC 480
DB 514 CTGTATGATTACATCAGTAGCGGCCACCGCTGAGTGAGCGGACCGCAGGCAATTTCTTC 573
QY 481 CGACAGATCGTGTCTCCCTGCACTACTGCACAGAAAGGGATCGTTTACCCAGATCTC 540
DB 574 CGACAGATCGTGTCTCCCTGCACTACTGCACAGAAAGGGATCGTTTACCCAGATCTC 633
QY 541 AAGCTGGAAAAACATCTCTTAGATGCCAATGGAAACATCAAGATTCGTGATTTGGCCTC 600
DB 634 AAGCTGGAAAAACATCTCTTAGATGCCAATGGAAACATCAAGATTCGTGATTTGGCCTC 693
QY 601 TCCAACTGTACCAAAAGCAAGTTCTCTCAGACGTTCTGTGGGAGCCCTCTCTAGGCC 660
DB 694 TCCAACTGTACCAAAAGCAAGTTCTCTCAGACGTTCTGTGGGAGCCCTCTCTAGGCC 753
QY 661 TCGCTTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGAGTGAGCAGCTGCTCTCTG 720
DB 754 TCGCTTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGAGTGAGCAGCTGCTCTCTG 813
QY 721 GCGTTCTCTCTGATCCTCTGTCATGTCATGCCATCCCTTTTTCACCGGAGGATCATATA 780
DB 814 GCGTTCTCTCTGATCCTCTGTCATGTCATGCCATCCCTTTTTCACCGGAGGATCATATA 873
QY 781 ACACCTGTCAGCAAAATCAGTAACGGGGCTTACCGTGAGCGCCCAAGCGCTCCGATGCC 840
DB 874 ACACCTGTCAGCAAAATCAGTAACGGGGCTTACCGTGAGCGCCCAAGCGCTCCGATGCC 933
QY 841 TGTGGCTCATTCGGTGGCTGTTTAAATGGTGAACCCCAACCCCGTCGGGCCCACTCTGGAGGAT 900
DB 934 TGTGGCTCATTCGGTGGCTGTTTAAATGGTGAACCCCAACCCCGTCGGGCCCACTCTGGAGGAT 993
QY 901 GTAGCCAGTCATTGTTGGGTCAATCGGGGTTACACACCGGAGTCGGGGAAACAGGAAGCC 960
DB 994 GTAGCCAGTCATTGTTGGGTCAATCGGGGTTACACACCGGAGTCGGGGAAACAGGAAGCC 1053

Qy	961	CTGCGTGAAGGAGTGGACACCTTAGTGTGACATTTGGCCGGGCTCCATGGCGAGCTGTTA	1020
Db	1054	CTGCGTGAAGGAGTGGACACCTTAGTGTGACATTTGGCCGGGCTCCATGGCGAGCTGTTA	1113
Qy	1021	CGTGCCTCTCGGCCCTCTCTGGAGAAATGGAGCCAAAGTGTGACGCTTCTTCAAGCAG	1080
Db	1114	CGTGCCTCTCTCGGCCCTCTCTGGAGAAATGGAGCCAAAGTGTGACGCTTCTTCAAGCAG	1173
Qy	1081	CACGTGCGGAGGTGAAGCAGTGTACCTGGGCTGGAGCGGCAACATCTCTTAAAGAAG	1140
Db	1174	CACGTGCGGAGGTGAAGCAGTGTACCTGGGCTGGAGCGGCAACATCTCTTAAAGAAG	1233
Qy	1141	TCCGAAAGGAGATGATGGCTCAAAATCTCAAGGTGACCCGGCTGAGGATACCTCT	1200
Db	1234	TCCGAAAGGAGATGATGGCTCAAAATCTCAAGGTGACCCGGCTGAGGATACCTCT	1293
Qy	1201	TCTGCCCTTGGCAGAGCAGCTTAACTTCGGAAGGCAATCTCAAGAAAGTCTCTCT	1260
Db	1294	TCTGCCCTTGGCAGAGCAGCTTAACTTCGGAAGGCAATCTCAAGAAAGTCTCTCT	1353
Qy	1261	ACCTCGTCAGGGAGGTACAGGAGACCTCAGGAATCAGACCGGTGCTGATCTCCA	1320
Db	1354	ACCTCGTCAGGGAGGTACAGGAGACCTCAGGAATCAGACCGGTGCTGATCTCCA	1413
Qy	1321	GGGAGCCTGTCTCTGTATCTCTCCCAAGGAAAGGCATCTTAAAGAGTCTCGA	1380
Db	1414	GGGAGCCTGTCTCTGTATCTCTCCCAAGGAAAGGCATCTTAAAGAGTCTCGA	1473
Qy	1381	CAGGTGAATCTGTGTTACTCTCTCAGAGCCAGCAGTCTGGGAACTCTTAGAC	1440
Db	1474	CAGGTGAATCTGTGTTACTCTCTCAGAGCCAGCAGTCTGGGAACTCTTAGAC	1533
Qy	1441	GCAGTGTATGTTGTGAGTGGGACCCGTCGAGCAGAGTCTCCACAGGCTTCAGGG	1500
Db	1534	GCAGTGTATGTTGTGAGTGGGACCCGTCGAGCAGAGTCTCCACAGGCTTCAGGG	1593
Qy	1501	CTCTCTCTCCACGCAAGGCGATTTCTCAAACTCAATGGCAAGTTCTCCGACAGCCTTA	1560
Db	1594	CTCTCTCTCCACGCAAGGCGATTTCTCAAACTCAATGGCAAGTTCTCCGACAGCCTTA	1653
Qy	1561	GAGGCACTACCTTAGCAGCTTTGGCTCCCTGGAGCAACCTGGCTCTCCCATCTCGCA	1620
Db	1654	GAGGCACTACCTTAGCAGCTTTGGCTCCCTGGAGCAACCTGGCTCTCCCATCTCGCA	1713
Qy	1621	GCCGGCCAGCCGCCCTCAGGGGCTGTGAGTGAGCAGCATCTCTGCTCCGAGTCC	1680
Db	1714	GCCGGCCAGCCGCCCTCAGGGGCTGTGAGTGAGCAGCATCTCTGCTCCGAGTCC	1773
Qy	1681	TTTGACCAATTGGACTTGGCTGAACGCTTTTCCCGAAACCCCACTGAGGGGCTGTGTCT	1740
Db	1774	TTTGACCAATTGGACTTGGCTGAACGCTTTTCCCGAAACCCCACTGAGGGGCTGTGTCT	1833
Qy	1741	GTGACAACTGAGGGGCTTGGAGCAGCTTCCCTCAGAAAGTCTGAAGCGATGTGGCAG	1800
Db	1834	GTGACAACTGAGGGGCTTGGAGCAGCTTCCCTCAGAAAGTCTGAAGCGATGTGGCAG	1893
Qy	1801	GAATCTTGGGGATAGCTCTTTCTCTGACAGCTGCCAAGAGGTGACTGCGAGCCTAC	1860
Db	1894	GAATCTTGGGGATAGCTCTTTCTCTGACAGCTGCCAAGAGGTGACTGCGAGCCTAC	1953
Qy	1861	AGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC	1893
Db	1954	AGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC	1986

RESULT 2

AK033672
LOCUS
DEFINITION
Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130215K18 product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) [Homo sapiens], full insert sequence.

ACCESSION

AK033672.1 GI:26329364

VERSION

HTC: CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

AUTHORS

TITLE
High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

20499374

PUBMED

11042159

REFERENCE

3

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

REFERENCE

4

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE

Functional annotation of a full-length mouse cDNA collection

JOURNAL

Nature 409, 685-690 (2001)

REFERENCE

5

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

REFERENCE

6

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

Direct Submission

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ac.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/

QY	1561	GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCTCCCTCCCTGCA	1620
Db	1653	GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCTCCCTCCCTGCA	1712
QY	1621	GCCCGGCCAGCCGCCCTCAGGGCTGTGAGTGAGGACAGCATCTGTCTCGAGTCC	1680
Db	1713	GCCCGGCCAGCCGCCCTCAGGGCTGTGAGTGAGGACAGCATCTGTCTCGAGTCC	1772
QY	1681	TTTGACCAATTGGACTTGGCTGAACGCTTCCCGAAACCCACTGAGGGCTGTGTCTCT	1740
Db	1773	TTTGACCAATTGGACTTGGCTGAACGCTTCCCGAAACCCACTGAGGGCTGTGTCTCT	1832
QY	1741	GTGGACAACCTGAGGGGCTTGAGCAGCCTCCCTCAGAAGGCTCTGAAGCGATGTCGAC	1800
Db	1833	GTGGACAACCTGAGGGGCTTGAGCAGCCTCCCTCAGAAGGCTCTGAAGCGATGTCGAC	1892
QY	1801	GAATCTTGGGGGATAGCTCTTTCTCTGACAGATGCGCAAGAGTGACTGCGAGCCTAC	1860
Db	1893	GAATCTTGGGGGATAGCTCTTTCTCTGACAGATGCGCAAGAGTGACTGCGAGCCTAC	1952
QY	1861	AGACAAGCCCTAGGAATCTCTCAAAGCTCAGC	1893
Db	1953	AGACAAGCCCTAGGAATCTCTCAAAGCTCAGC	1985
RESULT 3			
LOCUS	AK034082		
DEFINITION	Mus musculus adult male diencephalon cDNA, RIKEN full-length		
	enriched library, clone:9330154N24 product:weakly similar to		
	PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-)		
	[Homo sapiens], full insert sequence.		
ACCESSION	AK034082		
VERSION	AK034082.1	GI:26329672	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	1		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
	Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,		
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
	Yamanoto, R., Matsumoto, H., Sakeguchi, S., Ikegami, T., Kashiwagi, K.,		
	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,		
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
	sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the		
	FANTOM Consortium		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		

AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2869)
AUTHORS	Adachi, J., Aizawa, K., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@res.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
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	/mol_type="mRNA"
	/strain="C57BL/6J"
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	/db_xref="taxon:10090"
	/clone="9330154N24"
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	/dev_stage="adult"
	98. .2017
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	/db_xref="GI:26329673"
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ORIGIN	
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QY	1 ATGGAGTCGTGGCCTTACTCCAGCCCGAGCAGGCTCCCTCGGCTCCGCCCTGGCC 60

Db	98	ATCGAGTCGGGGCTTTACTCCAGCGCCCGAGCCAGGCTCCCTCGGCTCCGCGCTGGCC	157
Qy	61	TCGAGAGCGCCGGCGCTGGCGGACGGGCTCATCAAGTCGCTTAAACCTCTGATGAAG	120
Db	158	TCGAGAGCGCCCGCGCGCTGGCGGACGGGCTCATCAAGTCGCTTAAACCTCTGATGAAG	217
Qy	121	AAGCAGCGGTGAAGCGGCACCATCAAAACAAACACCACTCGCGCACCGCTACGAGTTCCCTG	180
Db	218	AAGCAGCGGTGAAGCGGCACCATCAAAACAAACACCACTCGCGCACCGCTACGAGTTCCCTG	277
Qy	181	GAGACGCTGGCAAGGGGCACCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGCGT	240
Db	278	GAGACGCTGGCAAGGGGCACCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGCGT	337
Qy	241	CTGTGGCCATCAAGTCATCAGAGAAAGACAAATCAAGATGAGCAGGATCTGCTGCAC	300
Db	338	CTGTGGCCATCAAGTCATCAGAGAAAGACAAATCAAGATGAGCAGGATCTGCTGCAC	397
Qy	301	ATACGGAGGGAGATTGAGATCATCTCTTCACTCAACCAACCCACATCATTTGCCATCCAT	360
Db	398	ATACGGAGGGAGATTGAGATCATCTCTTCACTCAACCAACCCACATCATTTGCCATCCAT	457
Qy	361	GA-----GTGTTTGAGAAATAGCAACAAGATTGTAATGTC	396
Db	458	GAAGTGGGCAGATCACGCTTAGTGACTGTGTTTGAGAAATAGCAGCAAGATTGTAATGTC	517
Qy	397	ATGAGATATGCACGCGAGGGCGATCTGTATGATTTACATCATGAGCGCGCACGGCTGAGT	456
Db	518	ATGAGATATGCACGCGAGGGCGATCTGTATGATTTACATCATGAGCGCGCACGGCTGAGT	577
Qy	457	GAGCGGAGCGCAGGCATTTCTCCGACAGATCGTGTCTGCCCTGCACTACTGCGCACCG	516
Db	578	GAGCGGAGCGCAGGCATTTCTCCGACAGATCGTGTCTGCCCTGCACTACTGCGCACCG	637
Qy	517	AACGGGATCGTTTCAACCGAGATCTCAAGCTGGAACACATCTTCTAGATGCCAATGGAAC	576
Db	638	AACGGGATCGTTTCAACCGAGATCTCAAGCTGGAACACATCTTCTAGATGCCAATGGAAC	697
Qy	577	ATCAAGATTGCTGACTTTGGCTCTCACAACCTGTACCAAGGCAAGTTCTCCAGACG	636
Db	698	ATCAAGATTGCTGACTTTGGCTCTCACAACCTGTACCAAGGCAAGTTCTCCAGACG	757
Qy	637	TTCTGTGGAGCCCTCTCTACGCTCGCTCAGATAGTCAACGGGAAGCCCTATGTGGC	696
Db	758	TTCTGTGGAGCCCTCTCTACGCTCGCTCAGATAGTCAACGGGAAGCCCTATGTGGC	817
Qy	697	CCAGAGTGGACAGCTGGTCTCTGGGCGCTTCTCTGTATCACTCTGGTGCATGGCACCATG	756
Db	818	CCAGAGTGGACAGCTGGTCTCTGGGCGCTTCTCTGTATCACTCTGGTGCATGGCACCATG	877
Qy	757	CCCTTTGACGGGCGAGATCAATAAACATCTGTGTAAGCAATCAGTAACGGGCTTACCGT	816
Db	878	CCCTTTGACGGGCGAGATCAATAAACATCTGTGTAAGCAATCAGTAACGGGCTTACCGT	937
Qy	817	GAGCGCCCAAGCCGTCGATCGCTGTGCGCTGTATCGGTGCGCTGTTAAATGGTGAACCC	876
Db	938	GAGCGCCCAAGCCGTCGATCGCTGTGCGCTGTATCGGTGCGCTGTTAAATGGTGAACCC	997
Qy	877	ACCCGTCGGGCCACACTGGAGGATAGCCAGTCAATTGGTGGGTCAACTGGGGTTACCC	936
Db	998	ACCCGTCGGGCCACACTGGAGGATAGCCAGTCAATTGGTGGGTCAACTGGGGTTACCC	1057
Qy	937	ACCGAGTGGGGAAACAGAAAGCCCTCGTGAGGCTGGGCAACCTAGTGGTACTTTGGC	996
Db	1058	ACCGAGTGGGGAAACAGAAAGCCCTCGTGAGGCTGGGCAACCTAGTGGTACTTTGGC	1117
Qy	997	CGGGCTCATGCGCGACTGGTTACGTCTCTCGGCCCTCTCTCGGAGAAATGGAGCC	1056
Db	1118	CGGGCTCATGCGCGACTGGTTACGTCTCTCGGCCCTCTCTCGGAGAAATGGAGCC	1177
Qy	1057	AAGGTTGTCAGCTTCTTCAAGCAGCACGTGCGGAGGTGGAAGCACTGTACTCTGGGCTG	1116

Db	1178	AAAGTGTGCAGCTTCTTCAAGCAGCAGCTGCCGGGAGGTGGAAAGCACTGTACTCTGGGCTG	1233
Qy	1117	GAGCGGCAACATTTCTTTAAGAAAGTCCGAAAGAGAAATGACATGGCTCAAAATCTGCAA	1176
Db	1238	GAGGGGCAATTTCTTTAAGAAAGTCCGAAAGAGAAATGACATGGCTCAAAATCTGCAA	1297
Qy	1177	GGTGACCCGGCTGAGGATACCTTTCTCGCCCTGGCAAGAGAGCCTTTAAGCTTCCGAAA	1236
Db	1298	GGTGACCCGGCTGAGGATACCTTTCTCGCCCTGGCAAGAGAGCCTTTAAGCTTCCGAAA	1357
Qy	1237	GGCAATTTCTCAAGAAAGTCCCTACTCTCTCAGGGGAGGTACAGGAGGACCCCTCAGGAA	1296
Db	1358	GGCAATTTCTCAAGAAAGTCCCTACTCTCTCAGGGGAGGTACAGGAGGACCCCTCAGGAA	1417
Qy	1297	CTCAGACCGGTGCTGATCTACTCCAGGGCAGCCTGTCCCTCTGTATCCCTGCTCCCAAGG	1356
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Qy	1357	AAAGGCATCCTTTAAGAAAGTCTCGACAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCC	1416
Db	1478	AAAGGCATCCTTTAAGAAAGTCTCGACAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCC	1537
Qy	1417	AGCGAGTCTGGGAACTCTTAGAGCGCCAGTGAATGTTGTGTAGTGGGGACCCCGTGGAG	1476
Db	1538	AGCGAGTCTGGGAACTCTTAGAGCGCCAGTGAATGTTGTGTAGTGGGGACCCCGTGGAG	1597
Qy	1477	CAGAAGTCTCCACAGGCTTCAGGGCTCCTCTCCACCGCAAGGGCATTCTCAAACTCAAT	1536
Db	1598	CAGAAGTCTCCACAGGCTTCAGGGCTCCTCTCCACCGCAAGGGCATTCTCAAACTCAAT	1657
Qy	1537	GGCAAGTCTCCCGCACAGCTTTAGAGGCGACTACCCCTAGCAGCCTTTGGCTCCCTGGAC	1596
Db	1658	GGCAAGTCTCCCGCACAGCTTTAGAGGCGACTACCCCTAGCAGCCTTTGGCTCCCTGGAC	1717
Qy	1597	CAACTGGCTCCTCCCATCTCTGACGCCGGGCCACAGCCGCCCTCAGGGGCTGTGAGTGAG	1656
Db	1718	CAACTGGCTCCTCCCATCTCTGACGCCGGGCCACAGCCGCCCTCAGGGGCTGTGAGTGAG	1777
Qy	1657	GACAGCATCTGTCTCCGAGTCTCTTGAACCAATTTGAGTCTGAACTCTTCCCGGAA	1716
Db	1778	GACAGCATCTGTCTCCGAGTCTCTTGAACCAATTTGAGTCTGAACTCTTCCCGGAA	1837
Qy	1717	ACCCCACTGAGGGGCTGTGTCTGTGCGACAACTGAGGGGGCTTGAGCAGCCCTCCCTCA	1776
Db	1838	ACCCCACTGAGGGGCTGTGTCTGTGCGACAACTGAGGGGGCTTGAGCAGCCCTCCCTCA	1897
Qy	1777	GAAGGTCTGAAGCGATGGTGCAGGAATCTCTTGGGGATAGTCTCTTTCTGACAGAC	1836
Db	1898	GAAGGTCTGAAGCGATGGTGCAGGAATCTCTTGGGGATAGTCTCTTTCTGACAGAC	1957
Qy	1837	TGCCAAGAGGTGACTGCAGCCTACAGACAGCCCTAGGATCTGCTCAAGCTCAGC	1893
Db	1958	TGCCAAGAGGTGACTGCAGCCTACAGACAGCCCTAGGATCTGCTCAAACTCAGC	2014

RESULT 4
AV399041

A1393041
 LOCUS
 DEFINITION

STAFFING

ACCESSION

VERSION
KEYWORDS

KEYWORDS
SOURCE

SOURCE
ORGANISMS

11

REFERENCES

AUTHORS

Gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1896)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1896
/organism="Mus musculus"
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Best Local Similarity 93.7%; Pred. No. 0;
Matches 1773; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
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DB 121 AAGCAGCGGTGAAGCGGACCATCAAAACACAACTCGGCGACCGCTACGAGTTCCTG 180
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QY 661 TCCCTGAGATAGTCAACGGAAGCCCTATGTGGGCCGAGAGTGGACAGCTGCTCTG 720
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DB 1441 GCCAGT 1500
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QY 1861 AGACAAGCCCTAGGAATCTGCTCAAAAGCTCAGC 1893
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DEFINITION Homo sapiens HCM0091 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY399039
VERSION AY399039.1 GI:39755028
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1887)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1887)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1887
/organism="Homo sapiens"
/mol_type="genomic DNA"
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<1..>1887
/locus_tag="HCM0091"
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ORIGIN
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Best Local Similarity 78.4%; Pred. No. 0;
Matches 1458; Conservative 0; Mismatches 380; Indels 21; Gaps 2;

QY 47 CCTCCGCGCTGGCTCGAGAGCGCCGCGCTGGCGGACGGCTCATCAAGTCGCTA 106
Db 35 CCATCCCTCGGCGCAGAGCTAGCCCGCGCTGGCGGAGGGCTGATCAAGTCGCCA 94

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Db 95 AGCCCTTAATGAAGACGCGGTGAAGCGGACCATCAACAACAACTGGGCGACC 154

QY 167 GTACAGAGTTCTGGAGACGCTGGGCAAGGSCACTACGGGAAGGTGAAGAGCGACG 226
Db 155 GCTACAGAGTTCTGGAGACCTGGGCAAGGSCACTACGGGAAGGTGAAGAGCGCGG 214

QY 227 AGAGCTCGGCGCTGCTGGTGGCCATCAAGTCCATCAGAAAGACAAAATCAAGATGAGC 286
Db 215 AGAGCTCGGCGCGCTGCTGGTGGCCATCAAGTCCATCAGAAAGACAAAATCAAGATGAGC 274

QY 287 AGGATCTGCTGCATACGAGGAGATGAGATCATGCTTCACTCAACACCCCCACA 346
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QY 407 CCAGCGGAGCGGATCTGTATGATTACATCAGTGAAGCGGCACGGCTGTGAGTGAAGCGGAGC 466
Db 395 CCAGCGGAGCGGACCTTTATGACTACATCAGCGGAGCGGACGAGCTCACTGAGCGCGGAAG 454

QY 467 CCAGGCAATTTCTCCGACAGATCGTGTGCGCTGCACCTACTGCCACACAGAGCGGATCG 526
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QY 647 GCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGAGTGG 706
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QY 827 AGCCGTCCTGATGCTGTGCGCTGATCCGCTGGCTGTAAATGGTGAACCCACCCCGCTGGG 886
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QY 887 CCACACTGGAGGATGTAGCAGTCAATTTGGTGGTCAACTGGGTTTACACACCGAGTGC 946
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QY 1127 ATTCTCTTAAGAGTCCGAAAGAGATCAGATGCTCAAAATCTGCAAGTGTACCCGG 1186
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 Db 718 GGCATTCTC 726
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 IMAGE:30665389 5', mRNA sequence.

CO424322
 CO424322.1 GI:49670481
 EST.
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS
 TITLE NIH-MGC http://mgc.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.
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 /note="Organ: Eye; Vector: pYX-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AATTAATACG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH)."

Query Match 35.5%; Score 672; DB 7; Length 672;
 Best Local Similarity 100.0%; Pred. No. 3e-164;
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RESULT 9

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CK781308 655 bp mRNA linear EST 23-FEB-2004
 UI-M-GIO-clp-g-23-0-UI.r1 NIH_BMAP_G10 Mus musculus cDNA clone
 IMAGE:30619078 5', mRNA sequence.

CK781308

CK781308.1 GI:42746986

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 655)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
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/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 34.5%; Score 652.4; DB 7; Length 655;
Best Local Similarity 99.7%; Pred. No. 4e-159;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1114 CTGGAGCGGCAACATTTCTTTAAGAGTCCCGAAGAGAGATGACATGGCTCAAAATCTG 1173
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QY 1174 CAGGTGACCGGCTGAGGATACCTTCTTCGCCCTGCCAGAGCAGCTTAAGCTTCCG 1233
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QY 1294 GAACTCAGACCGGTGCCTGATACCTCAGGAGCAGCTGCTCCCTGCTGTATCCTGTCCCA 1353
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QY 1354 AGGAAAGGATCTTAAAGAGTCTCGACAGCTGATCTGTTACTCTCTCTCCAGAG 1413
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QY 1534 AATGCCAAGTTCTCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTG 1593
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QY 1594 GACCAACTGGGCTCTCCCATCTCTCAGCCCGGCCAGCCGCCCTCAGGGGCTGTGAGT 1653
DB 541 GACCAACTGGGCTCTCTCNCATCTCTCAGCCCGGCCAGCCGCCCTCAGGGGCTGTGAGT 600

QY 1654 GAGGACAGCATCTCTCTCTCCGAGTCTCTTGACCAATTTGGACTTCCTGGAAGTCT 1708
DB 601 GAGGACAGCATCTCTCTCTCCGAGTCTCTTGACCAATTTGGACTTCCTGGAAGTCT 655

RESULT 10

BG174288
LOCUS
DEFINITION
602334589F1 NCI_COAP_Mam1 Mus musculus cDNA clone IMAGE:4457398 5',
mRNA sequence.

ACCESSION
BG174288

VERSION
BG174288.1 GI:12680591

KEYWORDS
EST.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
1 (bases 1 to 805)
NIH-MGC http://mgs.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE
Unpublished (1999)

JOURNAL
Contact: Robert Strausberg, Ph.D.

COMMENT
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLNL0254 row: b column: 23

High quality sequence stop: 704.

Location/Qualifiers
1. .805
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/clone_lib="NCI CGAP Mam1"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

FEATURES

source

ORIGIN

Query Match 34.4%; Score 651.6; DB 4; Length 805;
Best Local Similarity 96.6%; Pred. No. 6.9e-159;
Matches 709; Conservative 0; Mismatches 19; Indels 6; Gaps 4;

QY 379 AGCAAGATTGTGATTTGTCTGAGTATGCCAGCGGCGCATCTGTATGATTACATCAGT 438
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QY 439 GAGCGGCGCATGCTGAGTGTGAGCGGAGCCAGGCAATTTCTCCAGACAGATCGTGTCTGCC 498
DB 61 GAGCGGCGCATGCTGAGTGTGAGCGGAGCCAGGCAATTTCTCCAGACAGATCGTGTCTGCC 120

QY 499 CTGCACTACTGCCACCAAGAGGAGTCTTTCACCGAGATCTCAAGCTTGGAACATCTT 558
DB 121 CTGCACTACTGCCACCAAGAGGAGTCTTTCACCGAGATCTCAAGCTTGGAACATCTT 180

Qy	559	CTAGATGCCAATGGAACATCAAGATTGCTGACTTTGGCCTCTCCAACTGTACACAAA	618
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Db	301	GGGAAGCCCTATGTGGGCCACAGAGGTGGACAGCTGGTCTCTGGGCGCTTCTCTGTATCATC	360
Qy	739	CTGCTGATGSCACCATGCCCTTTGACGGGCAAGGATCATAAACACTGGTGAAGCAAAATC	798
Db	361	CTGCTGATGSCACCATGCCCTTTGACGGGCAAGGATCATAAACACTGGTGAAGCAAAATC	420
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Db	421	AGTAAACGGGGTTACCGTGAAGCCGCCCAAGCCGTCCGATGCTGTGACCTGATCCGGTGG	480
Qy	859	CTGTTAATGGTGAACCCCAACCCGTCGGGCCACACCTGGAGGATGTAGCCAGTTCATTGGTGG	918
Db	481	CTGTTAATGGTGAACCCCAACCCGTCGGGCCACACCTGGAGGATGTAGCCAGTTCATTGGTGG	540
Qy	919	GTCAACTGGGGTTACACACCGGAGTCGGGGACAGGAAGCCCTCGCTGAGGGTGGGCAC	978
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Db	715	AGCACTGTACTGG	728

RESULT 11	646 bp	mRNA	linear	EST 04-MAY-2001
BG694881				
LOCUS	NISC iv05h10.w1 Soares NMBP2 pituitary Mus musculus cDNA clone			
DEFINITION	IMAGE:4317546 5', mRNA sequence.			
ACCESSION	BG694881			
VERSION	BG694881.1			
KEYWORDS	GI:13954237			
SOURCE	EST.			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 646)			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)			
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov cDNA Library Preparation: M. Bento Soares Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov MGI:1598314			
COMMENT	Plate: LUAM9921 row: 0 column: 19 Seq primer: T7 primer. Location/Qualifiers 1..646			
FEATURES				
source				

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5'-AACTCGAAGAATTCGGCGCGCGCGCTTTTCTTTTCTTTT-3';
double-stranded cDNA was ligated to EcoRI adaptors
5'-AATCGCAGCAGG-3' AND 5'-CCTCGTCGC-3' (Pharmacia),
digested with NotI and cloned into the NotI and EcoRI
sites of the pT7T3D-pacI vector. Library went through one
round of normalization, and was constructed in the
laboratory of M. Bento Soares (University of Iowa)."

```

ORIGIN

Query Match	34.1%	Score 646;	DB 4;	Length 646;
Best Local Similarity	100.0%;	Pred. No. 1.9e-157;		
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Qy	1193	ATACCTCTTTCTCGCCCTGGCAAGCAGCCTTAAGCTTCCGAAAGGCATTCTCAAGNAAA	1252	
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[illegible]

5', mRNA sequence.
BF789245
VERSION
BF789245.1 GI:12094281
EST.
Mus musculus (house mouse)
Mus musculus
ORGANISM
REFERENCE
1 (bases 1 to 948)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9811 row: g column: 12
High quality sequence stop: 651.
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FEATURES
source
Query Match 34.1%; Score 645.8; DB 2; Length 948;
Best Local Similarity 96.3%; Pred. No. 2.3e-157;
Matches 683; Conservative 0; Mismatches 22; Indels 4; Gaps 2;
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DB 12 GGTGAACCCACCGGCTCGGGCCACACTGGAGATGTAGCCAGTCAATGGTGGTCAACTG 71
QY 927 GGGTTACACACCGGAGTGGGGAAACAGGAAGCCCTGCTGAGGTGGGCAACCTTAGTGG 986
DB 72 GGGTTACACACCGGAGTGGGGAAACAGGAAGCCCTGCTGAGGTGGGCAACCTTAGTGG 131
QY 987 TGACTTTGGCGGGCTCATGGCGGACTGGTACGTCTGCTCGGCCCTCCCTCTGGA 1046
DB 132 TGACTTTGGCGGGCTCATGGCGGACTGGTACGTCTGCTCGGCCCTCCCTCTGGA 191
QY 1047 GAATGGAGCAAGGTGTGAGCTTCTTCAAGCAGCAGCTGCGGGAGGTGGAAGCACTGT 1106
DB 192 GAATGGAGCAAGGTGTGAGCTTCTTCAAGCAGCAGCTGCGGGAGGTGGAAGCACTGT 251
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QY 1287 CCCTCAGGAACCTCAGACCGGTGCTGATCTTCAGGGCAGCTGTCCTGCTGTATCCCT 1346
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DB 492 GCTCCCAAGGAAGGCATCCTTAAGAACTCTCGACAGCTGAATCTGTTACTACTCTC 551
QY 1407 TCCAGAGCCAGCAGTCTGGGGAACTCTTACAGCCCACTGATGTGTTGTAGTGGGA 1466
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QY 1467 CCCGTGGAGCAGAAAGTCTCCACAGCTTCAGGGTCTCTCCACCGCAGGGCATCT 1526
DB 612 CCCGTGGAGCAGAAAGTCTCCACAGCTTCAGG--CTCTCTCCACCGCAGGGCATCT 669
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DB 670 CAA--CTCATGCAAGTCTCTCCGACAGCTTAAAGACTACCTAGTACT 716
RESULT 13
LOCUS
CA319312
DEFINITION
UI-M-FW0-cbz-i-16-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6816569 5', mRNA sequence.
ACCESSION
CA319312
VERSION
CA319312.1 GI:24537436
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
REFERENCE
1 (bases 1 to 795)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1..795
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/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 20:17:54 ; Search time 989.334 Seconds
(without alignments)
10994.228 Million cell updates/sec

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Perfect score: 1893
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues
Total number of hits satisfying chosen parameters: 8600550

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1893	100.0	2902	15	US-10-355-975-4
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4	1883.4	88.9	2026	17	US-10-343-514-27
5	1683.4	88.9	2929	17	US-10-343-514-1
6	1360.2	71.9	1884	9	US-09-963-159-3
7	1360.2	71.9	1884	16	US-10-423-543-45
8	1360.2	71.9	3353	9	US-09-963-159-1
9	1360.2	71.9	3353	16	US-10-423-543-43
10	1357.6	71.7	3360	16	US-10-311-034-38
11	1357	71.7	3404	17	US-10-322-281-25
12	1357	71.7	3463	18	US-10-618-941-11

13	1355.4	71.6	2501	16	US-10-302-172-215	Sequence 215, App
14	1355.4	71.6	3443	18	US-10-370-715B-639	Sequence 639, App
15	1071.4	56.6	1186	17	US-10-343-514-13	Sequence 13, Appl
16	1059.4	56.0	37278	17	US-10-322-281-21	Sequence 21, Appl
17	943.4	49.8	1186	17	US-10-343-514-70	Sequence 70, Appl
18	840.2	44.4	2616	17	US-10-363-829-151	Sequence 151, App
19	840.2	44.4	2619	17	US-10-363-829-250	Sequence 250, App
20	723	38.2	39699	17	US-10-322-281-24	Sequence 24, Appl
21	648	34.2	707	17	US-10-343-514-91	Sequence 91, Appl
22	648	34.2	712	17	US-10-343-514-31	Sequence 31, Appl
23	644.2	34.0	661	17	US-10-343-514-93	Sequence 93, Appl
24	613.6	32.4	741	17	US-10-343-514-32	Sequence 32, Appl
25	592	31.3	734	17	US-10-343-514-92	Sequence 92, Appl
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27	557.4	29.4	660	17	US-10-343-514-33	Sequence 33, Appl
28	533	28.2	578	17	US-10-343-514-95	Sequence 95, Appl
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30	510.6	27.0	579	17	US-10-343-514-35	Sequence 35, Appl
31	506.4	26.8	1986	9	US-09-780-949-3	Sequence 3, Appl
32	506.4	26.8	2884	9	US-09-780-949-5	Sequence 5, Appl
33	506.4	26.8	6828	9	US-09-780-949-1	Sequence 1, Appl
34	506.4	26.8	6828	15	US-10-354-358-81	Sequence 81, Appl
35	506.4	26.8	6828	15	US-10-172-118-1541	Sequence 1541, Ap
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40	483.8	25.6	548	17	US-10-343-514-36	Sequence 36, Appl
41	448.2	23.7	521	17	US-10-343-514-94	Sequence 94, Appl
42	417.8	22.1	521	17	US-10-343-514-34	Sequence 34, Appl
43	383.4	20.3	439	17	US-10-343-514-10	Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-10-355-975-4
; Sequence 4, Application US/10355975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/579,664B
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-355-975-4

Query Match	100.0%;	Score 1893;	DB 15;	Length 2902;
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Qy	61	TCGAGAGCCCGCGGCTTGGCGGAGCTATCAAGTCGCTAAACCTCTGATGAAG	120	
Db	183	TCGAGAGCCCGCGGCTTGGCGGAGCTATCAAGTCGCTAAACCTCTGATGAAG	242	

121 AAGCAGCGGTGAGCGGCAACCATCAAAACACAACTCGGGCAACCGTACGAGTTCTCTG 180
Db
243 AAGCAGCGGTGAGCGGCAACCATCAAAACACAACTCGGGCAACCGTACGAGTTCTCTG 302
Qy
181 GAGACGCTGGGCAAGGCACTACGGGAAGGTGAAGAGGACGAGAGAGCTCGGGGCGT 240
Db
303 GAGACGCTGGGCAAGGCACTACGGGAAGGTGAAGAGGACGAGAGAGCTCGGGGCGT 362
Qy
241 CTGGTGCCATCAAGTCCATCAGAAAGACAAATCAAAAGATGAGCAGGATCTGCTGCAC 300
Db
363 CTGGTGCCATCAAGTCCATCAGAAAGACAAATCAAAAGATGAGCAGGATCTGCTGCAC 422
Qy
301 ATACGGAGGAGATGAGATCATGTCTTCACTCAACACCCCAACATCAATGCGCATCAT 360
Db
423 ATACGGAGGAGATGAGATCATGTCTTCACTCAACACCCCAACATCAATGCGCATCAT 482
Qy
361 GAAGTGTTCAGAAATAGCAGCAAGATTGTGATTGTCTCATGGATGATGCGAGCGAGGCGAT 420
Db
483 GAAGTGTTCAGAAATAGCAGCAAGATTGTGATTGTCTCATGGATGATGCGAGCGAGGCGAT 542
Qy
421 CTGTATGATTACATCAGTAGCGGCCACCGGTGAGTGAGCGGGACGCGCAGGCAATTTCTTC 480
Db
543 CTGTATGATTACATCAGTAGCGGCCACCGGTGAGTGAGCGGGACGCGCAGGCAATTTCTTC 602
Qy
481 CGACAGATCGTGTCTGCCCTGCACTACTGSCACCAAGACCGGATCGTTCAACGAGATCTC 540
Db
603 CGACAGATCGTGTCTGCCCTGCACTACTGSCACCAAGACCGGATCGTTCAACGAGATCTC 662
Qy
541 AAGCTGAAACATCTCTTAGATGCCAATGGAAACATCAAGATTGTGCTGATTTGGGCTC 600
Db
663 AAGCTGAAACATCTCTTAGATGCCAATGGAAACATCAAGATTGTGCTGATTTGGGCTC 722
Qy
601 TCCAACTGTACCAAAAGGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTCTACGCC 660
Db
723 TCCAACTGTACCAAAAGGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTCTACGCC 782
Qy
661 TCCGCTGAGATGATCAACGGGAGCCCTATGTGGCCCGCAGAGTGGACAGCTGCTCTCTG 720
Db
783 TCCGCTGAGATGATCAACGGGAGCCCTATGTGGCCCGCAGAGTGGACAGCTGCTCTCTG 842
Qy
721 GCGGTTCTCTGTACATCTCTGTGTCATGCGCACCATGCCCCCTTTGACGGGCAAGGATCAAAA 780
Db
843 GCGGTTCTCTGTACATCTCTGTGTCATGCGCACCATGCCCCCTTTGACGGGCAAGGATCAAAA 902
Qy
781 AACTGTGTGAAGCAAAATCAGTAACGGGCTTTACCGTGAGCGGCCCAAGCGCTCGATGCC 840
Db
903 AACTGTGTGAAGCAAAATCAGTAACGGGCTTTACCGTGAGCGGCCCAAGCGCTCGATGCC 962
Qy
841 TGTGGCCTGATCCGGTGGCTGTTAATGTTGTAACCCACCCGTCGGGCCACACTGGAGGAT 900
Db
963 TGTGGCCTGATCCGGTGGCTGTTAATGTTGTAACCCACCCGTCGGGCCCAACTGGAGGAT 1022
Qy
901 GTAGCCAGTCAATGTGGGTCAACTGGGGTTTACACCAACCGAGTCCGGGCAACGAGAGCC 960
Db
1023 GTAGCCAGTCAATGTGGGTCAACTGGGGTTTACACCAACCGAGTCCGGGCAACGAGAGCC 1082
Qy
961 CTGCGTGAGGGTGGGCAACCTAGTGTGATCTTTGGCCGGGCTTCCATGGCGGAGCTGTTTA 1020
Db
1083 CTGCGTGAGGGTGGGCAACCTAGTGTGATCTTTGGCCGGGCTTCCATGGCGGAGCTGTTTA 1142
Qy
1021 CGTCCGCTCTCGGCCCTCTCTGGAGAAATGGAGCCAAAGTGTGACAGCTTCTTCAAGCAG 1080
Db
1143 CGTCCGCTCTCGGCCCTCTCTGGAGAAATGGAGCCAAAGTGTGACAGCTTCTTCAAGCAG 1202
Qy
1081 CAGTGCCGGGAGGTGAAGCACTGTACTCTGGGTGAGCGGCAACATTTCTTTAAGAAG 1140
Db
1203 CAGTGCCGGGAGGTGAAGCACTGTACTCTGGGTGAGCGGCAACATTTCTTTAAGAAG 1262
Qy
1141 TCCGGAAGGAGATGATGCTCAAAATCTGCAAGTGACCCGGGTGAGGATACCTCT 1200
Db
1263 TCCGGAAGGAGATGATGCTCAAAATCTGCAAGTGACCCGGGTGAGGATACCTCT 1322

1201 TCTCGCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAGGCAATTTCTCAAGAAAAGTCTCTCT 1260
Db
1323 TCTCGCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAGGCAATTTCTCAAGAAAAGTCTCTCT 1382
Qy
1261 ACCTCGTCAGGGAGGTACAGAGGAGCCCTCAGGAACTCAGAGCCGGTGCCTGATCTCCA 1320
Db
1383 ACCTCGTCAGGGAGGTACAGAGGAGCCCTCAGGAACTCAGAGCCGGTGCCTGATCTCCA 1442
Qy
1321 GGGAGCCTGCTCCCTGCTGTATCCCTGCTCCAAAGAAAGGCAATCTTAAGAAAGTCTCGA 1380
Db
1443 GGGAGCCTGCTCCCTGCTGTATCCCTGCTCCAAAGAAAGGCAATCTTAAGAAAGTCTCGA 1502
Qy
1381 CAGCGTAATCTGTTACTACTCTCTCAGAGCCAGAGGCTCTGGGAACTCTTAGAC 1440
Db
1503 CAGCGTAATCTGTTACTACTCTCTCAGAGCCAGAGGCTCTGGGAACTCTTAGAC 1562
Qy
1441 GCCAGTGATGTTGTTGAGTGGGACCCCGTGGAGCAAGTCTCCACAGGCTTCAGGG 1500
Db
1563 GCCAGTGATGTTGTTGAGTGGGACCCCGTGGAGCAAGTCTCCACAGGCTTCAGGG 1622
Qy
1501 CTCTCTCTCACCAGAGGCAATCTCAAACTCAATGGCAAGTCTTCCCGCACAGCCTTA 1560
Db
1623 CTCTCTCTCACCAGAGGCAATCTCAAACTCAATGGCAAGTCTTCCCGCACAGCCTTA 1682
Qy
1561 GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCCTCTCCATCTCGCA 1620
Db
1683 GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCCTCTCCATCTCGCA 1742
Qy
1621 GCCCGGCCACAGCCCTCTCAGGGGCTGTGAGTGAGGACAGCATCTCTCTCCGAGTCC 1680
Db
1743 GCCCGGCCACAGCCCTCTCAGGGGCTGTGAGTGAGGACAGCATCTCTCTCCGAGTCC 1802
Qy
1681 TTTGACCAATTTGACTTGCCTGAACTTTCCGAAACCCCACTAGAGGGCTGTGTGTCT 1740
Db
1803 TTTGACCAATTTGACTTGCCTGAACTTTCCGAAACCCCACTAGAGGGCTGTGTGTCT 1862
Qy
1741 GTGCAACACTGAGGGGCTTTGAGCAGCCTCTCAGAGGCTCTGAAGCGATGTTGGCAG 1800
Db
1863 GTGCAACACTGAGGGGCTTTGAGCAGCCTCTCTCAGAGGCTCTGAAGCGATGTTGGCAG 1922
Qy
1801 GAATCTCTGGGGATAGTGTCTTTCTTGACAGACTGCCAAGAGGTGACTGCAGCCTAC 1860
Db
1923 GAATCTCTGGGGATAGTGTCTTTCTTGACAGACTGCCAAGAGGTGACTGCAGCCTAC 1982
Qy
1861 AGACAAGCCTTAGGAATCTGCTCAAAAGCTCAGC 1893
Db
1983 AGACAAGCCTTAGGAATCTGCTCAAAAGCTCAGC 2015

RESULT 2

US-10-322-281-22
; Sequence 22, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945201000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-281-22

Query Match 100.0%; Score 1893; DB 17; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGTTCGGTGGCTTACTTCCAGCGCCGAGCAGGCTCCCTCGGCTCCGCGCTCGCC 60

Db 92 ATGGAGTCGTGGGCTTACTCCAGCGCCGAGCAGGCTCCCTCGGCTCCGCGCTGGCC 151
Qy 61 TCGGAGAGCGCCGCGCTGGCGGACGGCTCATCAAGTCGCTAAACCTCTGTATGAAG 120
Db 152 TCGGAGAGCGCCGCGCTGGCGGACGGCTCATCAAGTCGCTAAACCTCTGTATGAAG 211
Qy 121 AAGCAGCGGTGAAGCGGCAACCATCAAAACACAACTCGGCGCACCGCTACGAGTTCCTG 180
Db 212 AAGCAGCGGTGAAGCGGCAACCATCAAAACACAACTCGGCGCACCGCTACGAGTTCCTG 271
Qy 181 GAGACGCTGGGCAAGGCACTAGCGGAAGGTGAAGAGGCAAGAGAGCTCGGGCGT 240
Db 272 GAGACGCTGGGCAAGGCACTAGCGGAAGGTGAAGAGGCAAGAGAGCTCGGGCGT 331
Qy 241 CTGGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAGATGAGCAGGATCTGTGCAC 300
Db 332 CTGGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAGATGAGCAGGATCTGTGCAC 391
Qy 301 ATACGAGGAGGATTTGAGATCATGTCTTCACTCAACACCCCAACATCATTTGCCATCCAT 360
Db 392 ATACGAGGAGGATTTGAGATCATGTCTTCACTCAACACCCCAACATCATTTGCCATCCAT 451
Qy 361 GAAGTGTTCGAGATACAGCAAGATTTGATGTCTATGAGTATGCCAGCGAGGCGAT 420
Db 452 GAAGTGTTCGAGATACAGCAAGATTTGATGTCTATGAGTATGCCAGCGAGGCGAT 511
Qy 421 CTGTATGATTACATCAGTAGCGGCGCACGCTGAGTGAGCGGAGCGGCGATTTCTTC 480
Db 512 CTGTATGATTACATCAGTAGCGGCGCACGCTGAGTGAGCGGAGCGGCGATTTCTTC 571
Qy 481 CGACAGATCTGTCTGCGCTGCACTACTGCGCACAGGAGCGGATCGTTTCAACGAGATCTC 540
Db 572 CGACAGATCTGTCTGCGCTGCACTACTGCGCACAGGAGCGGATCGTTTCAACGAGATCTC 631
Qy 541 AAGCTGAAACATCTCTTAGATGCOATGGAACATCAAGATTTGATGCTGTGCTGCTG 600
Db 632 AAGCTGAAACATCTCTTAGATGCOATGGAACATCAAGATTTGATGCTGTGCTGCTG 691
Qy 601 TCCAACTGTACCAACAAAGCAAGTTCCTCCAGACGTTCTGTGGAGCCCTCTCTAGGCC 660
Db 692 TCCAACTGTACCAACAAAGCAAGTTCCTCCAGACGTTCTGTGGAGCCCTCTCTAGGCC 751
Qy 661 TCGCTGAGATAGTCAACGGGAGCCCTATGTGGGCGCCAGAGTGAGAGTGTGCTGCTG 720
Db 752 TCGCTGAGATAGTCAACGGGAGCCCTATGTGGGCGCCAGAGTGAGAGTGTGCTGCTG 811
Qy 721 GCGCTTCTCTGTACATCTCTGTGATGCGCAACATGCGCTTTGACGGGCGAGGATCAATA 780
Db 812 GCGCTTCTCTGTACATCTCTGTGATGCGCAACATGCGCTTTGACGGGCGAGGATCAATA 871
Qy 781 ACAGTGTGAAGCAAAATCAGTAGCGGGCTTACCGTGAGCGGCCCAAGCGCTCGATGCC 840
Db 872 ACAGTGTGAAGCAAAATCAGTAGCGGGCTTACCGTGAGCGGCCCAAGCGCTCGATGCC 931
Qy 841 TGTGGCTGTATCCGGTGGCTTTAATGAGTGAACCCCAACCGCTCGGGCCACACTGGAGGAT 900
Db 932 TGTGGCTGTATCCGGTGGCTTTAATGAGTGAACCCCAACCGCTCGGGCCACACTGGAGGAT 991
Qy 901 GTAGCCAGTCAATGTTGGGTCAACTGGGGTTACACCAACCGAGTTCGGGGAACAGGAAGCC 960
Db 992 GTAGCCAGTCAATGTTGGGTCAACTGGGGTTACACCAACCGAGTTCGGGGAACAGGAAGCC 1051
Qy 961 CTGGCTGAGGGTGGGCAACCTAGTGTGACTTTGGCGGGCCCTCATGGGCGAGTGTGTA 1020
Db 1052 CTGGCTGAGGGTGGGCAACCTAGTGTGACTTTGGCGGGCCCTCATGGGCGAGTGTGTA 1111
Qy 1021 CGTGGCTCTCGCGCCCTCTCTGAGAAATGAGGCAAGGTGTCAGCTTCTTCAAGCAG 1080
Db 1112 CGTGGCTCTCGCGCCCTCTCTGAGAAATGAGGCAAGGTGTCAGCTTCTTCAAGCAG 1171
Qy 1081 CAGTGCCTGGAGGTGAAGCACTGTACCTGGGCTGGAGCGGCAACATCTCTTAAAGAG 1140

Db 1172 CACGTGCCGGAGGTGAAGACACTGTACTCTGGGCTGGAGCGGCAACATCTCTTAAAGAG 1231
Qy 1141 TCCGAAAGAGAGATGACATGGCTCAAAATCTCAAGGTGACCGGCTGAGGATACCTCT 1200
Db 1232 TCCGAAAGAGAGATGACATGGCTCAAAATCTCAAGGTGACCGGCTGAGGATACCTCT 1291
Qy 1201 TCTCGCTTGGCAAGAGCAGCTTAAAGTTCGAAAGGCAATCTCAAGAAAAAGTCTCTCT 1260
Db 1292 TCTCGCTTGGCAAGAGCAGCTTAAAGTTCGAAAGGCAATCTCAAGAAAAAGTCTCTCT 1351
Qy 1261 ACCTCTCAGGGAGGTACAGGAGGACCTTCAGGAACTCAGACCGGTGCTGATCTCCA 1320
Db 1352 ACCTCTCAGGGAGGTACAGGAGGACCTTCAGGAACTCAGACCGGTGCTGATCTCCA 1411
Qy 1321 GGGCAGCTGTCTCTGCTGTATCCCTGCTCCCAAGGAAAGGCAATCTTAAAGAGTCTCGA 1380
Db 1412 GGGCAGCTGTCTCTGCTGTATCCCTGCTCCCAAGGAAAGGCAATCTTAAAGAGTCTCGA 1471
Qy 1381 CAGCGTGAATCTCTGCTGTATCTCTCTCAGAGCCGAGAGTCTGGGGAATCTTTAGAC 1440
Db 1472 CAGCGTGAATCTCTGCTGTATCTCTCTCAGAGCCGAGTCTGGGGAATCTTTAGAC 1531
Qy 1441 GCCAGTGTGTCTGTGAGTGGGACCCCGTGGAGCAGAGTCTCCACAGGCTTCAGGG 1500
Db 1532 GCCAGTGTGTCTGTGAGTGGGACCCCGTGGAGCAGAGTCTCCACAGGCTTCAGGG 1591
Qy 1501 CTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGCAAGTCTCCCGCACAGCCTTA 1560
Db 1592 CTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGCAAGTCTCCCGCACAGCCTTA 1651
Qy 1561 GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCTCTCTCCCATCTGCA 1620
Db 1652 GAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCTCTCTCCCATCTGCA 1711
Qy 1621 GCCCGGCCACCGCCCTCAGGGCTGTGAGTGAGGACAGCATCTGTCTCGAGTCC 1680
Db 1712 GCCCGGCCACCGCCCTCAGGGCTGTGAGTGAGGACAGCATCTGTCTCGAGTCC 1771
Qy 1681 TTTGACCAATTTGAGCTTGGCTGAACTCTTCCGAAACCCCACTGAGGGGCTGTGTGCT 1740
Db 1772 TTTGACCAATTTGAGCTTGGCTGAACTCTTCCGAAACCCCACTGAGGGGCTGTGTGCT 1831
Qy 1741 GTGCAACACTGAGGGGCTTGAAGAGCTCTCTCAGAGGCTCTGAAGCGATGGTGGCAG 1800
Db 1832 GTGCAACACTGAGGGGCTTGAAGAGCTCTCTCAGAGGCTCTGAAGCGATGGTGGCAG 1891
Qy 1801 GAATCTTGGGATAGTGTCTTTCTGTGACAGCTGCCAAGAGGTGACTGAGCCTAC 1860
Db 1892 GAATCTTGGGATAGTGTCTTTCTGTGACAGCTGCCAAGAGGTGACTGAGCCTAC 1951
Qy 1861 AGACAGCCCTAGGAATCTGCTCAAAAGCTCAGC 1893
Db 1952 AGACAGCCCTAGGAATCTGCTCAAAAGCTCAGC 1984

RESULT 3

US-10-343-514-87

; Sequence 87, Application US/10343514

; Publication No. US2004013205A1

; GENERAL INFORMATION:

; APPLICANT: DRUCKER, Daniel J.

; APPLICANT: ROSEN, Cheryl F.

; APPLICANT: LEFEBVRE, Diana L.

; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK

; FILE REFERENCE: DPA-DRUC2/PCT

; CURRENT APPLICATION NUMBER: US/10/343,514

; PRIOR FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: PCT/CA01/01109

; PRIOR FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: US 60/222,650

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: US 60/274,613

; PRIOR FILING DATE: 2001-03-12

;; PRIOR APPLICATION NUMBER: CA 2,340,780
;; PRIOR FILING DATE: 2001-03-28
;; NUMBER OF SEQ ID NOS: 109
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 87
;; LENGTH: 2027
;; TYPE: DNA
;; ORGANISM: MOUSE
US-10-343-514-87

Query Match 99.7%; Score 1888.2; DB 17; Length 2027;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1890; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	ATGGAGTCGGTGGCTTACTCCAGCGCCGAGCCAGGCTCCCTCGGCTCGCCCTGGCC	60
Db	75	ATGGAGTCGGTGGCTTACTCCAGCGCCGAGCCAGGCTCCCTCGGCTCGCCCTGGCC	134
Qy	61	TCGGAGAGCGCCCGCGCTGGCGGACGGGCTCATCAAGTCGCCCTAAACCTCTGATGAAG	120
Db	135	TCGGAGAGCGCCCGCGCTGGCGGACGGGCTCATCAAGTCGCCCTAAACCTCTGATGAAG	194
Qy	121	AAGCAGCGGTGAAGCGGACCATCAAAACAACCTGGGACACCGGTACGATTCCTG	180
Db	195	AAGCAGCGGTGAAGCGGACCATCAAAACAACCTGGGACACCGGTACGATTCCTG	254
Qy	181	GAGACGCTGGGCAAGGCGCCTACGGGAGGTGAAGAGCAGCAGAGAGCTCGGGCGT	240
Db	255	GAGACGCTGGGCAAGGCGCCTACGGGAGGTGAAGAGCAGCAGAGAGCTCGGGCGT	314
Qy	241	CTGGTGGCCATCAAGTCCATCAGAAAGACAAATCAAGATGAGCAGGATCTGCTGCAC	300
Db	315	CTGGTGGCCATCAAGTCCATCAGAAAGACAAATCAAGATGAGCAGGATCTGTTGCAC	374
Qy	301	ATACGAGGAGATTGATGATCATGTTCTCACTCAACCAACCCCAATCATGTCATCCAT	360
Db	375	ATAAGGAGGAGATCGAGATCATGTTCTCACTCAACCAACCCCAATCATGTCATCCAT	434
Qy	361	GAAGTGTTCAGATACAGCAGATTGATGTTGTCATGAGTATGCGAGCGGAGCGAT	420
Db	435	GAAGTGTTCAGATACAGCAGATTGATGTTGTCATGAGTATGCGAGCGGAGCGAT	494
Qy	421	CTGTATGATTACATCAGTGAAGCGCCACGGCTGAGTGAGCGGAGCGCCAGGCAATTTCTC	480
Db	495	CTGTATGATTACATCAGTGAAGCGCCACGGCTGAGTGAGCGGAGCGCCAGGCAATTTCTC	554
Qy	481	CGACAGATCGTGTCTGCCCTGCATCTGCGACAGAAACGGGATCGTTTCAACGAGATCTC	540
Db	555	CGACAGATCGTGTCTGCCCTGCATCTGCGACAGAAACGGGATCGTTTCAACGAGATCTC	614
Qy	541	AAGCTGAAACATCTCTTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCCTC	600
Db	615	AAGCTGAAACATCTCTTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCCTC	674
Qy	601	TCCAACCTGTACCAAAAGGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTCTACGCC	660
Db	675	TCCAACCTGTACCAAAAGGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTCTACGCC	734
Qy	661	TCGCCTGAGATAGTCAACGGGAGCCCTATGTGGGCCACAGAGTGGAACAGTGTCTCTG	720
Db	735	TCGCCTGAGATAGTCAACGGGAGCCCTATGTGGGCCACAGAGTGGAACAGTGTCTCTG	794
Qy	721	GGCGTCTCTGTACATCTCTGGTGCATGGCACCATGCCCTTTGACGGGAGGATCATAAA	780
Db	795	GGCGTCTCTGTACATCTCTGGTGCATGGCACCATGCCCTTTGACGGGAGGATCATAAA	854
Qy	781	ACACTGTGTAAGCAAAATCAGTAAACGGGCTTACCGTGAGCGGCCCAAGCCGTCCGATGCC	840
Db	855	ACACTGTGTAAGCAAAATCAGTAAACGGGCTTACCGTGAGCGGCCCAAGCCGTCCGATGCC	914
Qy	841	TGTGGCCCTGATCCGGTGGCTGTTAATGGTGAACCCCAACCCGTCGGGCCACACTGGAGGAT	900
Db	915	TGTGGCCCTGATCCGGTGGCTGTTAATGGTGAACCCCAACCCGTCGGGCCACACTGGAGGAT	974

RESULT 4

US-10-343-514-27

; Sequence 27, Application US/10343514

Publication No. US20040132025A1
GENERAL INFORMATION:
APPLICANT: DRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: LEBEVRE, Diana L.
TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUC2/PCT
CURRENT APPLICATION NUMBER: US/10/343,514
PCT/CA01/01109
PRIORITY FILING DATE: 2003-01-31
PRIORITY FILING DATE: 2001-08-02
PRIORITY FILING DATE: 2000-08-03
PRIORITY FILING DATE: 2000-08-03
PRIORITY FILING DATE: 2001-03-12
PRIORITY FILING DATE: 2001-03-12
PRIORITY FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 109
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 2026
TYPE: DNA
ORGANISM: RAT
US-10-343-514-27

Query Match 88.9%; Score 1683.4; DB 17; Length 2026;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1769; Conservative 0; Mismatches 121; Indels 3; Gaps 1;
1 ATGAGTCGTGGCTTACTCCAGCGCCGAGCCAGGCTCCCTCGCGCTCCGCGCTCGGCC 60
75 ATGAGTCGTGGCTTACTACCGCGCGGGAACCTGGCTCCCTCGCGCTCCGCGCTCGGCC 134
61 TCGAGAGCCCGCGCGCTGGCGGAGCGGCTCATCAAGTCGCTAAACCTCTGATGAAG 120
135 ACGAGAGCCCGCGCGCTGGCGGAGCGGCTCATCAAGTCGCGCAACCTCTGATGAAG 194
121 AAGCAGCGGTGAAGCGGCACCATCAAAACACAACTCGCGGCACCGCTACGAGTTCCTG 180
195 AAGCAGCGGTGAAGCGGCACCATCAAAACACAACTCGAGGACCGCTACGAGTTCCTG 254
181 GAGACGTGGGCAAGGCACTACGGAAGGTGAAGAGGCAAGAGAGCTCGGGCGT 240
255 GAGACCTGGGCAAGGCACTACGGAAGGTGAAGAGGCAAGAGAGCTCGGGACGC 314
241 CTGCTGCCATCAAGTCATCAGGAAAGACAAATCAAGATGAGCAGGATCTGCTGCAC 300
315 CTGCTGCCATCAAGTCATCAGGAAAGACAAATCAAGATGAGCAGGATCTGTTGCAC 374
301 ATACGAGGAGATTCAGATCATGTCTTCACTCAACCCACCCACCATCATTTGCCATCCAT 360
375 ATAAGGAGGAGATTCAGATCATGTCTTCACTCAACCCACCCACCATCATTTGCCATCCAT 434
361 GAAGTGTTCAGATTCAGCAGCAAGATTCAGTTCATGTCATGAGTATGTCAGCCAGGCGAT 420
435 GAAGTGTTCAGCAGCAGCAAGATTCAGTTCATGTCATGAGTATGTCAGCCAGGCGAT 494
421 CTGATGATTCATCAGTTCAGGCGGCACCGCTGAGTTCAGGCGGCACCGGATTTCTTC 480
495 CTGATGATTCATCAGTTCAGGCGGCACCGCTGAAATGAGCGGACCGCAGGATTTCTTC 554
481 CGACAGATTCGTGTGTCCTTCGACTACTGTCACACAGAAACCGGATTCGTTACCCAGATCTC 540
555 CGACAGATTCGTGTGTCCTTCGACTACTGTCACACAGAAACCGGATTCGTTACCCAGGACCTC 614
541 AAGCTGGAACAACTCTTCATGATGCAATTCGAAACATCAAGATTCGTCATTTGGCCTC 600
615 AAGCTGGAACAACTCTTCATGATGCAATTCGAAACATCAAGATTCGTCATTTGGCCTC 674
601 TCCAACTGTACCAAGGCAAGTTCCTTCAGACGTTCTGTGGGAGCCCTCTCTAGCC 660
675 TCCAACTGTATCACAAAGCAAGTTCCTTCAGACGTTCTGTGGGAGCCCTCTCTATGCC 734

QY 661 TCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTGGACAGCTGGTCTCTG 720
DB |||||
735 TCACCTGAGATCGTCAACGGGAAGCCCTATGTGGGCCAGAGGTGGACAGCTGGTCTCTG 794
QY 721 GGGTTCCTCTGTACATCTCTGGTGCATGGCAACCATGCTTTTACCGGCGAGGATCATAAA 780
DB |||||
795 GGGTTCCTCTGTACATCTCTGGTGCATGGCAACCATGCTTTTACCGGCGAGGATCATAAA 854
QY 781 ACATCTGTGAAGCAAAATCAGTAACGGGCTTACCGTGGAGCGCCCAAGCCGTCGATGCC 840
DB |||||
855 ACCCTGTGAACAAATCAGTAGGGGCTTACCGAGAGCGGTGCAAAACCGCTCTGATGCC 914
QY 841 TGTGGCTGATCCGGTGGCTGTTAATGGTGAACCCACCGCTCGGGGCACACCTCGAGGAT 900
DB |||||
915 TGTGGCTGATCCGGTGGCTGTTAATGGTGAACCCACCGCTCGGGGCACCTCTGAGGAT 974
QY 901 GTAGCCAGTCAATTTGGTGGTCAACTGGGGTTACACACCGAGGTTCGGGGAACAGGAAGCC 960
DB |||||
975 GTAGCCAGTCAATTTGGTGGTCAACTGGGGTTACAGCACCCGCAATTTGGGGAACAGGAAGCT 1034
QY 961 CTGCTGAGGTGCGGCACCCCTAGTGGTGACTTTTGGCGGGCCCTCCATGGCGGACTGGTTA 1020
DB |||||
1035 CTGCGAGAGGTGGGCACCCCTAGCGGTGACTCTGGCGGGCCCTCTATGGCGGACTGGTTA 1094
QY 1021 CGTCTGCTCTCGCGCCCTCTCTCGAGAAATGGAGCAAGGTGTGACGCTTCTTCAAGCAG 1080
DB |||||
1095 CGTCTGCTCTCTCGCGCCCTCTCTCGAGAAATGGAGCAAGGTGTGACGCTTCTTCAAGCAG 1154
QY 1081 CAGTTCGGGAGGTGAAGCACTGTACTGGGTGTGAGCGGCAACATTTCTTTAAGAAG 1140
DB |||||
1155 CATGTGCGGGAGGTGAAGCACTGTACTGGGTGTGAGCGGCAACATTTCTTTAAGAAG 1214
QY 1141 TCCGGAAGAGAGATGACATGGCTCAAAATCTCAAGGTGACCGGCTGAGGATACCTCT 1200
DB |||||
1215 TCCGGAAGAGAGATGACATGGCTCAAGTCTCAGACTCTCAGAAATGACCAAGTGAAGTACTTCC 1274
QY 1201 TCTCGCCCTCGGCAAGAGCAGCTTAAAGCTTTCGAAAGGCAATTTCTCAAGAAAGGCTCTCT 1260
DB |||||
1275 TCTCGCCCTCGGCAAGAGCAGCTTAAAGCTTTCGAAAGGCAATTTCTCAAGAAAGGCTCTCT 1334
QY 1261 ACCTGTTCAGGAGGTGACAGAGGACCTTCAGAGAACTCAGACCGGTGCTGTATCTCA 1320
DB |||||
1335 CCCTCATTCGGGAGGTGACAGAGGCGCTTCAGAGAACTCAGACGAGTGTCCAATACCCCA 1394
QY 1321 GGGCAGCTGTCTCTGTATCTCTGCTCCCAAGGAAGGCAATCTTTAAGAAAGTCTCGA 1380
DB |||||
1395 GGGCAGCTGTCTCTGTATCTCTGCTCCCAAGGAAGGCAATCTTTAAGAAAGTCTCGG 1454
QY 1381 CAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCCGAGTCTGGGGAACCTCTTAGAC 1440
DB |||||
1455 CAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCCGAGTCTGGGGAACCTCTTAGAC 1514
QY 1441 GCAGTGTATGTTGTGAGTGGGACCCCGTGGAGAGAGTCTTCCACAGGCTTCAGGG 1500
DB |||||
1515 GCAGTGTATGTTGTGAGTGGGACCCCGTGGAGAGGATCTTCCACAGGCTTCAGGG 1574
QY 1501 CTCTCTCTCCAGCGAAGGCAATTTCAAACTCAATGGCAAGTTCCTCCCGCAGAGCCTTA 1560
DB |||||
1575 ---CGCTCTCATCGAAGGCAATTTCAAACTCAATGGCAAGTTCCTCCCGCAGAGCCTTA 1631
QY 1561 GAAGGCACTACCCCTAGCAGCTTTGGCTCTCTCGAGCAACTGGGCTCTCTCCCATCTTCGA 1620
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1632 GAAGGCACTACCCCTAGCAGCTTTGGCTCTCTCGAGCAACTGGGCTCTCTCCCATCTTCGA 1691
QY 1621 GCCCGCCAGCGCCCTTCAGGGCTGTGAGTGAAGAGCAGCATCTCTCTCGAGTTC 1680
DB |||||
1692 GCCCGCCAGCGCCCTTCAGGGCTGTGAGTGAAGAGCAGCATCTCTCTCGAGTTC 1751
QY 1681 TTTGACCAATTTGACCTGCTGAACCTTTCCCGAAGCCCACTGAGGGGCTGTGTGCT 1740
DB |||||
1752 TTTGACCAATTTGACCTGCTGAACCTTTCCCGAAGCCCACTGAGGAGCTGTGTGCT 1811
QY 1741 GTGGCAAACTGAGGGGCTTTGAGCAGGCTCTCTCAGAGGCTCTGAAGCAGATGTTGGCAG 1800

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Db 1812 GTGGCAACCTGAGGAGCTTGAGAGCTCCCTCAGAGGCTAAACGATGGTGGCAG 1871
Qy 1801 GAATCTTGGGGATAGTCTCTTTCTCTGACAGCTGCGCAAGAGGTGATGCGAGCCTAC 1860
Db 1872 GAATCTTGGGGATAGCGCTTTCTCTGACAGCTGCGCAAGAGGTGACAGAGCCTAC 1931
Qy 1861 AGACAGCCCTAGGAATCTCTCAAGCTCAGC 1893
Db 1932 AGACAAGCCCTAGGAATCTCTCAAGCTCAGC 1964

RESULT 5
US-10-343-514-1
; Sequence 1, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; APPLICANT: LEBEVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; PRIOR FILING DATE: 2003-01-31
; CURRENT FILING DATE: 2003-PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2929
; TYPE: DNA
; ORGANISM: RAT
US-10-343-514-1

Query Match 88.9%; Score 1683.4; DB 17; Length 2929;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1769; Conservative 0; Mismatches 121; Indels 3; Gaps 1;

Qy 1 ATGAGTTCGTGGCTTACTCCAGCGCCCGAGCGGCTCATCAAGTCGCCCTAAACCTCTGATGAAG 120
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Qy 61 TCGGAGAGCGCCCGCGCTGGCGGACGGGCTCATCAAGTCGCCCTAAACCTCTGATGAAG 120
Db 143 ACGGAGAGCGCCCGCGCTGGCGGACGGGCTCATCAAGTCGCCCTAAACCTCTGATGAAG 202
Qy 121 AAGCAGCGGTGAAGCGGACCATCAACACAACTGGCGGACCGGCTAGAGTTCTG 180
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Qy 181 GAGACGCTGGCAGGCGACCTACGGAGGTGAAGAGGACGAGAGCTCGGGCGT 240
Db 263 GAGACCTGGCAGGCGACCTACGGAGGTGAAGAGGACGAGAGCTCGGGAGC 322
Qy 241 CTGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAGATGAGCAGGATCTGCTGCAC 300
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Qy 421 CTGTATGATTACATCAGTAGCGGCCAGCGGCTGAGTGAGCGGAGCGGAGCATTTCTTC 480
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Qy 1801 GAATCTTTGGGGATAGTCTGTTTTCTTGACAGACTGCCAAGAGGTGACTGACGCTAC 1860
Db 1880 GAATCTTTGGGGATAGTCTGTTTTCTTGACAGACTGCCAAGAGGTGACTGACGCTAC 1939
Qy 1861 AGCAAGCCCTAGGAATCTGCTCAAGCTCAGC 1893
Db 1940 AGCAAGCCCTAGGAATCTGCTGAAGCTCAGC 1972

RESULT 6
US-09-963-159-3
; Sequence 3, Application US/09963159
; Patent No. US20020077312A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-5001
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-159-3

Query Match
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;
Qy 47 CCTCCGCTCGGCTCGGAGAGCGCCGCGCTGGCGGAGCGGCTCATCAAGTCGCTTA 106
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Qy 107 AACCTCTGATGAAGACGCGGTGAAGCGGACCATCAAAACAAACCAACTCGCGCAC 166
Db 95 AGCCCTAATGAAGACGCGGTGAAGCGGACCATCAAAACAAACCAACTCGCGCAC 154
Qy 167 GCTACGAGTTCTGGAGAGCTCGGCAAGGCGCCTACGGGAAGGTGAAGAGGACGAG 226
Db 155 GCTACGAGTTCTGGAGAGCTCGGCAAGGCGCCTACGGGAAGGTGAAGAGGCGCGG 214
Qy 227 AGAGCTCGGGGCTGTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 286
Db 215 AGAGCTCGGGGCGCTGTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 274
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Qy 347 TCATTGCCATCCATGAAGTGTGTTGAGATAGCAGCAAGATTGTGATGTCAGGATG 406

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Db 395 CGAGCCGAGCGATCTGTATGATATCATCATGAGTGGCGGCACCGCTGAGTGGCGGACG 454
Qy 467 CGAGGCAATTTCTCCGACAGATCGTGTCTCCCTGCACTACTGCGCACAGAAACGGGATCG 526
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Db 875 CCACCTCGAGGATGTGGCCAGTCACTGGTGGTCAACTGGGCTACGCCACCGAGTGG 934
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Db 995 TGGCTGACTGGCTCCGGCTTCTCTCCCGCCCTCTCGGAGAAATGGGCGCAAGTGTGCA 1054
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Db 1766 GAAAGCTCCCTGAGGCGCTGGCGGAGGATCTTTGGGGGACAGCTGTCTTTCTGTGACAG 1825
Qy 1835 ACTGCCAAGAGGTGACTGAGCTTACAGACAGCCCTAGGAATCTGCTCAAGCTCAGC 1893
Db 1826 ACTGCCAAGAGGTGACAGCAGCCTTACCGACAGGCACTGAGGGGTCTGTCTCAAGCTCACC 1884
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RESULT 8

US-09-963-159-1

; Sequence 1, Application US/09963159

; Patent No. US20020077312A1

; GENERAL INFORMATION:

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; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700. A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-5001
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3268)
; NAME/KEY: unsure
; LOCATION: (3270)
; NAME/KEY: unsure
; LOCATION: (3272)
; US-09-963-159-1
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Query Match 71.9%; Score 1360.2; DB 9; Length 3353;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;

Qy 47 CTTCCGCGCTGGCTCGGAGAGCGCGCGCTGGCGGAGCGGCTCATCAAGTCGCGCTA 106
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Qy 287 AGGATCTGTGCACATACGAGGAGGATTCAGATCATGTCTTCACTCAACACCCACACA 346
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Db 1802 TGTCTCTGTAGTCTTTGACAGCTGTGACTGTGTAACGCTTCCGAGACCCCACTGC 1861
Qy 1727 GGGGCTGT 1780
Db 1862 GGGGCTGT 1921
Qy 1781 -----GTCTGAAGCGATGTGGCAGGAATCTTTGGGGGATAGTGTCTTTCTGTACAG 1834
Db 1922 GAAGCTGCTGAGCGCTGGCGGAGGATCTTTTGGGGGAGCAGTGTCTTTTCCCTGACAG 1981

Qy 1835 ACTGCCAGAGGTGACTGCGAGCCTACAGACAAGCCCTAGGAATCTCTCAAGCTCAGC 1893
Db 1982 ACTGCCAGAGGTGACAGGACCTACCGACAGCACTAGGGTCTGCTCAAGCTCACC 2040

RESULT 9

US-10-423-543-43
; Sequence 43, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Teai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williamson, Mark J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638.
; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-023OWNIM
; CURRENT APPLICATION NUMBER: US/10/423,543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 3353
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3353)
; OTHER INFORMATION: n = A,T,C or G

US-10-423-543-43

Query Match 71.9%; Score 1360.2; DB 16; Length 3353;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;

Qy 47 CCTCCGCTGGCTCGAGAGCGCCGCTGCGGACGGGCTCATCAAGTCGGCTA 106
Db 191 CCACTCCCTCGCGCGCAGAGCTAGCCGCTGCGGAGGGCTGATCAAGTCGCCCA 250
Qy 107 AACCTCTGATGAAGAAGAGCGGCTGAAGCGGCACCATCAAAACAAACCTCGGCACC 166

Db 251 AGCCCTTAATGAAGCAGCGGTGAAGCGGCACCAACCAAGCAAACTCGGCGACC 310
Qy 167 GCTACGAGTTCTCGAGACGCTGGCAAGGCACCTACGGGAAGGTGAAGGACGAG 226
Db 311 GCTACGAGTTCTCGAGACGCTGGCAAGGCACCTACGGGAAGGTGAAGGACGCGGG 370
Qy 227 AGAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 286
Db 371 AGAGCTCGGGCGCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 430
Qy 287 AGAGTCTGCTGCACATACGAGGAGATGAGATCATGTCTTCACTCAACACCCCA 346
Db 431 AAGATCTGATGACATACGAGGAGATGAGATCATGTCTCACTCAACACCCCTCA 490
Qy 347 TCATTGCCATCCATGAAGTGTTCAGAAATACAGCAAGATGATGATGATGATGATG 406
Db 491 TCATTGCCATCCATGAAGTGTTCAGAAATACAGCAAGATGATGATGATGATGATG 550
Qy 407 CCAGCCGAGCGATCTGTATGATACATCAGTGAAGCGGCCACCGCTGAGTGAAGCGGACG 466
Db 551 CCAGCCGAGCGACCTTTATGACTATACATCAGGAGCGGACGACTCAGTGAAGCGGAG 610
Qy 467 CCAGGCAATTTCTCCGACAGATCGTGTCTGCTGCTGCACTACTGCAACAGAAAGCGGATCG 526
Db 611 CTAGGCAATTTCTCCGCGAGATCGTCTGCTGCTGCACTACTGCAACAGAAAGCGGATG 670
Qy 527 TTACCCGAGATCTCAAGCTGGAACATCTCTTAGATGCCAATGGAACATCAAGATTG 586
Db 671 TCCACCGAGATCTCAAGCTGGAACATCTCTTAGATGCCAATGGAACATCAAGATTG 730
Qy 587 CTGACTTTGGGCTCTCAACCTGTACCAAGCAAGTTCTCTCAGACGTTCTGTGGGA 646
Db 731 CTGACTTTGGGCTCTCAACCTGTACCAAGCAAGTTCTCTCAGACATCTGTGGGA 790
Qy 647 GCGCTCTTACGCTCGCTGAGATGATCAACGGGAAGCCCTATGTGGGCCAGAGTGG 706
Db 791 GCGCCCTCTATGCTCGCCAGAGATGTCTCAATGGGAAGCCCTACACAGGCGCCAGAGTGG 850
Qy 707 ACAGCTGCTCTGCGGCTCTCTCTGTACATCTCTGTGATGCCATGCCATGCCCTTTGACG 766
Db 851 ACAGCTGCTCTGCGGCTCTCTCTGTACATCTCTGTGATGCCATGCCATGCCCTTTGATG 910
Qy 767 GGCAGGATCATAAACACTGTGTGAAGCAATACAGTAACGGGGCTTACCGTGAGCGGCCA 826
Db 911 GGCATGACCATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGTGAGCCACTA 970
Qy 827 AGCCGTCGATGCTGTGGCTGATCCGGTGGCTGTTAATGGTGAACCCCAACCCGTCGGG 886
Db 971 AACCTCTGATGCTGTGGCTGATCCGGTGGCTGTTGATGGTGAACCCCAACCCGTCGGG 1030
Qy 887 CCACACTGGAGGATGATGACGATCATTTGGTGGGTCAACTGGGGTTACACACCGGATCG 946
Db 1031 CCACCTTGGAGGATGTGGCAGTCACTGGTGGGTCAACTGGGGTTACGCGCCAGTGG 1090
Qy 947 GGGAAAGGAGCCCTGCTGAGGCTGGGACCCCTAGTGGTACTTTGGCGGGCCCTCCA 1006
Db 1091 GAGAGGAGGAGCTCCGATGAGGCTGGGACCCCTGGCAGTACTCTGCCGCGCCCTCCA 1150
Qy 1007 TGGCGGATGCTGTTACGTCTGCTCTCGGCGCCCTCTCTGGAGAATGGAGCCAAAGTGTGCA 1066
Db 1151 TGGCTGACTGCTCGGCTTCTCTCCGCGCCCTCTCTGGAGAATGGGCGCAAGTGTGCA 1210
Qy 1067 GCTTCTTCAAGCAGCAGTGGCGGAGGTGAAGCACTGTACTGGGCTGAGCGGCAAC 1126
Db 1211 GCTTCTTCAAGCAGCAGTGCACCTGGTGGGGAAGCACCACCCCTGGGCTGGAGCGCAGC 1270
Qy 1127 ATTCTCTTAAGAGTCCCGAAGAGAGATGACATGGCTCAAAATCTCAAGGTTGACCCGG 1186
Db 1271 ATTGCTCAAGAGTCCCGAAGAGAGATGACATGGGCCCCAGTCTCTCCAGTGTACACGG 1330
Qy 1187 CTGAGGATACCTCTTCTCGCCCTGGCAAGCAGCCTTAAAGCTTCCGAAAGGCAATCTCA 1246

Db 1331 CTGATGACACTGCCACTCGCCCTGGCAAGCAACCTCAAGCTGCCAAAGGCAATCTCA 1390
Qy 1247 AGAAAGAGTCTCTACTCTCTGCTAGGAGGAGTACAGGAGGACCCCTCAGGAATCTCAGACGG 1306
Db 1391 AGAAGAGAGTGTGAGCTCTGCAAGAGGGGTACAGGAGGACCCCTCCGGAGCTCAGCCAA 1450
Qy 1307 TGCTGTATCTCCAGGCGAGCTGTCTCTCTGCTATCTCTCTGCTGCCAAGGAAGGCAATCC 1366
Db 1451 TCCTGCGAGCCCGAGGCGAGCTGCCCC-----CCCTGCTCCCCCAAGAGGCAATTC 1501
Qy 1367 TTAAGAGAGTCTCAGACAGCTGAATCTGGTTACTACTCTCTCAGAGCCCGAGAGTCTG 1426
Db 1502 TCAAGAGAGCCCGACAGCGAGTCTGGCTACTACTCTCTCCGAGCCCGAGTGAATCTG 1561
Qy 1427 GGAAGCTCTTAGAGCGCCAGTGTGTTTGTAGTGGGAGCCCGTGGAGCAGAAAGTCTC 1486
Db 1562 GGGAGCTCTTGGAGCGAGGCGAGCTGTTTGTAGTGGGATCCCAAGGAGCAGAGGCTC 1621
Qy 1487 CACAGGCTTCAGGCGCTCTCTCCACGCAAGGCGCAATCTCAAACTCAATGGCAAGTTCT 1546
Db 1622 CGCAAGCTTCAGGCGCTCTCTCTCCATCGCAAGGCAATCTCAAACTCAATGGCAAGTTCT 1681
Qy 1547 CCAGCAGAGCTTAGAAGGCACTACCCCTAGACACTTTTGGCTCCCTGGACCAACTGGCCT 1606
Db 1682 CCAGACAGCTTAGAGCTCGCGGCGCCCAACCACTTCGGCTCCCTGGATGAATCGCCC 1741
Qy 1607 CTCCCATCTCGAGCGCCCGCCAGCGCCCTCAGGGGCTGTAGTGAGGAGCAGCATCC 1666
Db 1742 CACTCGCCCCCTGGGCGCGGCGAGCGGACCTCAGGGGCTGTGAGGAGGAGCAGCATCC 1801
Qy 1667 TGTCTCTCCGAGTCTTTGACCAATTTGGACTTGGCTGAACTCTTCCGAAACCCCACTGA 1726
Db 1802 TGTCTCTGAGTCTTTGACCACTGGACTTGGCTGAACTGGCTCCAGAGCCCGCCACTGC 1861
Qy 1727 GGGCTGTGTGTCTGTGGACAACTCAGGGGGCTGTGAGCAGCTTCTCTCAGAAAG----- 1780
Db 1862 GGGCTGTGTGTCTGTGGACAACTCAGGGGGCTGTGAGGAGCCCGCTCAGAGGGCCCTG 1921
Qy 1781 -----GTCTGAAGCAGTGTGGCAGGAACTCTTTGGGGGATAGCTGCTTTCTCTGACAG 1834
Db 1922 GAAGCTGCTGTGAGGCGCTGGCGGAGCATCTTTTGGGGGAGCAGCTGCTTTTCCCTGACAG 1981
Qy 1835 ACTGCCAAGAGGTGACTGACGCTCAGAGCCCTCAGCAAGCCCTTAGGAATCTGCTCAAAGCTCAGC 1893
Db 1982 ACTGCCAAGAGGTGACAGGACCTACCGACAGGCACTGAGGGTCTGCTCAAAGCTCACC 2040

RESULT 10

US-10-311-034-38

; Sequence 38, Application US/10311034

; Publication No. US20040023242A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: YUE, Henry

; APPLICANT: LAL, Preeti

; APPLICANT: BANDMAN, Olga

; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: AU-YOUNG, Janice

; APPLICANT: LU, Yan

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: YAO, Monique G.

; APPLICANT: LU, Dyrong Aina M.

; APPLICANT: GREENWALD, Sara R.

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: KEARNEY, Liam

; APPLICANT: BURFORD, Neil

; APPLICANT: NGUYEN, Dannel B.

; APPLICANT: TANG, Y. Tom

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: HE, Ann

APPLICANT: THORNTON, Michael
APPLICANT: HAPALIA, April
APPLICANT: ARVIZU, Chandra S.
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: LO, Terence P.
APPLICANT: KHAH, Farrah A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Yalda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GREYER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Saiteev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311.034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 38
LENGTH: 3360
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: incyte ID No. US20040023242A1 4841542CB1
US-10-311-034-38

Query Match 71.7%; Score 1357.6; DB 16; Length 3360;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1569; Conservative 0; Mismatches 284; Indels 21; Gaps 2;

QY	32	GCACGGTCCCTCGGCTCGCCCTCGGCTCGGAGAGGCGCCGCGCTGGCGGACGGGC	91
Db	98	GCAGCGGCTCGGCGCCCACTCCCTCGGCGCAGAGCTAGCCCGCGCTGGCGAAGGC	157
QY	92	TCATCAAGTGCCTAAACCTCTGATGAAGACGAGCGGTGAAGCGCACCATCACAAAC	151
Db	158	TGATCAAGTGCCTAAACCTCTGATGAAGACGAGCGGTGAAGCGCACCATCACAAAC	217
QY	152	ACAACTCGGCGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAGGCAACCTACGGGAAG	211
Db	218	ACAACTCGGCGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAGGCAACCTACGGGAAG	277
QY	212	TGAGAGGACGAGAGAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACA	271
Db	278	TGAGAGGACGAGAGAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACA	337
QY	272	AAATCAAGATGACGAGATCTGCTGCACATACGAGGAGATGAGATCATGCTTTCAC	331
Db	338	AAATCAAGATGACGAGATCTGATGCACATACGAGGAGATGAGATCATGCTTCGC	397
QY	332	TCAACCAACCCACATCATTTGCCATCCATGAAGTGTGTTGAGAATAGCAGCAAGATTGGA	391
Db	398	TCAACCAACCCATCATTTGCCATCCATGAAGTGTGTTGAGAATAGCAGCAAGATTGGA	457
QY	392	TTGTTCATGAGATGACGAGGAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACA	451
Db	458	TCGTTCATGAGATGACGAGGAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACA	517
QY	452	TGAGTGCAGGAGCGGACGAGGATTTCTTCCGACAGATCGTGTCTGCGCTGCACTACTGCC	511
Db	518	TCAGTGCAGGAGCGGATGAGGATTTCTTCCGACAGATCGTGTCTGCGCTGCACTACTGCC	577
QY	512	ACCAGAACGGATCGTTCCACCGAGATCTCAAGCTGGAAACATCTTCTAGATGCCAATG	571
Db	578	ATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAAACATCTTCTAGATGCCAATG	637

QY	572	GAAACATCAAGATTGCTGACTTTGGGCTCTCCAACTGTACCAACGAAAGCAAGTTCTCTCC	631
Db	638	GGAATATCAAGATTGCTGACTTTGGGCTCTCCAACTGTACCAACGAAAGTTCTCTCC	697
QY	632	AGACGTTTCTGTGGGAGCCCTCTCTAGCCCTCGGCTGAGATAGTCAACGGAAGCCCTATG	691
Db	698	AGACATTTCTGTGGGAGCCCTCTATGCTTCGCGAGAGATTGTCAATGGGAAGCCCTACA	757
QY	692	TGGGCCAGAGGTGGAACAGCTGTCTCTGGGCTTCTCTGTATCATCTCTGGTGAATGGA	751
Db	758	CAGGCCAGAGGTGGAACAGCTGTCTCTGGGCTTCTCTGTATCATCTCTGGTGAATGGA	817
QY	752	CCATGCCCTTTGACGGGCGAGATCAATAAACACTGCTGAGCAAAATCAGTAAGGGGCTT	811
Db	818	CCATGCCCTTTGATGGGCATGACCAATAAGATCTCTAGTGAACAGATCAGCAAGGGGCT	877
QY	812	ACCGTGAGCGCCCAAGCCGCTCGATGCTGCTGGCTGATCCGGTGGCTCTTAATGGTGA	871
Db	878	ACCGGAGCCACCTAAACCTCTGATGCTGCTGGCTGATCCGGTGGCTCTTAATGGTGA	937
QY	872	ACCCACCGCTCGGGCCACACTGGAGAGATGAGCAGTCAATGGTGGGTCAACTGGGGTT	931
Db	938	ACCCACCGCTCGGGCCACACTGGAGAGATGAGCAGTCAATGGTGGGTCAACTGGGGCT	997
QY	932	ACACCAACCGAGTGGGGACAGAGCCCTGCTGAGGTGGGCGCCCTAGTGGTGACT	991
Db	998	ACGCCACCGAGTGGGGACAGAGCCCTGCTGAGGTGGGCGCCCTAGTGGTGACT	1057
QY	992	TTGGCCGGGCTCCATGGGGACTGGTTACGTGCTCGCTCGCGCCCTCTCTGGAGAAATG	1051
Db	1058	CTGCCCGGCTCCATGGGTGACTGGCTCGGGCTTCTCTCGGCCCTCTCTGGAGAAATG	1117
QY	1052	GAGCCAGGTGTGAGCTTCTTCAAGCAGCAGCTGCGGGAGGTGGAAGCACTGTACTCTG	1111
Db	1118	GGGCCAAGGTGTGAGCTTCTTCAAGCAGCAGCTGCGGGAGGTGGAAGCACTGTACTCTG	1177
QY	1112	GGCTGAGCGGCAACATCTCTTAAAGAGTCCCGAAGGAGATGACATGGCTCAAAATC	1171
Db	1178	GGCTGAGCGGCAACATCTCTTAAAGAGTCCCGAAGGAGATGACATGGCTCAAAATC	1237
QY	1172	TGCAAGGTGACCGGGCTGAGGATACCTTCTCGCCCTTGGCAAGAGCAGCTTTAAGCTTC	1231
Db	1238	TCCACAGTGAACGCGCTGATGACACTGCCCTCGCCCTGGCAAGAGCACTCAAGCTGC	1297
QY	1232	CGAAAGCATTTCTCAAGAAAGTCTCTTACCTGCTCAGGGAGGTACAGAGACCTTC	1291
Db	1298	CAAAGGCGATTTCTCAAGAAAGTGTGAGCTCTGCGAAGGGGTACAGAGAGACCTTC	1357
QY	1292	AGGAATCTCAGACGCTGCTGATCTCCAGGGCAGCTGCTCCCTGCTGTATCTCTGCTCC	1351
Db	1358	CGAGCTCAGCCCAATCCCTGCGAGCCAGGGCAGGCTGCC-----CCCTGCTCC	1408
QY	1352	CAAGGAAAGGCATCTTAAAGAGTCTCGACAGCGTGAATCTGGTTACTCTCTCTCCAG	1411
Db	1409	CCAAGAGGCGATTTCTCAAGAAAGTCTCGACAGCGGAGTCTGGCTACTCTCTCTCCG	1468
QY	1412	AGCCAGCGAGTCTGGGAACTCTTAGACCGCAGTGAATGTTTGTGAGTGGGACCCCG	1471
Db	1469	AGCCAGCGATTAATCTGGGAGCTCTTGAGCGCAGCGGACGCTGTTGTGAGTGGGATCCCA	1528
QY	1472	TGAGCAGAGATCTCCACAGGCTTCCAGGGCTCTCTCCACCGCAAGGGCATTTCTCAAC	1531
Db	1529	AGGAGCAGAGCTCTCGAAGCTTTCAGGGCTGCTCTCTCATCGCAAGGATCTCTCAAC	1588
QY	1532	TCAATGGCAGTTCTCCCGCAGCAGCTTAGAAGGCACTACCCCTAGCAGCTTTGGTCTCC	1591
Db	1589	TCAATGGCAGTTCTCCCGCAGCAGCTTAGAAGTCTCGGGCCCCCACCACCTTCGGCTCC	1648
QY	1592	TGACCAACTGGGCTCTCCATCTCTGAGCGCGCCAGCCCTCTAGGGGCTGTGA	1651
Db	1649	TGATGAACCTCGGCCCACTCTCGCCCTCTGGCCCCGGGCCAGCCCTCAGGGGCTGTGA	1708


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Db 1654 CGCAAGCTTCAGGGCTGCTCCTCCATCGCAAGGCATCCTCAAACTCAATGGCAAGTTCT 1713
Qy 1547 CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACTTTGGCTCCCTGGACCAACTGGCCT 1606
Db 1714 CCCAGACAGCCTTAGAGTCGCGGCCCCCAACACCTTCGGCTCCCTGGATGAATCGGCC 1773
Qy 1607 CCTCCATCTCTGACGCGCCGCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1666
Db 1774 CACCTGCGCCCTTGCGCGCGCGAGCGACCTCAGGGGCTGTGAGGAGGACAGCATCC 1833
Qy 1667 TGTCTCCGAGTCTTTGACCAATTGACTTGCCTGAACGTCTTCCGAAACCCCACTGA 1726
Db 1834 TGTCTCTGAGTCTTTGACCAAGTGGACTTGCCTGAACGTCTTCCGAAACCCCACTGC 1893
Qy 1727 GGGGCTGTGCTGTGTGCAACACTGAGGGGCTTGTGAGCAGCCTCCCTCAGAAG----- 1780
Db 1894 GGGGCTGTGCTGTGTGCAACACTCAGGGGCTTGTGAGGAGCCCCCTCAGAGGGCCCTG 1953
Qy 1781 -----GTCTGAAGCGATGTGGCAGGAATCCTTTGGGGATAGCTGCTTTTCTCTGACAG 1834
Db 1954 GAAGCTGCTGAGGCGCTGGCGGCGAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGACAG 2013
Qy 1835 ACTGCCAAGGCTGACTGACGCTTACAGAACGCCCTTAGGAATCTGCTCAAAGCTCAGC 1893
Db 2014 ACTGCCAAGGCTGACAGCGACCTTACCAGAGGCACTGAGGGTCTGCTCAAAGCTCACC 2072

RESULT 13
US-10-302-172-215
; Sequence 215, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Dmanac, Radjoje T.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids an
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 ICNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 215
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(1989)
US-10-302-172-215

Query Match 71.6%; Score 1355.4; DB 16; Length 2501;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;

Qy 47 CCTCCGCGCTGGCTCGAGAGCGCCCGCGCTGGCGGAGGGCTCATCAAGTCGCCTA 106
Db 140 CCACTCCTCGCGCGAGAGCTAGCCCGCGCTGGCGGAGGGCTGATCAAGTCGCCCA 199
Qy 107 AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCAACCATCAAAACACAACCTCGCGCAC 166
Db 200 AGCCCTTAATGAAGAAGCAGCGGTGAAGCGGCAACCATCAAAACACAACCTCGCGCAC 259
Qy 167 GCTACGAGTCTCTGGAGACGCTGGGCAAGGCACTTACGGGAAGGTGAAGAGGCAAG 226
Db 260 GCTACGAGTCTCTGGAGACGCTGGGCAAGGCACTTACGGGAAGGTGAAGAGGCAAG 319
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Qy 227 AGAGTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGAAAGACAAAATCAAGATGAGC 286
Db 320 AGAGTCGGGCGCTCTGGTGGCCATCAAGTCAATCCGGAAGGACAAAATCAAGATGAGC 379
Qy 287 AGGATCTGCTGCACATACGAGGGAGATTGAGATCATGTCTTCACTCAACACACCCCA 346
Db 380 AAGATCTGATGCACATACGAGGGAGATTGAGATCATGTCTCATCACTCAACACACCTCA 439
Qy 347 TCATTGCCATCCATGAAGTCTTTGAGAAATAGCAGCAAGATTGTGATTGTCTCATGAGTATG 406
Db 440 TCATTGCCATCCATGAAGTCTTTGAGAAACAGCAGCAAGATTGTGATTGTCTCATGAGTATG 499
Qy 407 CCAGCCGAGGCGATCTGTATGATTACATCAGTGAAGCGGCACAGCTCAGTGAAGCGGACG 466
Db 500 CCAGCCGAGGCGATCTTTATGACTACATCAGCAGCGGCGAGCAGCTCAGTGAAGCGGACG 559
Qy 467 CCAGGCAATTTCTCCGACAGATCGTGTCTCCCTGCACTACTGCCACAGAACCGGATCG 526
Db 560 CTAGGCAATTTCTCCGCGAGATCGTCTCTCGGTGCATATTGCCATCAGAACAGAGTTG 619
Qy 527 TTACCCGAGATCTCAAGCTGGAAAAACATCTCTTAGATGCCAATGGAAAAACATCAAGATTG 586
Db 620 TCCACCGAGATCTCAAGCTGGAGAACATCTCTTTGGATGCCAATGGGAATATCAAGATTG 679
Qy 587 CTGACTTTGGCCTCTCCAACTGTACCACAAAGCAAGTTCTCTCAGACGTTCTGTGGGA 646
Db 680 CTGACTTTGGTCTCTCCAACTGTACCATCAGGCAAGTTCTCTGACACATCTCTGGGA 739
Qy 647 GCGCTCTCTAGGCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCGCAGAGTTG 706
Db 740 GCGCCCTCTATGCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCGCCAGAGTTG 799
Qy 707 ACAGCTGGTCTCTGGGCGTTCTCTCTGTACATCTCTGTGATGGCAGCACCATGCCCTTTGACG 766
Db 800 ACAGCTGGTCTCTGGGCGTTCTCTCTACATCTCTGTGATGGCAGCACCATGCCCTTTGATG 859
Qy 767 GGCAAGGATCATAAACACTCGTGAAGCAAACTAGTAACGGGCTTACCGTGAGCGGCCA 826
Db 860 GGATGACCATAGATCTTAGTGAACAGATCAGAACGGGCGCTACCGGAGGACCACTA 919
Qy 827 AGCGTCCGATGCTGTGGCTGATCCGGTGGCTTTAATGGTGAACCCCAACCGCTCGGG 886
Db 920 AACCTCTGATGCTGTGGCTGATCCGGTGGCTTTGATGGTGAACCCCAACCGCTCGGG 979
Qy 887 CCACACTGGAGGATGATAGCCAGTCACTGGTGGTCACTGGGTTACACACCGGAGTCG 946
Db 980 CCACCTCTGGAGGATGTGGCAGTCACTGGTGGGTCAACTGGGCTACGCCACCGGAGTTG 1039
Qy 947 GGGAAACAGGAAGCCCTGCGTGAGGCGGCAACCTAGTGTGACTTTGGCGGGCGCTCCA 1006
Db 1040 GAGAGCAGGAGGCTCGCATGAGGTTGGGCAACCTTGGCAGTGAATCTGCGCGCGCTCCA 1099
Qy 1007 TGGCGGATGCTGTTACGTGCTCTCGCGCCCTCTCTGGAGAAATGGAGCAAGGTGTGCA 1066
Db 1100 TGGCTGACTGGCTCCGCGCTTCTCTCGCGCCCTCTCTGGAGAAATGGGCGCAAGGTGTGCA 1159
Qy 1067 GCTTCTTCAAGCAGCAGTCCCGGAGGTGGAAGCACTGTACCTGGGCTGAGGCGGCAAC 1126
Db 1160 GCTTCTTCAAGCAGCAGTCACTCTGGTGGGGAAGCACCACCCCTGGGCTGAGGCGCGAGC 1219
Qy 1127 ATTCTCTTAAGAAGTCCCGAAAGAGAAATGACATGGCTCAAAATCTCAAGGTGACCCGG 1186
Db 1220 ATTCTCTCAAGAAGTCCCGCAAGAGAAATGACATGGCCAGTCTCTCCACAGTGACAGG 1279
Qy 1187 CTGAGGATACCTTTCTCGCCCTGGCAAGAGCAGCCTTAAGCTTTCGAAAGGCAATCTCA 1246
Db 1280 CTGATGACACTGCCCCCTGGCAAGAGCAACCTCAAGCTGCCAAGAGGCAATCTCA 1339
Qy 1247 AGAAAAAGTCTCTACTCTGTGAGGGAGGTACAGGAGGACCTCAGGAACCTCAGACCGG 1306
Db 1340 AGAAGAAAGTGTGAGCCTCTGACAGAGGGGTACAGGAGGACCTCCGCGGAGCTCAGCCCAA 1399
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Qy 1187 CTGAGGATACCTTTCTCGCCCTGGCAAGACGAGCCTTAAGCTTCCGAAAGGCATTCTCA 1246
Db 1302 CTGATGACACTGCCATCGCCCTGGCAAGACCACTCAAGCTGCCAAGGGCAATTCTCA 1361
Qy 1247 AGAAAAAGTCTCTACTCTGTGTCAGGGAGGTACAGGAGGACCTTCAGAACTCAGACGG 1306
Db 1362 AGAAGAAGGTGTACGCTCTGACAGGGGTACAGGAGGACCTTCGAGCTCAGGCCAA 1421
Qy 1307 TGCCTGATACCTCAGGAGGAGCTGTCCCTGTGTATCCCTGCTCCCAAGGAAGGCATCC 1366
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Qy 1367 TTAAGAAAGTCTCGACAGCGGTGAATCTGTGTACTACTCTCTCCAGAGCCCAAGCGAGTCTG 1426
Db 1473 TCAAGAAAGCCCGACAGCGGAGTCTGGCTACTACTCTCTCCAGAGCCCAAGTGAATCTG 1532
Qy 1427 GGGAACTCTTAGACCGCAGTGTATGTTGTGAGTGGGAGCCCGTGGAGCAGAAAGTCTC 1486
Db 1533 GGGAGCTCTTGGAGCGCAGCGACGTGTTGTGAGTGGGAGTCCCAAGGAGCAGAAGCTC 1592
Qy 1487 CACAGGCTTCAGGCGCTCTCTCTCCACCGCAGGCGATTCCTCAAACTCAATGGCAAGTCT 1546
Db 1593 CGCAAGCTTCAGGCGCTCTCTCTCCATCGCAAGGCACTCTCAAACTCAATGGCAAGTCT 1652
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Qy 1781 -----GTCTGAAGCGATGTGGCAGGAATCCTTTGGGGATAGTGTCTTTCTGACAG 1834
Db 1893 GAAGCTGCTGAGGCGCTGGCGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGACAG 1952
Qy 1835 ACTGCCAAGGTCAGCTGACGCTCAGACAGCCCTAGGNACTGTCTCAAGCTCAGC 1893
Db 1953 ACTGCCAAGGTCAGCAGCGACCTACCGACAGGCACTGAGGGTCTGTCTCAAGCTCACC 2011

RESULT 15
US-10-343-514-13
; Sequence 13, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; APPLICANT: LEBEVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13

; LENGTH: 1186
; TYPE: DNA
; ORGANISM: RAT
US-10-343-514-13

Query Match 56.6%; Score 1071.4; DB 17; Length 1186;
Best Local Similarity 94.0%; Pred. No. 0;
Matches 1114; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 70 GCCCGCGCTGGCGGACGGGCTCATCAAGTCGGCTTAAACCTCTGTATGAAGAAGCAGCG 129
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Qy 130 GTGAAGCGGACCATCAAAACAAACCTCTCGGCACCGCTACGAGTTCCTGGAGACCGCTG 189
Db 61 GTGAAGCGGACCATCAAAACAAACCTCTCGGCACCGCTACGAGTTCCTGGAGACCGCTG 120
Qy 190 GGCAAGGCGACCTACCGGAAAGGTGAAGAAAGCAAGAGAGCTCGGGCGCTCTGGTGCC 249
Db 121 GGCAAGGCGACCTACCGGAAAGGTGAAGAAAGCAAGAGAGCTCGGGACGCTCGGTGGCC 180
Qy 250 ATCAAGTCCATCAGGAAGACAAATCAAAAGATGAGCAGGATCTGTGCACATACGAGG 309
Db 181 ATCAAGTCTATCAGGAAGACAAATCAAAAGATGAGCAGGATCTGTGTGCACATACGAGG 240
Qy 310 GAGATTGAGATCATGTCTTCACTCAACCCACATCATTTGCCATCCATGAAGTGTCT 369
Db 241 GAGATGAGATCATGTCTTCACTCAACCCACATCATTTGCCATCCATGAAGTGTCT 300
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Qy 490 GTGTCTGCCCTGCACTACTGCCACAGAGCGGATCGTTCCACGAGATCTCAAGCTCGAA 549
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Qy 730 CTGTACATCTCTGTGATGSCACCATGCCCTTTTGGCGGAGGATCATATAACACTGGTG 789
Db 661 CTGTACATCTCTGTGATGSCACCATGCCCTTTTGGCGGAGGATCATATAACACTGGTG 720
Qy 790 AAGCAATCAGTAAACGGGCTTACCTGAGCGCGCCAGCCGCTCCGATGCTGTGGGCTG 849
Db 721 AAGCAATCAGTAAACGGGCTTACCGAGAGCCGCTGCAAAACCGTCTGTATGCTGTGGGCTG 780
Qy 850 ATCCGGTGGCTGTAAATGGTGAACCCACCCGCTCGGSCACACTGGAGGATGTAGCCAGT 909
Db 781 ATCCGGTGGCTGTAAATGGTGAATCCATCCGCTGGGCGACTCTGGAGGATGTAGCCAGT 840
Qy 910 CATTTGGTGGTCAACTGGGTTTACACCCGAGTCCGGGAAACAGGAAGCCCTGCGTGAG 969
Db 841 CATTTGGTGGTCAACTGGGTTTACAGCACCCGAATTTGGGAAACAGGAAGCTCTGCGAGAG 900
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Qy	1030	TCGGGCCCCCTCTCTGGAGATGGAGCCAAAGGTGTGCAGCTTCTTCAAGCAGCAGCTGCCG	1089
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Qy	1090	GGAGGTGGAGCACTGTACCTGGCTCGAGCGGCACATTTCTTTAAGAGTCCCAGAAAG	1149
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Qy	1150	GAGAAATGACATGGCTCAAAATCTGCAGAGGTGACCCGGCTGAGGATACCTTCTTCGCCCT	1209
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Db	1141	GGCAAGAACAGCCTCAAGCTTCGAAAGGTATCTCAAGAAAAG	1185

Search completed: January 25, 2005, 07:55:10
Job time : 996.334 secs

QY 361 GAAGTGTGTTGAGAAATAGCAGCAAGATTCTGTGATTGTCTATGGAGTATGCCAGCCGAGGCGAT 420
DB 483 GAAGTGTGTTGAGAAATAGCAGCAAGATTCTGTGATTGTCTATGGAGTATGCCAGCCGAGGCGAT 542
QY 421 CTGTATGATTATCATCAGTACGAGCGGCCAGCGGTGAGTGAAGCGGAGCGCCAGGCAATTTCTTC 480
DB 543 CTGTATGATTATCATCAGTACGAGCGGCCAGCGGTGAGTGAAGCGGAGCGCCAGGCAATTTCTTC 602
QY 481 CGACAGATCGTGTCTGCCCTGCACTAATGCGCAACAGAAACGGGATCGTTTCAACGAGATCTC 540
DB 603 CGACAGATCGTGTCTGCCCTGCACTAATGCGCAACAGAAACGGGATCGTTTCAACGAGATCTC 662
QY 541 AAGCTGGAACATCTCTTCTAGATGCAATGGAACATCAAGATGCTGATTTGGGCTC 600
DB 663 AAGCTGGAACATCTCTTCTAGATGCAATGGAACATCAAGATGCTGATTTGGGCTC 722
QY 601 TCCAACTGTATACCAAGGCAAGTTCTCTCAGACGTTCTGTGGGAGCCCTCTCTACGCC 660
DB 723 TCCAACTGTATACCAAGGCAAGTTCTCTCAGACGTTCTGTGGGAGCCCTCTCTACGCC 782
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QY 721 GGCCTTCTCTGTATCTCTGTCATGCGCACCATGCTTTTACGGGCGAGATCATAAA 780
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DB 963 TGTGGCTGTATCCCGTGGCTGTTAATGTGTAACCCCAACCGTCCGGGCAACACTGGAGAT 1022
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DB 1023 GTAGCCAGTCAATGTGGTCAATGTGGGTATACACACCGAGTCCGGGCAACAGGAGCC 1082
QY 961 CTGCGTGAAGGTGGCAACCCCTAGTGTGTTGTTGCTGGGCGGCTCCATGGCGGACTGGTTA 1020
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QY 1021 CGTGGCTCTCGCCGCCCTCTCGAGAAATGAGAGCAAGTGTGACGTTCTTCAAGCAG 1080
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QY 1081 CAGTGGCGGAGGTGGAAGCACTGTACTGGGTGGAGCGGCAACATTTCTTTAAGAAG 1140
DB 1203 CAGTGGCGGAGGTGGAAGCACTGTACTGGGTGGAGCGGCAACATTTCTTTAAGAAG 1262
QY 1141 TCCGGAAGGAGATGATGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCT 1200
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QY 1201 TCTCGCCCTCGCAGAGCAGCTTAAGTCTCCGAAAGGCAATTTCAAGAAAGTCTCT 1260
DB 1323 TCTCGCCCTCGCAGAGCAGCTTAAGTCTCCGAAAGGCAATTTCAAGAAAGTCTCT 1382
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DB 1503 CAGCGTGAATCTGTTTACTACTCTCTCCAGAGCCAGCGAGTCTGGGAACTCTTAGAC 1562
QY 1441 GCCAGTGAATGTTTGTGTGAGTGGGAGCCCGTGGAGCAGAAAGTCTCCACAGGCTTCAGGG 1500

DB 1563 GCCAGTGAATGTTTGTGTGAGTGGGAGCCCGTGGAGCAGAAAGTCTCCACAGGCTTCAGGG 1622
QY 1501 CTCTCTCTCCACCGCAAGGCAATTTCAAACTCAATGGCAAGTCTTCCCGCAGACGCTTA 1560
DB 1623 CTCTCTCTCCACCGCAAGGCAATTTCAAACTCAATGGCAAGTCTTCCCGCAGACGCTTA 1682
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QY 1801 GAATCTTTGGGGATAGCTGCTTTTCTCAGACAGCTGCCAAGAGTGTGACGCTAC 1860
DB 1923 GAATCTTTGGGGATAGCTGCTTTTCTCAGACAGCTGCCAAGAGTGTGACGCTAC 1982
QY 1861 AGACAAGCCCTAGGAATCTGTCTCAAAAGCTCAGC 1893
DB 1983 AGACAAGCCCTAGGAATCTGTCTCAAAAGCTCAGC 2015

RESULT 2

US-10-355-975A-4
; Sequence 4, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-355-975A-4

Query Match 100.0%; Score 1893; DB 4; Length 2902;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 243 AAGCAGCGGTGAAGCGGCAACATCAAAACAACTCGCGCACCGCTACAGTTCCTG 302
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Qy 301 ATACGGAGGAGATTGAGATCATGTCTTCACTCAACCAACCCCAACATCATTTGCCATCAT 360
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Qy 423 ATACGGAGGAGATTGAGATCATGTCTTCACTCAACCAACCCCAACATCATTTGCCATCAT 482
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Qy 483 GAACTGTTTGAATATGAGCAAGATTGTGATTGTCTGAGATGACAGCCGAGGCGAT 542
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Qy 1261 ACCTCGTCAGGGAGGTACAGGAGGACCTCAGGAATCAGACCGGTGCTGATCTCA 1320
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Qy 1383 ACCTCGTCAGGGAGGTACAGGAGGACCTCAGGAATCAGACCGGTGCTGATCTCA 1442
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Qy 1321 GGGCAGCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCTCTAAAGATCTCGA 1380
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Qy 1503 CAGCGTGAATCTGTTACTACTCTCTCCAGAGCCAGCAGTCTGGGAACTCTTAGAC 1562
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Qy 1563 GCCAGTCAATCTGTTGAGTGGGACCCGCTGGAGCAGAGTCTCCACAGGCTTCAGGG 1622
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Qy 1623 CTCTCTCCACCCAGGCGCATTTCTCAAACTCAATGGCAAGTCTCCCGCAGCCTTA 1682
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Qy 1683 GAAGGCACTACCCCTAGCACCCTTTGGCTCCCTGGACCAACTGGGCTCTCCCATCTGCA 1742
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Qy 1621 GCCGGCCAGCCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCTCTGCTCCGAGTCC 1680
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Qy 1743 GCCGGCCAGCCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCTCTGCTCCGAGTCC 1802
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Qy 1681 TTTGACCAATTGGACTTGCCTGAACGCTTCTCCGAAACCCACCTGAGGGGCTGTGTCT 1740
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Qy 1803 TTTGACCAATTGGACTTGCCTGAACGCTTCTCCGAAACCCACCTGAGGGGCTGTGTCT 1862
Db |||||
Qy 1741 GTGCAACCTGAGGGGCTTTGAGCAGCCTCCCTCAGAAGTCTGAAGCAGATGTGCGAG 1800
Db |||||
Qy 1863 GTGCAACCTGAGGGGCTTTGAGCAGCCTCCCTCAGAAGTCTGAAGCAGATGTGCGAG 1922
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Qy 1801 GAATCTCTGGGGATAGTCTCTTTCTCTCAGACACTGCCAAGAGGTGACTGCGAGCCTAC 1860
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Qy 1923 GAATCTCTGGGGATAGTCTCTTTCTCTCAGACACTGCCAAGAGGTGACTGCGAGCCTAC 1982
Db |||||
Qy 1861 AGACAAGCCCTAGGAATCTCTCTCAAAAGCTCAGC 1893
Db |||||
Qy 1983 AGACAAGCCCTAGGAATCTCTCTCAAAAGCTCAGC 2015
Db |||||

RESULT 3

US-09-799-451-215
; Sequence 215, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yuning
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799, 451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 215
; LENGTH: 2501

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(1989)
US-09-799-451-215

Query Match 71.68; Score 1355.4; DB 4; Length 2501;
Best Local Similarity 84.08; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;

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200 AGCCCTTAATGAAGAAGCAGCGGCTGAAGCGGCAACCAACCAAGCAACCTCGCGGACC 259
167 GCTACGAGTTCTTGAGACGCTGGCAAGCGGCAACCTACGGGAGGTTGAAGAAGCAGGAG 226
260 GCTACGAGTTCTTGAGACGCTGGGCAAGCGGCAACCTACGGGAGGTTGAAGAAGCGCGGG 319
227 AGAGCTCGGCGGCTCGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAAAGATGAGC 286
320 AGAGCTCGGCGGCTCGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAAAGATGAGC 379
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380 AAGATCTGATGCATACGAGGAGGATGAGATCATGTCTTCACTCAACACCCCTCACA 439
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440 TCATTGCCATCCATGAAGTGTTCAGAAATAGCAGCAAGATGTGATGTGATGAGATG 499
407 CCAGCCGAGGCGATCTGTATGATATACATCAGTACGAGCGGCAACGCTGAGTGAGCGGAGC 466
500 CCAGCCGAGGCGATCTGTATGATATACATCAGTACGAGCGGCAACGCTGAGTGAGCGGAG 559
467 CCAGGCAATTTCTCGGAGAGATGTGTGCTGCGCTGCACTACTGCGGAGCGGATGCG 526
560 CTAGGCAATTTCTCGGAGAGATGTGTGCTGCGCTGCACTACTGCGGAGCGGATGCG 619
527 TTCAACGAGATCTCAAGCTGGAACATCTCTCTAGATGCAATGGAACATCAAGATG 586
620 TCCACCGAGATCTCAAGCTGGAACATCTCTCTAGATGCAATGGAACATCAAGATG 679
587 CTGACTTTGGGCTCTCAACCTGTACCAAGCAAGTTCCTCCAGACGTTCTGTGGGA 646
680 CTGACTTTGGGCTCTCAACCTGTACCAAGCAAGTTCCTCCAGACATTTCTGTGGGA 739
647 GCGCTCTCTACGCTCGGCTGAGATGATCAAGGGAAGCCCTATGTGGGCCAGAGTGG 706
740 GCGGCTCTATGCTCGGCTGAGATGATGATGGAAGGAGCCCTATCAAGGCGGCGAGAGTGG 799
707 ACAGCTGTCTCTGCGGCTCTCTGATACATCTGCTGATGAGGAGGAGGAGGAGGAGGAG 766
800 ACAGCTGTCTCTGCGGCTCTCTGATACATCTGCTGATGAGGAGGAGGAGGAGGAGGAG 859
767 GGCAAGGATCAATAAACAACCTGTGAGCAAAATCAGTAAGCGGCGCTTACCGTGAGCGGCCA 826
860 GGCAATGATCAATAAACAACCTGTGAGCAAAATCAGTAAGCGGCGCTTACCGTGAGCGGCCA 919
827 AGCGCTCGATGCTGTGGGCTGTATCGGCTGGCTGTAAATGGTGAACCCCAACCGTGGG 886
920 AACCTCTGATGCTGTGGGCTGTATCGGCTGGCTGTAAATGGTGAACCCCAACCGTGGG 979
887 CCACACTGGAGGATGTAGCAGTCAATGCTGGGCTCACTGGGCTTACACCAACCGGAGTGG 946
980 CCACCTGGAGGATGTGGCAGTCACTGCTGGGCTCACTGGGCTTACACCAACCGGAGTGG 1039
947 GGGAAACAGGAAGCCCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1006

RESULT 4

US-09-984-890-1
; Sequence 1, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306

1040 GAGAGCAGGAGGCTCCGCATGAGGGTGGGCAACCTGGCAGTGACTCTGCGCGCGCTCCA 1099
1007 TGGCGGACTGGTTACGTGCTCTCTCGCGCCCTCTCTGAGATGAGCAAGGTGCA 1066
1100 TGGCTGACTGGCTCCGGCGTCTCTCGCGCCCTCTCTGAGATGAGGCAAGGTGCA 1159
1067 GCTTCTTCAAGCAGACGTCGCGGAGGTGGAGCACTGTACTCTGGGCTGGAGCGCAAC 1126
1160 GCTTCTTCAAGCAGACGTCGCGGAGGTGGAGCACTGTACTCTGGGCTGGAGCGCAAC 1219
1127 ATTCTCTTAAAGAGTCCGAAAGAGAGATGACATGCTCAAAATCTGCAAGGTGACCGG 1186
1220 ATTCTCTTAAAGAGTCCGCAAGAGAGATGACATGCTCAAAATCTGCAAGGTGACCGG 1279
1187 CTGAGATACCTTCTTCTCGCGCTGGCAAGCAGCCTTAAGCTTCCGAAAGGATCTCA 1246
1280 CTGATCAGACTGCCCCATCGCCCTGGCAAGAGCAACCTCAAGCTGCCAAAGGATCTCA 1339
1247 AGAAAAGTCTCTTACTCTGTCAGGGAGGTACAGGAGACCTCAGGAACTCAGACCGG 1306
1340 AGAAGAGGTGTGAGCTCTGCAAGAGGGGTACAGGAGGACCTCCGAGCTCAGCCCA 1399
1307 TGCTGATCTCAGGGCAGCTCTCCCTGCTGTATCCCTGCTCCCAAGAAAGGATCC 1366
1400 TCCTCGAGCCCGAGGCGAGCTGCCCC-----CCCTGCTCCCAAGAGGATTC 1450
1367 TTAAGAGTCTCGACAGCGTGAATCTGTTACTTACTCTCTCCAGAGCCGAGGTCTG 1426
1451 TCAAGAGGCCCGACAGCGAGTCTGGCTACTTCTCTCCGAGCCCGAGTGAATCTG 1510
1427 GGGAACTCTTAGACGCGCAGTGTGTTGTGAGTGGGACCCCTGGAGCAGAAAGTCTC 1486
1511 GGGAGCTCTTGAACGAGCGAGCGTGTGTTGAGTGGGATCCCAAGGAGCAGAGCCTC 1570
1487 CAGAGGCTCAGGGCTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGCAAGTTCT 1546
1571 CGAAGCTTCAGGGCTGCTCTCCATCGCAAGGCAATCTCAAACTCAATGGCAAGTTCT 1630
1547 CCCGCAAGCTTAGAAGGCACTACCCCTAGACACCTTTGGCTCCCTGGACCAACTGGCCT 1606
1631 CCAGACAGCTTGGAGCTCGCGGCCCGAGCCCTCAGGGCTGTGAGCGAGCAGAGATCC 1690
1607 CTTCCCATCTCGACGCGCGCCCGCCCTCAGGGGCTGTGAGTGGAGCAGAGATCC 1666
1691 CACTCGCCCTCGCGCGCGCGCGAGCCCTCAGGGCTGTGAGCGAGCAGAGATCC 1750
1667 TGTCTCCGAGTCTTTGACCAATTTGACTTGGCTGNAAGTCTTCCGAAACCCCACTGA 1726
1751 TGTCTCTGAGTCTTTGACCAATTTGACTTGGCTGNAAGTCTTCCGAAACCCCACTGC 1810
1727 GGGGCTGTGTGTGTGGCAACCTGAGGGGGCTTGAGCAGGCTCCCTCAGAAAG----- 1780
1811 GGGGCTGTGTGTGTGGCAACCTCAGGGGGCTTGAGGAGCCCTCAGAGGGGCGCTG 1870
1781 -----GTCTGAAGCAGATGGTGGCAGAAATCTTGGGGGATAGTGTCTTTCTGTGACAG 1834
1871 GAAGTGCCTGAGCGCTGGCGCAGGATCTTTTGGGGGACAGCTGTCTTTCCCTGACAG 1930
1835 ACTGCCAAGAGGTGACTGAGCAGCTCAGACAGCCCTTAGAAATCTGCTCAAGGCTCAGC 1893
1931 ACTGCCAAGAGGTGACAGCGACCTTACCGACAGGCACTGAGGGTCTGCTCAAGGCTCACC 1989


```
; Sequence 1257, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1257
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1257

Query Match 10.0%; Score 189.2; DB 4; Length 484;
Best Local Similarity 64.3%; Pred. No. 6.2e-44;
Matches 284; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

Qy 233 CGGGGCTGTGGTCCATCAAGTCCATCAGGAAGAACAATAAAGATGAGCAGGATC 292
Db 442 CGGGCCAGGAGTGGCTATCAAAACCATCAAGAAGTCAAGATCGAGGCCGCGGATT 383
Qy 293 TGTGACATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCCAATCATTTG 352
Db 382 TGGTGGCATCCGTCGGAGGTGCAGATTATGAGCTCAGTGCATATCCCAATCATTC 323
Qy 353 CCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATTGTGATGAGATGATGCCAGCC 412
Db 322 ACATCTACGAAGTATTGAGAAATCGTGAGAAATGGTGTAGTATGATGAAATTTGCCGCTG 263
Qy 413 GAGGCGATCTGTATGATTATCATCAGTGCAGCGGCCACGGTGCAGTGCAGCGGAGCCAGGC 472
Db 262 GCGGCGAGCTCTACGACTATCTGTCTGAAGAGGAGGTCTCACCAGGAGGAGCGGAGAC 203
Qy 473 ATTTCTTCCGACAGATCGTGTCTGCCCTGCACCTACTGCCACCAAGACGGGATGTTCCACC 532
Db 202 GCATCTTCCGCGAGTGGCCACCGCGTCTACTGTCTACAAGCACAAGATCTGCCATC 143
Qy 533 GAGATCTCAAGCTGGAAAAACATCTTCTAGATCCCAATGGAACATCAAGATTGCTGACT 592
Db 142 GCGATCTCAAGCTGGAGAACATCTCTGTCGAGAGGAGGCAATGCTAAGATTGCTGATT 83
Qy 593 TTGGCTCTCAACCTGTACCAACAAAGGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTC 652
Db 82 TTGGGTTGTGCAATGTGTTGATGACGAGCTGCTGGGCACTTTTGGCGTTCCCCAC 23
Qy 653 TCTACGCTCGCCTGAGATAGT 674
Db 22 TCTATGCTCGCCGAAATTTGT 1

RESULT 8
US-09-930-181-1
; Sequence 1, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(2112)
US-09-930-181-1

Query Match 9.8%; Score 186.4; DB 4; Length 2908;
Best Local Similarity 53.5%; Pred. No. 1e-42;
Matches 413; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

Qy 166 CGGTACGAGTCTCTGGAGACGCTGGGCAAGGCGACCTTACCGGAAGGTGAAGAAGGCACGA 225
Db 157 CCTACCGCTGGAGAAGACGCTGGGCAAGGCGACAGGTCTGTGTGAAGCTGGGGGTT 216
Qy 226 GAGAGCTCGGGGCGTCTGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAG 285
Db 217 CACTGCGTCACTCCCAAGAGGTGGCCATCAAGATCGTCAACCGTGAAGAGCTCAGCGAG 276
Qy 286 CAGGATCTGTGCACATACCGGAGGAGATTGAGATCATGTCTTCACTCAACCCACCCAC 345
Db 277 TCGTGTGATGAAGTGGAGCGGAGATCCGATCTCTGAAGCTCATTTGAGCACCCAC 336
Qy 346 ATCATGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATTGTGATGAGTAT 405
```

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Db 337 GTCTAAAGCTGCACGAGCTTTATGAAACAAAAAATTTGTACCTGGTCTAGAACAC 396
Qy 406 GCACGCCGAGCGGATCTGTATGATTACATCAGTCAGCGGCCACCGCTGAGTGACGGGAC 465
Db 397 GTGTACGGTGGTGAAGCTCTTCGACTACTCTGGTGAAGAGGGGAGGCTGACGCCCTAAGGAG 456
Qy 466 GCCAGGCAATTTCTTCCGACAGATCGTGTCTGCCCTGCACACTGCCCCACGAGAAACGGGATC 525
Db 457 GCTCGAAGTCTTCTCCGCGAGATCATCTCTGCGCTGGACTTCTGCCACAGCCACTCCATA 516
Qy 526 GTTCACCGAGATCTCAAGCTGGAACATCTCTTCTAGATGCAATGGAACATCAAGATT 585
Db 517 TGCCACAGGGATCTGAACACCTGAAACCTCTCTGCTGGACGAGAAAGAAACAACATCCGCATC 576
Qy 586 GCTGACTTTGGCTCTCTCAACCTGTACACAAAGGCAAGTTCTCTCCAGAGCTTCTGTGGG 645
Db 577 GCAGACTTTGGCTGCGGTCTCTGCGAGTGTGCGGAGAGCTTGTGGAGACAGCTGTGGG 636
Qy 646 AGCCTCTCTACGCTCGCTCGCTGAGATAGTCAACGGGAGGCCCTATGTGGGCCACAGAGTG 705
Db 637 TCCCCCACTACGCTCGCTCGGAGGTGATCGGGGGGAGAGTATGACGGCGCGAAGCGC 696
Qy 706 GACAGCTGGTCTCTGGGGCTTCTCTGTACATCTCTGTGATGCAATGCAATGCTTTGAC 765
Db 697 GACGTGTGGAGCTGCGGCGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
Qy 766 GGGCAGGATCATAAACACACGTGTGAAGCAAAATCAGTAACGGGGCTTACCGTGAGCGGCC 825
Db 757 GATGACAACTTGGACAGCTGTGGAGAGGTGAAGCGGGCGGTGTTCCACATGCCGCCAC 816
Qy 826 ---AAGCCGTCGATGCTGTGGCTGATCCGGTGGCTGTTAATGTGTGAACCCCGCCGCT 882
Db 817 TTTATCCCGCCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGGAACGCGCAGC 876
Qy 883 CGGCGCACACTGGAGGATGTAGCCAGTCATTTGGTGGGTCAACTGGGGTTACA 934
Db 877 CGCCTCAGCTAGAGCACATTCAGAAACACATATGTTATAGGGGGCAAGA 928
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RESULT 9

```
US-08-557-006C-39
; Sequence 39, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR FILING DATE: 1996-03-06
; PRIOR FILING DATE: 1994-05-20
; PRIOR FILING DATE: 1993-05-21
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 2652
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
```

Query Match

9.6%; Score 182.4; DB 3; Length 2652;

```
Best Local Similarity 53.0%; Pred. No. 1.3e-41;
Matches 437; Conservative 0; Mismatches 381; Indels 6; Gaps 2;
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Qy 120 GAAGCAGCGGCTGAGCGGCACCATCACAAACACCAACCTCGGGCACCGTACGAGTTCTCT 179
Db 4 GAACATGGCTGAGAAGCAGAAGCAGCAGCGGCGGTGTAAGATCGGACACTACGTCGCTGGG 63
Qy 180 GGAGACGCTCGGCAAGGGCACCTACGGGAAAGGTGAAGAGCGCAGAGAGAGCTCG---GG 236
Db 64 GGACACCTCGGCGCTCGGCACCTTCGGCAAGTGAAGATTGGAGAAACATCAATTGACAGG 123
Qy 237 GCGTCTGGTGGCCATCAAGTCCATCAGAAAGAAACAAATCAAAAGATGAGCAGGATCTGCT 296
Db 124 CCATAAAGTGGCAGTTAAAGATCTTAAATAGACAGAGATTCGCAGATTAGATGTTGTTGG 183
Qy 297 GCACATACGGAGGGAGATTCAGATCATGCTTCACTCAACACCCACCATCATTTGCCAT 356
Db 184 AAAAAATAAACAGAAATTCAAAATCTTTAACTCTTTTCGTCATCTCTATATATCAAACT 243
Qy 357 CCATGAAGTGTTCAGAAATAGCAGCAAGATTGTGATTGTTCATGGAGTATGCCAGCCGAGG 416
Db 244 CTACCAAGTGTATCAGCACTCCACAGACTTTTTTATGTTAATGGAATATGTTCTGAGG 303
Qy 417 CGATCTGTATGATTACATCAGTCAGCGGCCACCGCTGAGTGAGCGGACCGCAGGCAATTT 476
Db 304 TGAATTGTTCCGACTACATCTGTAAACACGGGAGGGTTGAAGAGGTGAAGCTCGCCGCT 363
Qy 477 CTTCCGACAGATCGTGTCTGCCCTGCACACTTCCACCAGACGGGATCGTTTCCACGAGA 536
Db 364 CTTCCAGCAGATTCTGTCTGCCGTGGACTACTGTCTCAGGCACATGGTTGTCCACAGGA 423
Qy 537 TCTCAAGCTGGAACACATCTCTAGATGCAATGGAACATCAAGATTGCTGACTTTGG 596
Db 424 CTTGAAGCCAGAGAACTGTGTCTGACGCCAGATGATGCTAAGATAGCTGACTTTCGG 483
Qy 597 CTTCTCAACCTGTACCAAAAGCAAGTTCTTCCAGACGTTCTGTGGGAGCCCTCTCTA 656
Db 484 ACTCTCTAATATGATGTGAGTGTGAAATTTCTACGAACTAGCTGTGATCGCCAAATTA 543
Qy 657 CGCCTCGCTGAGATAGTCAACGGGAGCCCTATGTGGGCCAGAGGTGACAGCTGGTC 716
Db 544 TGCACACCGGAGGTCTATCTCAGGAAAGGCTGTATGCGGGTCTCTGAGGTGATATCTCGAG 603
Qy 717 TCTGGGCTTCTCTGTACATCTCTGTGATGTCACCATGCGCCATCGCCCTTTGACGGCAGGATCA 776
Db 604 CTGTGGTGTATCTGTATGCCCTTCTCTGTGACACCTCTCCGTTGACCATGAGCAGT 663
Qy 777 TAAACACCTGGTGAAGCAAAATCAGTAACGGGGCTTACCGTGAACCGCCCAAGCCGTCGA 836
Db 664 GCCTACGCTCTTTAAGAAAGATCCGAGGGGTGTGTTCTACATCCCGAGTATCTCAACCG 723
Qy 837 TGCCTGTGGC---CTGATCGGTGGCTGTTAATGTTGAACCCACCCGCTCGGGCCACT 893
Db 724 TTCTATTGCCACTCTCTGATGCACATGCTGCGAGTGGACCCCTTGAAGCGAGCAACTAT 783
Qy 894 GGAGGATGTAGCCAGTCATTGGTGGGTCAACTCGGGTTACACCA 937
Db 784 CAAAGACATACGAGAGCATGAATGTTTAAACAGGATTTGCCCA 827
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RESULT 10

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US-08-557-006C-24
; Sequence 24, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR FILING DATE: 1996-03-06
; PRIOR FILING DATE: 1994-05-20
; PRIOR FILING DATE: 1993-05-21
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 2652
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
```

Query Match

9.6%; Score 182.4; DB 3; Length 2652;

;; PRIOR FILING DATE: 1994-05-20
;; PRIOR APPLICATION NUMBER: GB 9310489.1
;; PRIOR FILING DATE: 1993-05-21
;; PRIOR APPLICATION NUMBER: GB 9318010.7
;; PRIOR FILING DATE: 1993-08-31
;; NUMBER OF SEQ ID NOS: 44
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 24
;; LENGTH: 2761
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: cDNA of rat
;; OTHER INFORMATION: liver AMP protein kinase
US-08-557-006C-24

Query Match 9.6%; Score 182.4; DB 3; Length 2761;
Best Local Similarity 53.0%; Pred. No. 1.3e-41;
Matches 437; Conservative 0; Mismatches 381; Indels 6; Gaps 2;
QY 120 GAAGCAGCGGTGAAGCGGCACCATCAAAACAACTCTGGGACCGCTACGAGTTCTT 179
DB 20 GAACATGCTGAGAAGCAGACGACGCGGTGAAGATCGACACTACGTCGTGG 79
QY 180 GGAGACGCTGGGCAAGGCGACCTACGGAAGGTGAAGAGCGCAGAGAGCTCG---GG 236
DB 80 GGACACCCCTGGCGCTGGCACCTTCGGCAAGTGAAGATTGGAGAACATCAATTGACAGG 139
QY 237 GCGTCTGTGGCCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCAGGATCTGCT 296
DB 140 CCATAAGTGCGAGTTAAGATCTTAATAGACAGAGATTCGCAAGTTAGATGTTGTGG 199
QY 297 GCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACACCCCGACATATGGCAT 356
DB 200 AAAAATAAACGAGAAATTCAAAATCTTAAACTCTTTCGTATCTCTATATTAACAAC 259
QY 357 CCATGAAATGTTGAGATAGCAGAGATGTGATGTCATGAGTATGATGATGCGCCGAGG 416
DB 260 CTACCAAGTATCAGACTCCACAGACTTTTTATGTAATGAATATGATGTCGTGAGG 319
QY 417 CGATCTGTATGATTACATCAGTGAAGCGCCACGCTGATGAGCGGGACGCGCATTT 476
DB 320 TGAATTGTTGACATACATCTGTAAACACGGGAGGTTGAAGAGTGAAGCTCCCGGCT 379
QY 477 CTTCGACAGATGCTGTCTGCTGCTACTAGTCCACAGACGGGATCTGTCACCGAGA 536
DB 380 CTTCAGCAGATTCTGTCTGCGTGGACTACTGTACAGGCACATGTTGTCTCCACAGGGA 439
QY 537 TCTCAAGCTGGAAACATCTTCTAGATGCCAATGGAACATCAAGATTGCTGACTTTGG 596
DB 440 CTTGAAGCCAGAAACGTTGCTGCGACGCCAGATGATGCTAAGATAGCTGACTTCGG 499
QY 597 CCTCTCCAACTGTACCAAGCAAGTTCTCTCAGAGTTCTGTGGAGCCCTCTCTA 656
DB 500 ACTCTCTAATATGATGTAGATGTTGAATTTCTACGAACTAGCTGTGATCGCCAAATTA 559
QY 657 GCGCTCGCTGATAGTCAAGCGGAGCCCTATGTGGCCGACAGGTGGACAGTGTGTC 716
DB 560 TGCAGACCGGAGGTCACTCTCAGGAAGGCTGTATCGGGTCTGAGGTTGATATCTGGAG 619
QY 717 TCTGGCGGTTCTCTGTATACATCTCTGTGATGGCACCATGCGCTTTGACGGGCGAGATCA 776
DB 620 CTGTGTTGTTATCTGTATGCTCTCTGTGGCACCTCTCCGTTTCGACGATGAGCAGT 679
QY 777 TAAACAACCTGTGAAGCAAAATCAGTAAACGGGCTTACCGTGAAGCGCCCAAGCGTCCGA 836
DB 680 GCGTACGCTCTTAAAGAGATCCGAGGGGCTGTGTTCTACATCCCGGAGTATCTCAACCG 739
QY 837 TGCTGTGCG---CTGATCCGTTGGTGTATGTTGAACCCACCCCGTGGGCCACACT 893
DB 740 TTCTATGTCACCTCTGTGATGACATGCTGAGGTGGACCCCTTGAAGCGAGCAACTAT 799
QY 894 GGAGGATGTAGCCAGTCAATTGGTGGTCAACTGGGGTTACACCA 937

DB 800 CAAAGACATACGAGAGCATGAATGGTTTAAACAGGATTTGCCCA 843
RESULT 11
US-08-557-006C-38
; Sequence 38, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forder, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Human AMP protein kinase
US-08-557-006C-38

Query Match 9.6%; Score 181.2; DB 3; Length 1742;
Best Local Similarity 53.1%; Pred. No. 2.3e-41;
Matches 434; Conservative 0; Mismatches 378; Indels 6; Gaps 2;
QY 126 GCGGTGAAGCGGCACCATCAAAACAACTCTGGGACCGCTACGAGTTCTCTGAGAC 185
DB 3 GGTGAGAAGAGAGACGACGCGGCTGTGAAGATCGGACACTTCTCTGGGGACAC 62
QY 186 GCTGGCAAGGGCACCTACGGAAGGTGAAGAGGACGAGAGAGCT---CGGGCGTCT 242
DB 63 CTGGGCGTGGCACCTTCGGCAAGTGAAGATTGGAGAACATCAATTGACAGGCCATAA 122
QY 243 GGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAGATGAGCAGGATCTCTGCACAT 302
DB 123 AGTGGCAGTTAAGATCTTAAATAGACAGAAAGATTTCAGTTTGTGTTGAAAAAT 182
QY 303 ACGGAGGAGATTGATCATGTCTTCACTCAACACCCCCACATCATTTGCCATCCATGA 362
DB 183 AAAACGAGAAATCAAAATCTTAACTCTTTCGTATCTCATATTTATCAAACTTACCA 242
QY 363 AGTGTGTTGAGATAGCAGCAAGATTGTGATTTGTTCATGGAGTATGCGAGCGGCGATCT 422
DB 243 AGTATCAGCACTCCAAACAGACTTTTATGTTAATGGAATATGTCTCTGGAGGTGAAT 302
QY 423 GTATGATTATCAGTGAAGCGGCACCGGTGAGTGAAGCGGACGCGGCAATTTCTTCG 482
DB 303 GTTTCAGTACATCTGTAAACACGCGGAGGTGAAGAGGTGAAGCTCGCGGCTCTTCCA 362
QY 483 ACAGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
DB 363 GCAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
QY 543 GCTGGAAACATCTCTTCTAGATGCCAATGGAACATCAAGATTGTGATCTTTCGCTCTC 602
DB 423 GCCAGAGAACGTGTGCTGGACGCCAGATGAATGCTTAAGATAGCTGACTTCGAGCTCTC 482
QY 603 CAACCTGTACCAAAAGGCAAGTTCTCCAGAGCTTCTGTTGGGAGCCCTCTCTACGCGTC 662
DB 483 TAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 542
QY 663 GCGTGTAGATAGTCAACGGGAGGCCCTATGTGGGCCAGAGAGTGGACAGTGGTCTCTGGG 722
DB 543 ACCGAGGTCTATCTCAGAGAGGCTGTATGCGGGTCTCTGAGGTTGATATCTCTGAGCTGTGG 602


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; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 112
; LENGTH: 2899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(2899)
US-09-774-528-112

Query Match          9.3%; Score 176.4; DB 4; Length 2899;
Best Local Similarity 52.4%; Pred. No. 7e-40;
Matches 412; Conservative 0; Mismatches 371; Indels 3; Gaps 1;

QY 113 TGATGAAGAGCAGCGCGTGAAGCGGCACCATCACAAACACAACTGCGGCACCGCTACG 172
Db 120 TGGTCATGGCGATGGCCCGAGGCACCTTGACGCGCGCGGTCCGGGTGGGTCTCTACG 179

QY 173 AGTTCTGGAGACGCTGGGCAAGGGACCTACGGGAAGGTGAAGAGGCACGAGAGCT 232
Db 180 ACATCGAGGGCAGCTGGCAAGGGCAACTTCGCTGTGTGAAGCTGGGCGGCACCGGA 239

QY 233 CGGGGCGTCTGTGGCCATCAAGTCCATCAGGAAGACAAAATCAAGATGAGCAGATC 292
Db 240 TCACCAAGACGGAGGTGGCAATAAATAATTCGATAAGTCTCAGCTGATGCACTGAAC 299

QY 293 TGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACACCCCAATCATTTG 352
Db 300 TTGAGAAAATCTACCGAGAGTACAAATAATGAAATGTTAGACCACTTACATAATCA 359

QY 353 CCATCCATGAAGTGTGAGNATAGCAGCAAGATTGTGATGTCATGAGTATGCCAGCC 412
Db 360 AACTTTATCAGGTAATGGAGACCAAAAGTATGTTGTACCTTGTGACAGAATATGCCAAA 419

QY 413 GAGCGGATCTGTATGATTACATCAGTGAGCGCCACCGCTGAGTGAGCGGACGCCAGGC 472
Db 420 ATGAGAGAAATTTTGAATCTTCTGCTAATCATGCGCGGTAAATGAGTCTGAAGCCAGGC 479

QY 473 ATTTCCTCCGACAGATCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 532
Db 480 GAAAATTTCTGGCAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539

QY 533 GAGATCTCAAGCTGGRAAACAATCTCTAGATGCCAATGGAAACATCAAGATTGCTGACT 592
Db 540 GTGACCTCAAGCTGAAATCTCTGCTGGATTAACAATGAAATTAACAATGACAGATT 599

QY 593 TTGGCCTCTCAACCTGTACCAAGCAAGTTCTCTCAGACGTTCTGTGGGAGCCCTC 652
Db 600 TCGGTTTTGGAAATTTCTTTAAAGTGTGAACTGTGGCAACATGGTGTGGCAGCCGCC 659

QY 653 TCTAGCCTCGCTGAGATAGTCAAGGGAAGCCCTATGTGGGCCAGAGGTGACAGCT 712
Db 660 CTTATGACGCCCAAGAGTCTTTGAAGGGCAGCAGTATGAAGGACCAAGCTGGACATCT 719

QY 713 GGTCTCTGGGCGTCTCTGTACATCTCTGTGTCATGGCACCATGCCCTTTTACCGGAGG 772
Db 720 GAGTATGGGAGTGTCTTTATGTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779

QY 773 ATCATAAACACATGCTGAAGCAAAATCAGTAACGGGGCTTTACCGTGAGCGGCCAAGCGGT 832
Db 780 CTCCTTCAATTTTGAAGCAGAGGGTCTTGAAGGAAGATTCGGAATTCGCTATTTTCATGT 839

QY 833 CGATGCTCTGTG---GCTGTATCCGGTGGCTGTTAATGTTGAACCCCAACCGCTGGGCCA 889
Db 840 CAGAGAATTTGCGAGCACCTTATCCGAAGAGATGTTGGTCTTAGACCCATCCAAACGGCTAA 899

QY 890 CACTGG 895
Db 900 CCATAG 905

RESULT 14
US-09-930-181-3
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; Sequence 3, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3
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Query Match          9.2%; Score 174; DB 4; Length 3364;
Best Local Similarity 53.4%; Pred. No. 3.6e-39;
Matches 414; Conservative 0; Mismatches 355; Indels 7; Gaps 2;

QY 166 CGTACGAGTTCTCTGGAGACGCTGGGCAAGGCACCTACGGGAAGGTGAAGAGCAGCA 225
Db 280 CCTACCGGCTGGAGAAGACGCTGGGCAAGGGGCAGACAGGTCTGCTGAAGCTGGGGGTT 339

QY 226 GAGAGCTCGGGGCGTCTGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAGATGAG 285
Db 340 CACTGGCTCACCTGCCAGAAAGGTGGCCATCAAGATCGTCAACCGTGAGAGCTCAGCGAG 399

QY 286 CAGGATCTCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCAACCCCCAC 345
Db 400 TCGTCTCATGAGGTGGAGCGGAGATCGCATCTGAAGCTCATTGAGCACCCCCAC 459

QY 346 ATCAITGGCCATCCATGAAGTGTGAGATAGCAGCAAGATTGTGATT-----GTCAATGA 401
Db 460 GTCTTAAAGCTGCACGACGTTTATGAAAAACAAAAATATTTGTAGGTACTGTGTGTAGA 519

QY 402 GTATGCCGCGGAGGATCTGTATGATTACATCAGTGAGCGGCCACGCTGAGTGAAGCG 461
Db 520 ACAGTGTGAGGTGGTGGTCTTTCGACTACCTGTGTAAGAGGGGAGGCTGAGCGCTAA 579

QY 462 GGACGCGCAGGCATTTCTTCCGACAGATCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 531
Db 580 GGAGGCTCGGAAGTTCTTCCGGCAGATCATCTCGCTGGACTTCTGCTGACAGCCACTC 639

QY 522 GATCGTTTACCGAGATCTCAAGCTGGAAACATCTCTTAGATGCCAATGGAAACATCAA 581
Db 640 CATATGCCACAGGGATCTGAAACCTGAAACCTCTGCTGGACGAGAAAGAACATATCCG 699

QY 582 GATTGCTGACTTTTGGCTCTCCAACTGTACCAAGGCAAGTCTCTCCAGACGTTCTG 641
Db 700 CATCGCAGACTTTGGGATGGCTGCTTCCAGAGTGGCAGACGCTGTTGGAGACCACTG 759

QY 642 TGGGAGCGCTCTCTACGCTTCCGCTGAGATGATGATCAACGGGAAGCCCTATGTGGGCCAGA 701
Db 760 TGGTCCCCCACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819

QY 702 GGTGGAAGCTGTCTCTGGCGCTTCTCTGTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 761
Db 820 GCGGACGCTGTGGAGCTGCGGCGCTCATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879

QY 762 TGACGGCAGGATCATAAAAACACTGGTGAAGCAAAATCAGTAACGGGGCTTTACCGTGAGCC 821
Db 880 CGACGATGACAACTTTCGACAGCTGCTGGAGAGGTGAAGCGGGCGCTGTTCCACATGCC 939

QY 822 GCCC---AAGCGTCCGATGCCCTGATCCGGTGGCTGTTAATGTTGAGACCCAC 878
Db 940 GCATTTATCCCGCCCGACTGCCAGAGTCTGTCACGGGGCATGATCGAGGTGAGACGCCG 999

QY 879 CCGTCGGGCCACACTGGAGGATGTAGCCAGTCAATTGGTGGTCAACTGGGGTTACA 934
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Db 1000 AGCCGCTCACGCTAGAGCACATTTCAGAAACACATATGGTATATAGGGGCAAGA 1055

RESULT 15

US-10-003-690-3

; Sequence 3, Application US/10003690

; Patent No. 6787345

; GENERAL INFORMATION:

; APPLICANT: RORY A.J. CURTIS

; TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase

; FILE OF INVENTION: and Uses Therefor

; FILE REFERENCE: MNI-206

; CURRENT APPLICATION NUMBER: US/10/003.690

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: 60/248,893

; PRIOR FILING DATE: 2000-11-15

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2334

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2334)

US-10-003-690-3

Query Match 9.1%; Score 173; DB 4; Length 2334;

Best Local Similarity 52.7%; Pred. No. 5.8e-39;

Matches 399; Conservative 0; Mismatches 355; Indels 3; Gaps 1;

Qy 165 CCGCTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACGGGAAGGTGAAGAGGCACG 224

Db 96 CCCCTATCGCTGGAGAGACGCTGGGCAAGGACACAGGCGCTGGTTAACTCGGGGT 155

Qy 225 AGAGAGTCGGGGCGTCTGGTGGCCATCAAGTCATCAGAAAGACAAATCAAAAGATGA 284

Db 156 CCACTGCATCAGGGTCAGAAGGTCGCCATCAAGATCGTGAACCGGGAGAAGCTGTCCGA 215

Qy 285 GCAGGATCTGTCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACACCCCA 344

Db 216 GTGGGTCTGATGAAGGTGGAGCGGGAGATCGCCATCTTGAAGCTCATCGAACACCCACA 275

Qy 345 CATCATTCGCCATCCATGAAGTGTGAGAGTAGCAGCAAGATTGTGATGTGATGAGTA 404

Db 276 TGTCTCAAGCTCACAGCGCTACGAGACAGAAATATTTGTACCTGGTTCTGGAGCA 335

Qy 405 TGCCAGCCGAGGCGATCTGTATGATTACATCAGTACGCGGCCACGGCTGAGTACGCGGA 464

Db 336 CGTCTCGGGGGTGAGCTATTTCGACTACCTGGTAAAGAGGGGAGACTGACGCCCAAGGA 395

Qy 465 GCGCAGCATTCTTCGACAGATCGTGTGCGCTGCACTACGACACAGAACGGAT 524

Db 396 GGCCCGAAAGTCTTCGCGCAGATTGTGTGCGCTGGACTTCTGCCACAGCTACTCCAT 455

Qy 525 CGTTACCGAGATCTCAAGCTGGAACATCTTCTAGATGCCAATGGAACATCAAGAT 584

Db 456 CTGCCACAGAGACCTAAAGCCGAGAACCTGCTTTTGGATGAGAAACAAACATCCGCAT 515

Qy 585 TGCTGACTTTGGCCCTCTCCAACTGTACCAAGGCAAGTTCTCCAGACGTTTCTGTGG 644

Db 516 TGCAGACTTCGGCATGGGTCCTTCGAGGTGGGGGACAGCTCTCTGGAGACCAGTCCGG 575

Qy 645 GAGCCCTCTCTACGCCCTCGGCTGAGATGATCAACGGGAAGCCCTATGTGGGCCAGAGGT 704

Db 576 GTCCCCCAATTATCGGTGTCCAGAGGTGATTAAAGGGGAAAAATATGATGCGCCCGGC 635

Qy 705 GGACAGCTGGTCTCTGGGCGTTCTCCTGTACATCTGTTGATGACCATGCCCTTTGA 764

Db 636 AGACATGTGAGAGTGTGAGGTATCTCTTCTGCGCCCTGCTCGTGGGGGCTCTGCCCTTTGA 695

Qy 765 CGGCGAGGATCATAAACACATGTTGAGCAAAATCAGTAAACGGGGCTTACCGTGTAGCCGC - 823

Db 696 TGACGACAACTCCGCCAGCTGTGGAGAAAGGTGAAACGGGGCGTCTTCCACATGCCCA 755

Qy 824 --CCAAGCCGTCCGATGCGCTGTGCGCTGATCCCGTGGCTGTTAATGTTGAACCCACCCG 881

Db 756 CTTTCATTCTCCAGATTGCCAGAGCTTCTTGAGGGGATGATCGAAGTGGAGCCCGAAAA 815

Qy 882 TCGGGCCACACTGGAGGATGTACCCAGTCAATTGGTGG 918

Db 816 AAGGCTCAGTCTGGAGCAAAATTCAGAAACATCCTTGG 852

Search completed: January 25, 2005, 01:59:45

Job time : 156.572 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 05:56:58 ; Search time 875.636 Seconds
(without alignments)
11348.500 Million cell updates/sec

Title: US-09-980-464-4_COPY_123_2015

Perfect score: 1893

Sequence: 1 atggagtcggtgccttact.....gaatcgtcctaagctcagc 1893

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1893	100.0	2902	4	AAC90433 Murine Ly
2	1683.4	88.9	2929	6	AAD31710 Rat SNF1/
3	1360.2	71.9	1884	12	ADL14162 Novel hum
4	1360.2	71.9	3353	6	ABK14000 cDNA enco
5	1360.2	71.9	3353	12	ADL14160 Novel hum
6	1357.6	71.7	3360	6	AAD26459 Human kin
7	1357	71.7	3395	4	AAK94280 Human ful
8	1357	71.7	3395	12	ADL30885 Full leng
9	1357	71.7	3463	12	ADJ96554 Human cal
10	1355.4	71.6	2043	6	ABZ11333 Human pol
11	1355.4	71.6	2501	12	Adm43851 Novel hum
12	1355.4	71.6	3443	5	ABX71420 Human cel
13	1355.4	71.6	3443	10	ADF76964 Novel hum
14	1355.4	71.6	3443	10	ADF81952 Leukemia
15	1355.4	71.6	3443	12	ADO20171 Human PRO
16	1338.8	70.7	2291	4	AAF44659 Novel pro
17	1338.8	70.7	2291	12	ADI29357 Human MAR
18	1314.2	69.4	3200	4	AAF75338 Human TGF
19	1230	65.0	1833	10	ABZ77163 Human pro
20	840.2	44.4	2616	6	ABQ72599 Human MDD
21	840.2	44.4	2619	6	ABQ72698 Human MDD

22	506.4	26.8	2884	4	AAD14328 Human pro
23	506.4	26.8	6828	4	AAD14327 Human pro
24	506.4	26.8	6828	10	ADE38420 Human pro
25	506.4	26.8	6828	11	ADN95767 Human BEC
26	506.4	26.8	6828	12	ADJ74808 Marker ge
27	506.4	26.8	6828	12	ADL25352 Human ARK
28	506.4	26.8	6828	12	ADQ19733 Human sof
29	506.4	26.8	6828	12	ADP43253 Human pro
30	506.4	26.8	6854	12	ADO233883 Human sof
31	356.8	18.8	3594	5	AAD033994 Human pro
32	348.8	18.4	587	4	AAK93296 Human CDN
33	348.8	18.4	587	4	AAK91887 Human CDN
34	348.8	18.4	587	12	ADL29723 5' end of
35	348.8	18.4	587	12	ADL28314 5' end of
36	296.8	15.7	1454	4	ABL21269 Drosophil
37	267	14.1	1723	4	AAH13802 Human CDN
38	236.6	12.5	1594	4	AAF44655 Novel pro
39	236.6	12.5	1594	8	AAAL60326 Human 207
40	236.6	12.5	1594	12	ADI29353 Mouse MAR
41	236.6	12.5	3170	6	ABA05737 Murine ne
42	236.6	12.5	3250	6	ABA05738 Murine ne
43	233.6	12.3	1549	6	ABE64386 Human ser
44	233.6	12.3	2085	8	AAD51409 Human mic
45	233.6	12.3	2085	10	ADG91747 Human mic

ALIGNMENTS

RESULT 1

AAC90433

ID AAC90433 standard; cDNA; 2902 BP.

AC AAC90433;

XX 19-MAR-2001 (first entry)

DT Murine Lymph node Stromal cell kinase 1 coding sequence.

DE Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder;

KW wound healing; periodontal disease; inflammatory disease; tumour;

KW infection; allergy; ss.

XX Mus musculus.

XX WO2000073468-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014696.

XX 28-MAY-1999; 99US-0136781P.

XX (IMMV) IMMUNEX CORP.

XX Bird TA, Virca GD, Martin U, Anderson DM;

XX WPI; 2001-061546/07.

XX P-PSDB; AAB50056.

XX Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.

XX Claim 1; Page 86-87; 106pp; English.

XX The present sequence is the coding sequence for Murine Lymph node Stromal cell kinase 1 (MLSK-1). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal infection

KW Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes;
 KW glucose deprivation; lipid metabolism; therapy; lipoprotein disorder;
 KW hyperglycaemic; drug screening; hypoglycaemia; ss.

XX Rattus sp.

XX Key Location/Qualifiers
 XX CDS 83..1975
 FT /*tag= a
 FT /product= "Rat SNARK protein"
 XX

XX WO200212456-A2.

XX 14-FEB-2002.

XX 02-AUG-2001; 2001WO-CA001109.

XX 03-AUG-2000; 2000US-0222650P.

XX 12-MAR-2001; 2001US-0274613P.

XX 28-MAR-2001; 2001CA-02340783.

XX (ONEO-) 1149336 ONTARIO INC.

XX Drucker DJ, Rosen CF, Lefebvre DL;

XX WPI; 2002-241747/29.

XX P-PSDB; AAE19885.

XX AMPK (AMP-activated protein kinase)-related kinase, designated SNARK
 PT polypeptides and polynucleotides, useful for treating or preventing
 PT diabetes, or other disorders of lipoprotein production leading to
 PT increased levels of cholesterol.

XX Example; Fig 2; 94pp; English.

CC The invention relates to an AMPK (AMP-activated protein kinase)-related
 CC kinase, designated SNARK polypeptides and polynucleotides. SNARK
 CC (SNIF/AMP-activated protein kinase) is involved in stress response to
 CC glucose deprivation. The polynucleotides are useful for expressing SNARK
 CC protein in isolated form or as a protein conjugate. Activation of SNARK
 CC stimulates liver CPT-1 thus enhances lipid metabolism in liver cells and
 CC in other cell types such as heart and skeletal muscles, as well as
 CC increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted
 CC to have insulin-like effects that would enhance the disposal of glucose
 CC into muscle and reduce plasma glucose for the treatment of diabetes and
 CC some type of disorders of lipoprotein production leading to increased
 CC levels of cholesterol or triglycerides. SNARK or its variants may be
 CC administered to a subject to treat or prevent a disease associated with
 CC decreased expression of SNARK, such as diabetes. SNARK antibodies are
 CC used to modulate SNARK activity either in vivo for therapeutic purposes,
 CC or in vitro, for drug screening and related investigational purposes.
 CC SNARK antagonists may be administered to increase fuel production,
 CC decrease glucose uptake and increase levels of blood glucose in a patient
 CC suffering from hypoglycaemia. The present sequence is rat SNARK cDNA

XX Sequence 2929 BP; 650 A; 788 C; 791 G; 700 T; 0 U; 0 Other;

Query Match 88.9%; Score 1683.4; DB 6; Length 2929;
 Best Local Similarity 93.4%; Pred. No. 0;
 Matches 1769; Conservative 0; Mismatches 121; Indels 3; Gaps 1;

QY 1 ATGGAGTCGGTGGCTTACTCCAGCGCCGAGCCAGGCTCCCTCGGCTCCGCGCTGGCC 60
 DB 83 ATGGAGTCGGTGGCTTACACCGCGGGGNAACCTGCTCCCTCGGCTCCGCGCTGGCC 142
 QY 61 TCGGAGAGCGCCCGCGCTGGCGGACGGGTCTCAATGCTGCTAAACCTCTGATGAAG 120
 DB 143 ACGGAGAGCGCCCGCGCTGGCGGACGGGTCTCAATGCTGCTAAACCTCTGATGAAG 202
 QY 121 AAGCAGCGGTGAAGCGGCACCATCACAAACAACTCGGCGACCGGTAGGATTCCTG 180
 DB 203 AAGCAGCGGTGAAGCGGCACCATCACAAACAACTCGGCGACCGGTAGGATTCCTG 262

QY 181 GAGACGCTGGGCAAGGCACCTACCGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGCGT 240
 DB 263 GAGACCTTGGGCAAGGCACCTACCGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGACG 322
 QY 241 CTGGTGGCCATCAAGTCCATCAGGAAAGACAATAATCAAGATGAGCAGGATCTCTGAC 300
 DB 323 CTGGTGGCCATCAAGTCTATCAGGAAGGACAAAATCAAGATGAGCAGGATCTCTGAC 382
 QY 301 ATACGAGGAGGATGAGATCATGTCTCACTCAACCAACCCACACATCATTTGCCATCAT 360
 DB 383 ATAGGAGGAGGATCGAGATCATGTCTCACTCAACCAACCCACACATCATTTGCCATCAT 442
 QY 361 GAAAGTGTTCAGAAATAGCAGCAAGATTTGATTTGTCTCATGTGATATGCAGCCGAGGCGAT 420
 DB 443 GAAAGTGTTCAGAAACAGCAGCAAGATTTGATTTGTCTCATGTGATATGCAGCCGAGGCGAT 502
 QY 421 CTGTATGATTTACATCAGTGAGCGGCCACGGCTCAGTGAGCGGACGCGGACGATTTCTTC 480
 DB 503 CTGTACGATTTACATCAGTGAGCGGCCACGGCTGAATGAGCGGACGCGGACGATTTCTTC 562
 QY 481 CGACAGATCGTGTCTGCCCTGCCTACTGCGCACCCAGAACCGGATTTGTTCACCGGAGCCTC 540
 DB 563 CGACAGATCGTGTCTGCCCTGCCTACTGCGCACCCAGAACCGGATTTGTTCACCGGAGCCTC 622
 QY 541 AAGCTGGAACACATTCCTTTCTAGATGCGCAATGGAACATCAAGATTTGTGAGCTTC 600
 DB 623 AAGCTGGAACACATTCCTTTCTAGATGCGCAGTGGCAACATCAAGATTTGTGAGCTTC 682
 QY 601 TCCAACTGTACCAACAAAGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTCTTAGGCC 660
 DB 683 TCCAACTGTATCACAAAGCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTCTTAGGCC 742
 QY 661 TCGCCTGAGATAGTCACGCGGAGAGCCCTATGTGGGCCAGAGGTGGACAGCTGCTCTG 720
 DB 743 TCACCTGAGATCGTCACGCGGAGAGCCCTATGTGGGCCAGAGGTGGACAGCTGCTCTG 802
 QY 721 GGGCTTCTCTGTACATCTCTGTGTCATGCGACCATGATGCCCTTTGACGGGACGAGATCAATA 780
 DB 803 GGGCTTCTCTGTACATCTCTGTGTCATGCGACCATGATGCCCTTTGACGGGACGAGATCAATA 862
 QY 781 ACATGCTGAAGCAAAATCAGTAAACGGGCTTACCGTGAGCGGCCCAAGCCGCTCCGATGCC 840
 DB 863 ACCCTGTGTAAACAAATCAGTAGCGGGCTTACCGAGAGCCGTGCAAAACCGCTCTGATGCC 922
 QY 841 TGTGGCTGTATCCGCTGGCTGTTAAATGGTGCAACCCACCCGCTGGGCCACACTGGAGAT 900
 DB 923 TGTGGCTGTATCCGCTGGCTGTTAAATGGTGCAATCCCATCCGCTGGGCCCACTCTGGAGGAT 982
 QY 901 GTAGCCAGTCATTTGGTGGGTCAACTGGGGTTACACACCGGAGTCGGGGGAAACAGGAAGCC 960
 DB 983 GTAGCCAGTCATTTGGTGGGTCAACTGGGGTTACAGCACCCGAATTTGGGGAACAGGAAGCT 1042
 QY 961 CTGCGTGAGGCTGGGACCCCTAGTGTGACTTTTGGCGGGCCCTCCATGGCGGACTGTTA 1020
 DB 1043 CTGCGAGAGGCTGGGACCCCTAGCGGTGACTCTGGCGGGCCCTCTATGGCGGACTGTTA 1102
 QY 1021 CGTGGCTCTCTCGCGCCCTCTCTGGAGAAATGGAGCCAAAGGTGTGACGCTTCTTCAAGCAG 1080
 DB 1103 CGTGGCTCTCTCGCGCCCTCTCTGGAGAAATGGAGCCAAAGGTGTGACGCTTCTTCAAGCAG 1162
 QY 1081 CAGGTGCGGGAGGAGTGAAGCACTGTACCTGGGCTGGAGCGGCAACATTTCTTTAAGAAG 1140
 DB 1163 CATGTGCGGGAGGAGTGAAGCACTGGGACCGGGCTGGAGCGGCAACATTTCTTTAAGAAG 1222
 QY 1141 TCCGGAAGGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCT 1200
 DB 1223 TCCGGAAGGAGAAATGACATGGCTCAGACTCTGAGAAATGACCCAGTTGAAGATACCTCT 1282
 QY 1201 TCTCGCCCTGGCAAGAGCAGCTTTAGCTTCCGAAAGGCAATTTCTCAGAAAGAAAGTCTCT 1260
 DB 1283 TCTCGCCCTGGCAAGAACAGCTTCAAGCTTCCGAAAGGATTCCTCAGAAAGAAAGGCTCT 1342
 QY 1261 ACCTCGTCAGGGGAGGTACAGGAGGACCCCTCAGGAACCTCAGACCGGTGCCTGATCTCCA 1320

Db 1343 CCCTCATCGGGAGGTACAGAGGGCCCTCAGAACTCAGACAGTGTCAATACCCCA 1402
Qy 1321 GGGCAGCTGTCTCTGTATCCCTGTCTCCAGAGAAAGCATCTTAAGAACTCTCGA 1380
Db 1403 GGGCAGCTGTCTCTGTATACCTGTCTCCAGAGAAAGCATCTTAAGAACTCTCGG 1462
Qy 1381 CAGCGTGAATCTGTTTACTACTCTCTCCAGAGCCCAAGCGAGTGTGGGAACTCTTAGAC 1440
Db 1463 CAGCGTGAATCTGTTTACTACTCTCTCCAGAGCCCAAGCGAGTGTGGGAACTCTTAGAC 1522
Qy 1441 GCCAGTGAATGTTTGTAGTGGGAGCCCGTGGAGCAGAGTCTCCACAGGCTTCAGGG 1500
Db 1523 GCAGGTGATGTTTGTAGTGGGAGCCCGTGGAGCAGAGTCTCCACAGGCTTCAGGG 1582
Qy 1501 CTCCTCTCCACCGCAAGGGCATCTCAAACTCAATGGCAAGTCTCTCCGACAGCCCTTA 1560
Db 1583 ---CGCTCCATCGAAGGGCATCTCAAACTCAATGGCAAGTCTCTCCGACAGCCCTTA 1639
Qy 1561 GAAGGCACTACCTCTAGACCTTTGGTCTCTTGAGCAAACTGGGCTCTCCATCTCTGCA 1620
Db 1640 GAAGGCACTGCCCCCTAGCACCTTTGGTCTCTTGAGCAAACTGGGCTCTCCATCTCTGCA 1699
Qy 1621 GCCCGGCCAGCCGCTCTCGGGAGCTGTAGTGAGGACAGCATCTCTCCGAGTCC 1680
Db 1700 GCCCGGCCAGCCGCTCTCGGGAGCTGTAGTGAGGACAGCATCTCTCTCCGAGTCC 1759
Qy 1681 TTTGACCAATGGACTTGGCTTGAACGTCTTCCGAAACCCCACTGAGGGGCTGTGTCT 1740
Db 1760 TTTGACCAATGGACTTGGCTTGAACGTCTTCCGAAACCCCACTGAGGAGCTGTGTCT 1819
Qy 1741 GTGACAACTGAGGGGCTTGGAGGCTCTCTGAGAGTCTGAGCGATGTGGCAG 1800
Db 1820 GTGACAACTGAGGGGCTTGGAGGCTCTCTGAGAGTCTGAGCGATGTGGCAG 1879
Qy 1801 GAATCTTTGGGGATAGTCTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGGCTTAC 1860
Db 1880 GAATCTTTGGGGATAGGCGCTTTCTCTGACAGACTGCCAAGAGGTGACAGGCTTAC 1939
Qy 1861 AGACAAGCCCTAGGAATCTGTCAAGCTCAGC 1893
Db 1940 AGACAAGCCCTAGGAATCTGTCTGAAGCTCAGC 1972

RESULT 3

ID ADL14162 standard; cDNA; 1884 BP.

XX AC ADL14162;

XX DT 17-JUN-2004 (first entry)

XX DE Novel human gene 3700 coding region.

KW cytosolic; cardiac; hypotensive; antiangiinal; osteopathic;
KW antiarthritic; antirheumatic; neuroprotective; antiinflammatory;
KW antiproliferative; antidiabetic; cardiovascular; virucide; analgesic; CNS;
KW angogenesis inhibitor; angogenesis stimulator; cerebroprotective;
KW nephrotropic; antithyroid; dermatological; immunomodulator;
KW cell proliferation disorder; cell differentiation disorder;
KW brain disorder; platelet disorder; breast disorder; colon disorder;
KW kidney disorder; renal disorder; lung disorder; ovarian disorder;
KW prostate disorder; cervical disorder; spleen disorder; thymus disorder;
KW thyroid disorder; testes disorder; haematopoietic disorder;
KW pancreatic disorder; skeletal muscle disorder; skin disorder;
KW dermal disorder; bone metabolism disorder; immune disorder;
KW inflammatory disorder; cardiovascular disorder;
KW endobelial cell disorder; liver disorder; viral disease; pain disorder;
KW metabolic disorder; neurological disorder;
KW central nervous system disorder; erythroid disorder;
KW blood vessel disorder; angioleptic disorder; cancer; heart failure;
KW hypertension; angina; osteoarthritis; rheumatoid arthritis;
KW multiple sclerosis; Crohn's disease; psoriasis; asthma;

KW cell proliferation; cell differentiation; cell growth; cell division;
KW human; gene; ss.

XX OS Homo sapiens.

XX PN US2004058355-A1.

XX PD 25-MAR-2004.

XX PF 25-APR-2003; 2003US-00423543.

XX PR 30-SEP-1998; 98US-00163821.

XX PR 27-JAN-1999; 99US-0117580P.

XX PR 25-MAR-1999; 99US-00276400.

XX PR 30-JUL-1999; 99US-00365162.

XX PR 09-SEP-1999; 99US-00392189.

XX PR 05-OCT-1999; 99US-00412210.

XX PR 23-NOV-1999; 99US-00448076.

XX PR 28-FEB-2000; 2000US-0186061P.

XX PR 28-APR-2000; 2000US-0200688P.

XX PR 19-MAY-2000; 2000US-0205447P.

XX PR 30-JUN-2000; 2000US-00608921.

XX PR 31-JUL-2000; 2000US-0221925P.

XX PR 25-SEP-2000; 2000US-0234922P.

XX PR 08-NOV-2000; 2000US-0246669P.

XX PR 14-NOV-2000; 2000US-0248325P.

XX PR 15-NOV-2000; 2000US-0248993P.

XX PR 22-DEC-2000; 2000US-0257511P.

XX PR 05-JAN-2001; 2001US-0260166P.

XX PR 28-FEB-2001; 2001US-00797039.

XX PR 27-APR-2001; 2001US-00845044.

XX PR 20-JUL-2001; 2001US-00909743.

XX PR 31-JUL-2001; 2001US-00920346.

XX PR 13-AUG-2001; 2001US-00928531.

XX PR 14-AUG-2001; 2001US-00929218.

XX PR 15-AUG-2001; 2001US-0312539P.

XX PR 25-SEP-2001; 2001US-00963159.

XX PR 08-NOV-2001; 2001US-00008016.

XX PR 13-NOV-2001; 2001US-00012055.

XX PR 15-NOV-2001; 2001US-00003690.

XX PR 30-JAN-2002; 2002US-00060763.

XX PR 25-MAR-2002; 2002US-00105989.

XX PR 12-APR-2002; 2002US-00121911.

XX PR 12-AUG-2002; 2002US-00217168.

XX PR 22-OCT-2002; 2002US-00278036.

XX PR 02-JAN-2003; 2003US-00336489.

XX PR 03-JAN-2003; 2003US-00336153.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA;

XX PI Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;

XX PI Silos-Santiago I, Bandaru R;

XX WPI: 2004-268788/25.

XX P-PSDB: ADL14161.

XX New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,

XX 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593

XX nucleic acid molecules and proteins, useful for treating, e.g. cancer,

XX heart failure and angina.

XX Claim 1; SEQ ID NO 45; 139pp; English.

XX The invention describes an isolated 21910, 56634, 55053, 2504, 15977,

XX 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,

XX 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising

XX any one of 40 nucleotide sequences (I). The nucleic acid molecules and

XX polypeptides are useful for diagnosing and treating a subject having a

XX disorder, or a subject at risk of developing a disorder, which is

XX associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,

Db 1766 GAAGCTGCCTGAGCGCTGGCGGACGATCCTTTGGGGACAGCTGCTTTTCCCTGACAG 1825
QY 1835 ACTGCCAAGAGGTGACTGCGAGCCCTACAGACAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
Db 1826 ACTGCCAAGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCAAAGCTCACC 1884
RESULT 4
ABK14000
ID ABK14000 standard; cDNA; 3353 BP.
XX AC
XX ABK14000;
XX 02-JUL-2002 (first entry)
XX cDNA encoding human protein kinase 3700.
XX Human; protein kinase 3700; PK; protein phosphorylation; tumorigenesis;
KW cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma;
KW tissue repair; tissue regeneration; atherosclerosis; blood-brain barrier;
KW cell proliferation disorder; cell differentiation disorder; carcinoma;
KW haematopoietic neoplastic disorder; metastatic disorder; leukaemia;
KW cytoskeletal; aniatherosclerotic; gene; ss.
XX OS
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 157..2043
XX /*tag= a
XX /product= "Protein kinase 3700"
XX /note= "The coding region (not including the terminator
XX codon) is specifically claimed in claims 7 and 28"
XX WO200224921-A2.
XX 28-MAR-2002.
XX 25-SEP-2001; 2001WO-US030115.
XX 25-SEP-2000; 2000US-0234922P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Curtis RAJ, Galvin KM;
XX WPI; 2002-352007/38.
XX P-PSDB; AAU79652.
XX Use of modulators of activity of 3700 protein for making medicament for
PT e.g., modulating protein phosphorylation or cell signaling, or for
PT treating or preventing cellular proliferative and/or differentiative
PT disorders.
XX Claim 28; Fig 1; 115pp; English.
XX The present invention relates to the isolation of a novel human protein
CC kinase designated 3700, and the polynucleotide sequence encoding it. The
CC invention also describes the use of a modulator of the activity of
CC protein kinase (PK) 3700 for making a medicament or pharmaceutical
CC composition for modulating the ability of a cell to phosphorylate an
CC amino acid residue of a substrate protein. Modulators of protein kinase
CC 3700 activity are useful for modulating protein phosphorylation, cell
CC signalling, tumorigenesis, mitogenesis, transcription of a gene,
CC angiogenesis, tissue repair, tissue regeneration, establishment or
CC progression of atherosclerosis, and signalling across the blood-brain
CC barrier. The polynucleotide and polypeptide molecules for protein kinase
CC 3700 may be used as diagnostic targets and therapeutic agents for
CC prognosticating, diagnosing, preventing, inhibiting, alleviating, or
CC curing PK-related disorders and cellular proliferative and/or
CC differentiative disorders (e.g. haematopoietic neoplastic disorders,
CC carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700
CC polynucleotide sequence can be used to express protein kinase 3700, to
CC detect a genetic alteration in a 3700 gene, in chromosome mapping, for

CC tissue typing, in forensic biology, and as surrogate markers. The present
CC sequence encodes human protein kinase 3700
XX Sequence 3353 BP; 754 A; 1022 C; 879 G; 695 T; 0 U; 3 Other;
SQ Query Match 71.9%; Score 1360.2; DB 6; Length 3353;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;
QY 47 CTTCCGCTTGGCTCGGAGAGCGCCCGCGCTGGCGGACGGGCTCATCAAGTCGCTTA 106
Db 191 CCACTCCCTCGGCGCGAGAGCTAGCCCGCGCTGGCGGAAGGCTCATCAAGTCGCGCA 250
QY 107 AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGACCATCAAAACACAACTCGGGCACC 166
Db 251 AGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGACCAACCAAGCAACCTCGGGCACC 310
QY 167 GCTACAGATTCTTGGAGAGCGCTGGGCAAGGGCACTTACGGGAAGGTGAAGAAGCGACGAG 226
Db 311 GCTACAGATTCTTGGAGAGCGCTGGGCAAGGGCACTTACGGGAAGGTGAAGAAGCGCGGG 370
QY 227 AGAGCTCGGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAAAGATGAGC 286
Db 371 AGAGCTCGGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAAAGATGAGC 430
QY 287 AGGATCTGTCACATACGAGGAGATTGAGATCATGTCTTCACTCAACCAACCCACACA 346
Db 431 AGATCTGATGCACATACGAGGAGATTGAGATCATGTCTTCACTCAACCAACCCACACA 490
QY 347 TCATTGCCATCCATGAAGTGTGGAGATAGACAGCAAGATTGTGATGTCATGGAGTATG 406
Db 491 TCATTGCCATCCATGAAGTGTGGAGATAGACAGCAAGATTGTGATGTCATGGAGTATG 550
QY 407 CCAGCCGAGCGATCTGTATGATTATCATCAGTGAGCGGCAACGGCTGAGTGAGCGGAGC 466
Db 551 CCAGCCGAGCGATCTGTATGATTATCATCAGTGAGCGGCAACGGCTGAGTGAGCGGAGC 610
QY 467 CCAGGCGATTCTTCCGACAGATGCTGTGCGCTGCACTACTGCGCACCAGAACGGATCG 526
Db 611 CTAGGCGATTCTTCCGCGAGATGCTGTGCGCTGCACTACTGCGCACCAGAACGGATCG 670
QY 527 TTCACCGAGATCTCAAGCTGGAAAAACATCTCTTAGATGCCAATGAAACATCAAGATTG 586
Db 671 TCACCGAGATCTCAAGCTGGAAAAACATCTCTTAGATGCCAATGAAACATCAAGATTG 730
QY 587 CTGACTTTGGCTCTCCAACTGTATACCAAAAGGCAAGTTCTTCCAGACGTTCTGTGGGA 646
Db 731 CTGACTTTGGCTCTCCAACTGTATGAAACAGATCAGCAACCGGGCTTACCAGGAGCCACTA 790
QY 647 GCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGAGTGG 706
Db 791 GCGCCCTCTATGCTCGCCAGAGATTGTCAATGGGAAGCCCTTACACAGGCCACAGAGTGG 850
QY 707 ACAGCTGGTCTCTGGGCGTTCTCTCTATACATCTCTGTGATGGCACCACATGCCCCCTTGACG 766
Db 851 ACAGCTGGTCTCTGGGCGTTCTCTCTATACATCTCTGTGATGGCACCACATGCCCCCTTGATG 910
QY 767 GGCGAGATCATAAACACATCTGGTGAAGCAATCAGTAACCGGGGTTTACCGTGAGCGCGCCA 826
Db 911 GGCGATGACCAATAGATCTTAGTGAACAGATCAGCAACCGGGGCTTACCAGGAGCCACTA 970
QY 827 AGCGGTCCGATGCTGTGGCTGATCCGGTGGCTGTAAATGGTGAACCCACCCCGCTCGGG 886
Db 971 AACCTCTCTATGCTGTGGCTGATCCGGTGGCTGTAAATGGTGAACCCACCCCGCTCGGG 1030
QY 887 CCACACTGAGAGATGATGACGAGTCAATTGGTGGTCAACTGGGGTTTACACACCGGAGTCG 946
Db 1031 CCACCTCTGAGGATGTGGCGAGTCACTGTGGTCACTGGGGCTACCGCCACCCGAGTGG 1090
QY 947 GGGAAACAGGAGCCCTCGCTGAGGTTGGGCAACCTTAGTGGTGACTTTGGCGGGGCTCCA 1006
Db 1091 GAGAGCAGGAGGCTCCGCATGAGGGTGGGCAACCTTGGCAGTGTACTCTGCCCGGCTCCA 1150

Db 1682 CCACAGAGCCTTAGAGCTCGCGGCCCCACACCTTCGGCTCCCTGGATGAATCGCC 1741
 QY 1607 CCTCCCATCTGACGCGCCGAGCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1666
 Db 1742 CACCTGCCCTCCGCGCGCCGAGCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1801
 QY 1667 TGTCTCCGAGTCTTTGACCAATTTGACTTGGCTGAACGTCTTCCGAAACCCCACTGA 1726
 Db 1802 TGTCTCTGAGTCTTTGACCAAGTCTGACCTGACCTGACCTGACCTGACCTGACCTG 1861
 QY 1727 GGGCTGTGTCTGTGGACAACTGAGGGGCTTGGAGAGCTCCCTCAGAG----- 1780
 Db 1862 GGGCTGTGTCTGTGGACAACTGAGGGGCTTGGAGAGCTCCCTCAGAGGGCCCTG 1921
 QY 1781 -----GTCTGAAGCGATGTGGCAGGAATCTTGGGGGATAGTCTTCTCTGACAG 1834
 Db 1922 GAAGTGTCTGAGCGCTGGCGGAGATCTTTGGGGGAGAGTCTTTTCTCTGACAG 1981
 QY 1835 ACTGCCAAGAGTGTGACCTGACGCTTACAGACAGCCCTTAGGAATCTGCTCAAGCTCAGC 1893
 Db 1982 ACTGCCAAGAGTGTGACGCTTACAGACAGCCCTTAGGAATCTGCTCAAGAGTCAAC 2040

RESULT 6

AAD26459

ID AAD26459 standard; cDNA; 3360 BP.

AC AAD26459;

XX 26-MAR-2002 (first entry)

DT Human kinase PKIN-12 cDNA.

DE Human; kinase; PKIN-12; cancer; leukaemia; adenocarcinoma; osteoporosis;

DE Immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;

DE Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;

DE allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;

DE autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;

DE Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;

DE rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;

DE hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;

DE cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;

DE congestive heart failure; ischaemic heart disease; lung tumour; gout;

DE fatty liver; Niemann-Pick's disease; gene therapy; ss.

XX Homo sapiens.

OS

XX

XX

FH Key Location/Qualifiers

FT CDS 181..1965

FT /*tag= a

FT /product= "Human PKIN-12 protein"

XX

FN W0200196547-A2.

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PI

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DR

DR

XX

XX

PT

PT

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

Sequence 3360 BP; 729 A; 1022 C; 882 G; 727 T; 0 U; 0 Other;

Query Match 71.7%; Score 1357.6; DB 6; Length 3360;

Best Local Similarity 83.7%; Pred. No. 0;

Matches 1569; Conservative 0; Mismatches 284; Indels 21; Gaps 2;

QY 32 GCAGAGCTCCCTCGGCTCCGCTCGGCTCGGCTCGGAGAGCGCCGCGCTCGGAGAGCGGC 91

Db 98 GCGCGGCTCGGCTCGGCTCCCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 157

QY 92 TCATCAAGTCCCTAAACCTCTCATGAAGAGCAGCGGCTGAAGAGCGGCACCATCACAAC 151

Db 158 TGATCAAGTCCGCTCAAGCGCCCTAATGAAGAGCAGCGGCTGAAGAGCGGCACCATCACAAC 217

QY 152 ACAACCTCGGCGCACCGCTACGAGTTCTTGAGAGCGCTGGGCAAGGCGCCTACGGGAAGG 211

Db 218 ACACCTCGGCGCACCGCTACGAGTTCTTGAGAGCGCTGGGCAAGGCGCCTACGGGAAGG 277

QY 212 TGAAGAGCGCAGAGAGCTCGGCGCTCTGCTGAGAGCGCTGGGCGCTCAAGTCAATCAGGAAGACA 271

Db 278 TGAAGAGCGCGGAGAGCTCGGCGCTCTGCTGAGAGCGCTGGGCGCTCAAGTCAATCAGGAAGACA 337

QY 272 AATCAAGATGAGCAGGATCTCTGCACATACGAGGAGGATGAGATCATGCTCTTAC 331

Db 338 AATCAAGATGAGCAGGATCTCTGCACATACGAGGAGGATGAGATCATGCTCTTAC 397

QY 332 TCAACCAACCCCAATCATTTGCCATCATGAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 391

Db 398 TCACCAACCCCAATCATTTGCCATCATGAAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 457

QY 392 TTGTCTAGGAGTATGCCAGCGGAGCGATCTGTATGATTACATCAGTACGAGCGGCACGCG 451

Db 458 TCGTCTAGGATATGCCAGCGGAGCGATCTGTATGATTACATCAGTACGAGCGGCACGCG 517

QY 452 TGAGTACGCGGAGCGCAGGATCTTCTTCGACAGATCTGTCTGCGCTGCTGCTGCTGCTGCTG 511

Db 518 TCAGTACGCGGAGCGGAGTGTGCTTCTTCGCGAGATCTGCTCTGCGCTGCTGCTGCTGCTG 577

Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

WPI; 2002-050207/12.

P-PSDB; AAE16266.

New polypeptides, useful for diagnosing, treating or preventing disorders

of growth and development, cardiovascular and lipid, and diseases such as

cancer, comprise human kinase polypeptides.

Claim 5; Page 184; 197pp; English.

The invention relates to human kinase PKIN proteins and their

corresponding cDNAs. A composition containing PKIN agonist is useful for

treating a disease or condition associated with decreased expression of

PKIN and a composition comprising PKIN antagonist is useful for treating

a disease or condition associated with overexpression of PKIN. The

disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,

myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder

(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,

atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,

autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes

mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,

osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,

rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,

bacterial, parasitic, fungal, viral, protozoal and helminthic infections)

growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,

Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio

vascular disease (arteriovenous fistula, hypertension, vasculitis,

aneurysms, congestive heart failure, angina pectoris, myocarditis,

ischaemic heart disease, chronic bronchitis, lung tumours); lipid

disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,

hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity

of a test compound and in gene therapy. The present sequence is human

PKIN-12 cDNA

Qy	512	ACGAAACGGGATCGTTTCAACGAGATCTCAAGCTGGAAAAATCCTTCTTAGATGCCAATG	571
Db	578	ATCAGAAACAGAGTTGTCTCACCGAGATCTCAAGCTGGAGAAATCCTCTTGGGTGCCAATG	637
Qy	572	GAAACATCAAGATTGCTGACTTTTGGCCCTCTCCAACTGTACCAAAAGGCAGTTCTCTCC	631
Db	638	GGAATATCAAGATTGCTGACTTTGGCCCTCTCAACCTCTACCATCAAGAGCAAGTTCTCTGC	697
Qy	632	AGACGTTCTGTGGAGGCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATG	691
Db	698	AGACATTTCTGTGGAGCCCCCTCTATGCCTGCCAGAGATTGTTCATATGGNAGCCCTACA	757
Qy	692	TGGCCCCAGAGGTGGACAGCTGTGTTCTGTGGCGTTTCTCCTGTATCATCTCTGTGCAATGGCA	751
Db	758	CAGGCCCAGAGGTGGACAGCTGTGTTCTGTGGGTGTTCTCTATACATCTGTGTGATGGCA	817
Qy	752	CCATGCCCTTTAGCGGCGAGGATCATAAACACTGTGTGAAGCAATCAGTAAACGGGGCTT	811
Db	818	CCATGCCCTTTGATGGGCGATGACCATAGATCTCTAGTGAATCCCTAGTGAACAGATCAGCAACGGGGCT	877
Qy	812	ACCGTGAGCGGCCCAAGCCGTCCGATGCTGTGGCCTGATCCGGTGGCTGTGTTAATGGTGA	871
Db	878	ACCGGAGCCACCTTAACCTCTCATGCTGTGGCTGTATCCGGTGGCTGTGTTAATGGTGA	937
Qy	872	ACCCACCCGTTGGGCCACACTGAGAGATGTAAGCAGTCAATGTGTGGGTCAACTGGGGTT	931
Db	938	ACCCACCCGCGGGCCACCTCGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCT	997
Qy	932	ACACCACGGAGTCGGGGMACAGAAAGCCCTGCTGAGGGTGGGCACCTCTAGTGGTGACT	991
Db	998	ACGCCACCCGAGTCGGGAGAGCAGAGAGCTCCGCATGAGGGTGGGCACCTCTGGCAGTGA	1057
Qy	992	TTGGCCGGGCTCCATGCGGACCTGGTTTACGTCTCTCTCGCGCCCTCTCTGGAGAGT	1051
Db	1058	CTGCCCGGCTCCATGGCTGACTTGGCTCGGCGTTCTCTCCGCCCCCTCTCTGGAGAGT	1117
Qy	1052	GAGCCAAAGGTGTGAGCTTTCTTAAGCAGACAGTCGCGGGAGGTGGAAGCACTGTACCTG	1111
Db	1118	GGGCCAAAGGTGTGAGCTTTCTTAAGCAGCATGCACTGGTGGGGAGCACCACCCCTG	1177
Qy	1112	GGCTGAGAGCGGCAATTTCTTTAAGAGTCCCGAAAGGAGATGACATGGCTCAAAATC	1171
Db	1178	GCCTGAGAGCGCCAGCATTTGCGTCAAGAAGTCCCGCAAGGAGATGACATGGCCCAAGTCTC	1237
Qy	1172	TGCAAGGTGACCCGGCTGAGATACCTTTCTCGCCCTGGCAAGCAGAGCCTTAAGCTTC	1231
Db	1238	TCCACAGTGACAGGCTGTATGACTGCCCATCGCCCTGGCAAGAGCACTCAAGCTGC	1297
Qy	1232	CGAAAGCATTTCTCAAGAAAAGTCTCTATCCTCGTCAGGGGAGGTACAGAGGACCCCTC	1291
Db	1298	CAAAAGGCATTTCTCAAGAAGAAGTGTACGCCCTCTGCAGAAGGGGTACAGGAGGACCCCTC	1357
Qy	1292	AGGAACTCAGACCGGTGCTGATTAATCTCAGGGCAGCTGTCCCTGTGTATTCCTCTGTCTCC	1351
Db	1358	CGGAGCTCAGGCCCAATCCCTCTCGAGCCACGGGCAGGTGCCCC-----CCCTGTCTCC	1408
Qy	1352	CAAGGAAGGCATCTTTAAGAAGTCTCGACAGCGTGAATCTGGTPTACTCTCTCTCCAG	1411
Db	1409	CCAAGAAGGCATTTCTCAAGAAGCCCCGACAGCCGAGTCTGGCTACTCTCTCTCCCG	1468
Qy	1412	AGCCACGAGTCTGGGGAACTTTAGACGCAGTGATGTGTTTGTGAGTGGGAGCCCGC	1471
Db	1469	AGCCAGTGAATCTGGGGAGCTCTTGAGCGCAGCGACGTGTTTGTGAGTGGGATCCCA	1528
Qy	1472	TGGAGCAGAAGTCTCCACAGGCTTACGGGTCTCTCTCCACCGCAAGGGCATTTCTCAAAC	1531
Db	1529	AGGAGCAGAAGCCTCCGCAAGCTTTAGGGGTGCTCTCTCCATCGCAAAAGGCATCTCTCAAAC	1588
Qy	1532	TCAATGCAAGTTCTCCCGCAGACGCTTTAGAGGCACTACCCCTAGCACCTTTGGCTCCC	1591
Db	1589	TCAATGCAAGTTCTCCACAGACGCTTTGAGTCTCGGGCCCCCACACCTTTGGGTCCC	1648
Qy	1592	TGGAACCAACTGGGCTCTCTCCATCTCTGCAGCGCCGGCCAGCGGCCCTCTCAGGGGCTGTGA	1651

Db	1649	TTGGATGAACCTCGCCCCACCTCGCCCCCTGGCCCGGGCCAGCCGACCTCAGGGGCTGTGA	1708
Qy	1652	GTGAGGACAGCATCTGTCTCTCCGAGTCCCTTTGACCAATTGGACTTGCCTGACGCTCTTC	1711
Db	1709	GCGAGGACAGCATCTGTCTCTGAGTCCCTTTGACCAAGCTGGACTTGCCTGAAACGGCTCC	1768
Qy	1712	CCGAAACCCCACTGAGGGGCTGTGTCTGTGGACAACCTCGAGGGGCTTTGAGCAGCCTC	1771
Db	1769	CAGAGCCCCCACTCGGGGGCTGTGTCTGTGGACAACCTCAGGGGCTTGAGAGCCCC	1828
Qy	1772	CCTCAGAAAG-----GTCGTAAGCGATGGTGGCAGGAATCTTTGGGGGATAGCT	1819
Db	1829	CCTCAGAGGGCCCTTGGAAAGCTGTCTCAGGGGCTCGGGCAGGATCTCTTTGGGGGACAGCT	1888
Qy	1820	GCCTTTCTCTGACAGACTGCTCAAGAGGTGACTGCAGCTACAGACAAGCCCTAGGAATCT	1879
Db	1889	GCCTTTTCCCTGACAGACTGCTCAGAGGTGACGCGACTTACCGACAGGCACTGAGGGTCT	1948
Qy	1880	GCTCAAGCTCAGC 1893	
Db	1949	GCTCAAGCTCACC 1962	
RESULT 7			
AAK94280			
ID	AAK94280	standard; cDNA; 3395 BP.	
AC	AAK94280;		
XX			
DT	06-NOV-2001	(first entry)	
XX			
DE	Human full-length cDNA, SEQ ID NO: 2918.		
XX			
KW	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	EPI130094-A2.		
XX			
PD	05-SEP-2001.		
XX			
PF	07-JUL-2000; 2000EP-00114089.		
XX			
PR	08-JUL-1999; 99JP-00194486.		
PR	11-JAN-2000; 2000JP-00118774.		
PR	02-MAY-2000; 2000JP-00183765.		
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Ota T, Nishikawa T, Isogai T, Hayaehi K, Ishii S, Kawai Y;		
PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;		
XX			
XX	WPI; 2001-524255/58.		
DR	P-PSDB; AAM93360.		
XX			
PT	830 Primers useful for synthesizing full length cDNA clones and their use		
PT	in genetic manipulation.		
XX			
PS	Claim 8; SEQ ID NO 2918; 1380pp + Sequence Listing; English.		
XX			
CC	The invention relates to primers for synthesizing full length cDNA		
CC	clones. 830 cDNA molecules encoding a human protein have been isolated		
CC	and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have		
CC	been determined. Primers for synthesizing the full length cDNA are useful		
CC	for clarifying the function of the protein encoded by the cDNA. The full		
CC	length clones were obtained by construction of full length enriched cDNA		
CC	libraries that were synthesised by the oligo-capping method. The primers		
CC	enable the production of the full length cDNA easily without any special		
CC	methods. The present sequence is a full length human cDNA of the		
CC	invention. Note: The sequence data for this patent did not form part of		
CC	the printed specification, but was obtained in CD-ROM format directly		
CC	from EPO		

XX	SQ	Sequence	3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;
		Query Match	71.7%; Score 1357; DB 4; Length 3395;
		Best Local Similarity	84.1%; Pred. No. 0;
		Matches 1563; Conservative	0; Mismatches 275; Indels 21; Gaps 2;
Qy	47	CCTCCGCCCTCGCTCGAGAGCCCGCGCGCTGGCGACGGGCTCATCAAGTCGGCTA	106
Db	152	CCACTCCCTCGCCGCGAGCTAGCCCGCGCTGGCGAAGGCGCTGATCAAGTCGCCCA	211
Qy	107	AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCACATCAAAACACAACTCGGGCACC	166
Db	212	AGCCCCAATGAAGAAGCAGCGGTGAAGCGGCACCAACAAGACACAACTCGGGCACC	271
Qy	167	GCTACGAGTTCTCTGGAGACGCTGGCAAGGSCACTACGGGAAGGCTGAAGAAGCACGAG	226
Db	272	GCTACGAGTTCTCTGGAGACCTGGCAAGGSCACTACGGGAAGGCTGAAGAAGCGCGGG	331
Qy	227	AGAGCTCGGGCGCTCTGGTGCCCATCAAGTCCATCAGGAAGAACAATAAATCAAGATGAGC	286
Db	332	AGAGCTCGGGCGCTCTGGTGCCCATCAAGTCAATCCGGAAGGACAAATCAAGATGAGC	391
Qy	287	AGGATCTGTGCATACATACGAGGGAGATTGAGATCATGTCTTACTCAACACACCCCA	346
Db	392	AAGATCTGTGCATACATACGAGGGAGATTGAGATCATGTCTTACTCAACACACCCCA	451
Qy	347	TCATTGCCATCATGAAGTGTTCAGAAATAGCAGCAAGATTGTGATTGTCTATCGAGTATG	406
Db	452	TCATTGCCATCCATGAAGTGTTCAGAAACAGCAGCAAGATCGTGATCGTATGGAGTATG	511
Qy	407	CCAGCCGAGGCGATCTGTATGATTACATCATAGTCAGCGGCCACGGCTCAGTCAGCGGACG	466
Db	512	CCAGCCGAGGCGACTTTATGACTACATCAGCAGCGCAGCAGCTCAGTCAGCGCGAAG	571
Qy	467	CCAGGCATTTCCTCCGACAGATCGTGTCTGCCCTGCACCTACTGCCACAGAGGATCG	526
Db	572	CTAGGCATTTCCTCCGCGAGATCGTCTCTGCCGTGSCACTATTGGCATCAGAACAGAGTTG	631
Qy	527	TTACCCGAGATCTCAAGCTGGAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG	586
Db	632	TCCACCGAGATCTCNAAGCTGAGAACATCCTCTTGGATGCCAATGGGAATATCAAGATTG	691
Qy	587	CTGACTTTGGCCTCTCCAACTGTACCAAAAGGCAAGTTCTCTCCAGACGTTCTGTGGGA	646
Db	692	CTGACTTTGGCCTCTCCAACTGTACCATCAAGGCAAGTTCTCTGCACATCTGTGGGA	751
Qy	647	GCCCTCTTACGCTTCGCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGAGTGG	706
Db	752	GCCCCCTCTATGCTTCGCCACAGATTGTCAATGGGAAGCCCTACACAGGCCACAGAGTGG	811
Qy	707	ACAGCTGGTCTCTGGGGGTCTCTGTGACATCCTGTGTGATGACCATGCGCTTTTACG	766
Db	812	ACAGCTGGTCCCTGGGGTGTCTCTCTCTACATCTGTGTGATGACCATGCGCTTTTATG	871
Qy	767	GGCAGGATCATAAACACTGGTGAAGCAATCAGTAAACGGGGTTACCGTGAGCGGCCCA	826
Db	872	GGCATGACCATAAGATCCTAGTGAACAGATCAGAACGGGGCTTACCGGGAGCCACCTA	931
Qy	827	AGCGGTCCGATGCCCTGTGGCCTGATCCGCTGGCTGTGTTAATGGTGAACCCCAACCGCTGGG	886
Db	932	AAACCTCTGATGCCCTGTGGCTGTATCCGCTGGGTGTGTGATGGTGAACCCCAACCGCTGGG	991
Qy	887	CCACATCGAGGATGATGACCACTATTGGTGGGTCACTGGGGTTACACCAACCGAGTCG	946
Db	992	CCACCTCGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGTTACCGCACCGAGTGG	1051
Qy	947	GGGAAACAGGAAGCCCTCGCTGAGGGTGGGCACCTCTAGTGTGACTTTGGCGCGGCTCTCA	1006
Db	1052	GAGACGAGGAGGCTCCGCATGAGGGTGGGCACCTCTGCACTGACTCTGCGCGGCTCTCA	1111
Qy	1007	TGGCGGACTGGTTACGTGCTCTCTCGCGCCCCCTCTCTGGAGAAATGGAGGCAAGGTGTGCA	1066

XX EPI396543-A2.
XX 10-MAR-2004.
XX 07-JUL-2000; 2003EP-00025638.
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183865.
XX 07-JUL-2000; 2000EP-00114089.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Oca T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
XX P-PSDB; ADL30886.
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
XX length human cDNAs.
XX Example 1; SEQ ID NO 2918; 1340bp; English.
XX This invention relates to a novel primers useful for synthesizing full
XX length cDNA molecules that encode human proteins. Specifically, it refers
XX to secretory or membrane proteins that are potential therapeutic agents/
XX target molecules in the field of medicine, and in particular genes
XX encoding proteins that are associated with signal transduction,
XX glycoproteins and transcription. The present invention describes a method
XX for efficiently cloning a full length human cDNA from both the 5' and 3'
XX ends using the oligo-capping method. This polynucleotide sequence is a
XX full length human cDNA clone of the invention.
SQ Sequence 3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;
Query Match 71.78; Score 1357; DB 12; Length 3395;
Best Local Similarity 84.18; Pred. No. 0;
Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;
QY 47 CCTCCGCCCTGGCTCGAGAGCGCCCGCGCTGGCGGAGGCTCATCAAGTCGCGCTA 106
DB 152 CCACTCCCTCGCGCGCAGAGCTAGCCCGCGCTGGCGGAGGCTGATCAAGTCGCGCA 211
QY 107 AACCTCTGATGAAGACGAGCGGTGAAGCGGACCATCAAAACACAACTCGCGGACC 166
DB 212 AGCCCCAATGAAGACGAGCGGTGAAGCGGACCATCAAGCAAACTCGCGGACC 271
QY 167 GCTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACGGGAAGGTGAAGGACGAG 226
DB 272 GCTACGAGTTCCTGGAGACCTGGGCAAGGCGACCTACGGGAAGGTGAAGGACGAG 331
QY 227 AGAGCTCGGGCGCTGCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 286
DB 332 AGAGCTCGGGCGCTGCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 391
QY 287 AGATCTGCTGCACATACGAGGAGAGATTGATGATCTTCACTCAACACACCCCA 346
DB 392 AAGATCTGATGCACATACGAGGAGAGATTGATGATCTTCACTCAACACACCCCA 451
QY 347 TCATTGCGCATCCATGAAGTGTTCAGAAATAGCAGAGATTGATGATCTTCACTCAAGGATG 406
DB 452 TCATTGCGCATCCATGAAGTGTTCAGAAATAGCAGAGATTGATGATCTTCACTCAAGGATG 511
QY 407 CCAGCGAGGCGATCTGTATGATTAATCATAGTACGAGGCGCCACGCTGAGTACGAGGACG 466
DB 512 CCAGCGGCGGCGATCTTATGACTACATCAGGAGGCGGACGCTCAGTACGAGGCGGAA 571
QY 467 CCAGGCAATTCCTCGGACAGATCGTGTGCTGCCCTGCACTACTGCGACACAGAACGGATCG 526
DB 572 CTAGGCATTTCTTCGGGAGATGCTCTCTCGCGTGCACTATTGCGCATCAGAAACAGATTG 631

QY 527 TTCACCGAGATCTCAAGCTGGAAAAATCCTTCTAGATGCCAATGAAACATCAAGATTG 586
DB 632 TCCACCGAGATCTCAAGCTGGAGAAATCCTTCTTGGATGCCAATGGAATATCAAGATTG 691
QY 587 CTGACTTTGGCTCTCCAACTGTACCAAAAGGCAAGTTCTCTCCAGAGCTTCTGTGGGA 646
DB 692 CTGACTTTGGCTCTCCAACTGTACCAAAAGGCAAGTTCTCTCCAGAGATTTCTGTGGGA 751
QY 647 GCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCGCCAGAGGTGG 706
DB 752 GCGCCCTCTATGCTCGCAGAGATTGTCAATGGGAAGCCCTACACAGGCGCCAGAGGTGG 811
QY 707 ACAGCTGGTCTCTGGGCGTTCCTCTATACATCTCTGTGTCATGCGACCATCTGTCACG 766
DB 812 ACAGCTGGTCTCTGGGCGTTCCTCTATACATCTCTGTGTCATGCGACCATCTGTCACG 871
QY 767 GGAGGATCATAAACACATGGTGAAGCAATAGTAACGGGGCTTACCGTAGCGCCGCCA 826
DB 872 GGCATGACCATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGGAGCCACCTA 931
QY 827 AGCGTCCGATGCTGTGGCTGATCCGGTGGCTGTAAATGGTGAACCCACCCCGTCGGG 886
DB 932 AACCTCTGATGCTGTGGCTGATCCGGTGGCTGTGATGGTGAACCCACCCCGTCGGG 991
QY 887 CCACACTGGAGATGTAGCCAGTCAATTGGTGGTCAACTGGGGTTACACACCGGAGTCG 946
DB 992 CCACCTTGGAGATGTGGCCAGTCACTGGTGGTCAACTGGGGCTACGCCACCGAGTCG 1051
QY 947 GGAACAGGAAGCCCTGCTGAGGTTGGGACCCCTAGTGGTACTTTGGCGGGCTTCCA 1006
DB 1052 GAGACAGGAGGCTCCGCATGAGGTTGGGACCCCTGGCAGTACTCTGCCCGGCTTCCA 1111
QY 1007 TGGCGACTGTTTACGTCGCTCTCGGCCCTCTCTGGAGATGAGGCCAACGAGTGTGCA 1066
DB 1112 TGGCTGACTGGCTCCGGCGTTCTCCGCCCTCTCTGGAGATGAGGCCAACGAGTGTGCA 1171
QY 1067 GCTTCTTCAAGCAGCAGCTGCCGGAGGTGGAAGCACTGTACTCTGGCTGGAGCGCAAC 1126
DB 1172 GCTTCTTCAAGCAGCAGCTGCCGGAGGTGGAAGCACTGTACTCTGGCTGGAGCGCAGC 1231
QY 1127 ATTCTCTTAAGAGTCCGAAAGGAGATGACATGCTCAAAATCTGCAAGGTGACCCGG 1186
DB 1232 ATTCTCTTAAGAGTCCGAAAGGAGATGACATGCTCAAAATCTGCAAGGTGACACGG 1291
QY 1187 CTGAGGATACCTCTCTCGCCCTGGCAAGCAGCAGCTTAAGCTTCCGAAAGGCAATCTCA 1246
DB 1292 CTGATGACTGCGCATCGCCCTGGCAAGCACTCAAGCTGCCAAGGAGATCTCA 1351
QY 1247 AGAAAAGTCTCTTACTCTGCTCAGGAGGAGTACAGGAGACCTCAGGAACTCAGACCGG 1306
DB 1352 AGAAGAAGGTGTGAGCTCTGCAAGAAGGGGTACAGGAGGACCTCCGGAGCTCAGGCCAA 1411
QY 1307 TGCTGATCTCAGGCGACCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAGGATCC 1366
DB 1412 TCCCTCGAGCCAGGCGAGGCTGCC-----CCCTGCTCCCAAGGAGGATTC 1462
QY 1367 TTAAGAAGTCTCCACAGCGTGAATCTGTTACTCTCTCCAGAGCCCGAGGAGTCTG 1426
DB 1463 TCAAGAAGCCCGACAGCGGAGTCTGGCTACTCTCTCCGAGCCCGAGTGAATCTG 1522
QY 1427 GGAAGCTCTTACAGCGCAGTGTGTGTTGTAGTGGGACCCCGTGGAGCAGAGTCTC 1486
DB 1523 GGGAGCTCTTGGACGCGAGCGAGTGTGTTGTAGTGGGATCCCAAGGAGCAGAGGCTC 1582
QY 1487 CACAGGCTTCAGGCTCTCTCCACCGCAAGGCGATCTCTCAAACTCAATGGAAGTTCT 1546
DB 1583 CGAAGCTTCAGGCTGCTCTCTCATCGCAAGGCGATCTCTCAAACTCAATGGAAGTTCT 1642
QY 1547 CCGGCAAGCTTTAGAGGCACTACCCCTAGACACTTTGGCTCCCTGGGACCAACTGGCCT 1606
DB 1643 CCGACAGAGCTTGGAGCTCGCGGCCCCCAACCTTGGCTCCCTGGATGAACTCGCC 1702
QY 1607 CTTCCCATCTCGAGCGCGGCCCCCGAGCGGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1666

Db 1703 CACCTCCGCCCTTGGCCCGCCAGCCGACCTCAGGGGCTGTGAGCGAGACAGCATCC 1762
 QY 1667 TGTCTCCGAGTCTCTTTGACCAATTGGACTTGGCTGAACGCTTTCCTCGAAACCCCACTGA 1726
 Db 1763 TGTCTCTGAGTCTTTGACCAAGTGGACTTGGCTGAACGCTTTCCTCGAAACCCCACTGC 1822
 QY 1727 GGGGCTGTGTCTGTGGCAACCTGAGCGGGCTTGGAGCGCTTCCCTCAGAAG----- 1780
 Db 1823 GGGGCTGTGTCTGTGGCAACCTCAGCGGGCTTGGAGCGCTTCCCTCAGAAG----- 1882
 QY 1781 -----GTCCTAAGCGATGGTGGCAGGAATCTTGGGGGATAGTGTCTTCTTGACAG 1834
 Db 1883 GAAGCTCCCTGAGCGCTGGCGGAGGATCTTTGGGGGACAGCTGCTTTTCCCTGACAG 1942
 QY 1835 ACTGCCAAGAGGTGACTGTCAGCCTTACAGCAAGCCCTAGGAATCTGTCTCAAGCTCAGC 1893
 Db 1943 ACTGCCAAGAGGTGACAGCGACCTTACCGACAGGCACTGAGGGTCTGTCTCAAGCTCACC 2001
 RESULT 9
 ADJ96554
 ID ADJ96554 standard; DNA; 3463 BP.
 XX ADJ96554;
 AC
 XX
 XX
 XX 06-MAY-2004 (first entry)
 DE Human calcium/calmodulin-dependent protein kinase NuaK2 DNA SeqID 11.
 XX
 KW gene; ds; kinase; human; SNP; single nucleotide polymorphism;
 KW tyrosine protein kinase; serine/threonine protein kinase; PKT; STK;
 KW gene therapy; cancer; immune-related disease; cardiovascular disease;
 KW brain; neuronal associated disease; metabolic; inflammatory disorder;
 KW cytosstatic; neuroprotective; immunomodulator; antiinflammatory;
 KW calcium/calmodulin-dependent protein kinase; NuaK2.
 XX
 OS Homo sapiens.
 OS 68.
 XX
 XX Location/Qualifiers
 FT variation /tag= a
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1727,a)
 FT /tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 XX
 PN W02004006838-A2.
 XX
 XX 22-JAN-2004.
 XX
 XX 15-JUL-2003; 2003WO-US021730.
 XX
 XX 15-JUL-2002; 2002US-0395632P.
 XX
 XX (SUGEN-) SUGEN INC.
 XX
 XX Whyte D, Manning G, Caenepeel S;
 XX
 XX WPI; 2004-122753/12.
 DR P-PSDB; ADJ96620.
 XX
 XX New nucleic acid molecule encoding a kinase polypeptide, useful for
 PT preparing a composition for treating diseases or disorders, e.g., cancer,
 PT or neurological, immunological or inflammatory disorders.
 XX
 XX Example 1; SEQ ID NO 11; 366pp; English.
 PS
 XX
 XX This invention relates to a novel isolated, enriched or purified nucleic
 CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
 CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
 CC as well as protein kinase-like enzymes. The present invention describes

CC screening methods to identify agonists, antagonists and antibodies that
 CC can be used to modulate the activity or function of the mammalian kinase
 CC enzymes. As such, these compositions can be used for gene therapy
 CC purposes to treat diseases or disorders including cancer, immune-related
 CC diseases, cardiovascular disease, brain or neuronal associated disease,
 CC metabolic and inflammatory disorders. Accordingly, they exhibit
 CC cytostatic, neuroprotective, immunomodulator and antiinflammatory
 CC activities. This polynucleotide sequence is a human kinase DNA sequence
 CC of the invention.
 XX
 SQ Sequence 3463 BP; 732 A; 1057 C; 919 G; 755 T; 0 U; 0 Other;
 Query Match 71.7%; Score 1357; DB 12; Length 3463;
 Best Local Similarity 84.1%; Pred. No. 0;
 Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;
 QY 47 CTTCCGCCCTTGGGCTCGAGAGCGCCGCGGCTGGCGGAGCGGCTCATCAAGTCGGCTA 106
 Db 223 CCACCTCCCTCGCGCCGAGAGCTAGCCGCGGCTGGCGGAGGGCTGATCAAGTCGCCCA 282
 QY 107 AACCTCTGATGAAGAAAGCAGGCGGTGAAGCGGCACCATCAAAACACAACTCTCGGCACC 166
 Db 283 AGCCCTTATGAAGAAAGCAGGCGGTGAAGCGGCACCATCAAAACACAACTCTCGGCACC 342
 QY 167 GCTACGAGTTCTCTGGAGAGCTCTGGCAAGGGCACCTACGGAAGGTGAAGAAGCGACGAG 226
 Db 343 GCTACGAGTTCTCTGGAGAGCTCTGGCAAGGGCACCTACGGAAGGTGAAGAAGCGCGGG 402
 QY 227 AGAGCTCGGGGCGCTGTGGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 286
 Db 403 AGAGCTCGGGGCGCTGTGGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 462
 QY 287 AGGATCTGTGCACATACCGAGGAGATGAGATCATGTCTTCACTCAACCAACCCCA 346
 Db 463 AAGATCTGTGCACATACCGAGGAGATGAGATCATGTCTTCACTCAACCAACCCCA 522
 QY 347 TCATTGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATTGTCTCATGAGTATG 406
 Db 523 TCATTGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATTGTCTCATGAGTATG 582
 QY 407 CAGCGCGAGCGGATCTGTATGATTACATCAGTGAAGCGGCCACCGCTGAGTGAGCGGACG 466
 Db 583 CCAGCGCGGGCGGACCTTTATGACTACATCAGCGAGCGGCGCAGCTCAGTGAGCGCGAAG 642
 QY 467 CCAGGCAATTTCTTCCGACAGATCGTCTGCGCTGCACTACTGCCACCAAGCGGATCG 526
 Db 643 CTAGGCAATTTCTTCCGCGAGATCGTCTGCGCGTGCACATATTGCCATCAGAACAGATTG 702
 QY 527 TTCACCGAGATCTCAAGCTGGAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG 586
 Db 703 TCACCGGAGATCTCAAGCTGGAAACATCCTTCTGGATGCCAATGGGAATATCAAGATTG 762
 QY 587 CTGACTTTGGGCTCTCAACCTGTATACCAAGGCAAGTTCTTCCAGACCTTCTGTGGGA 646
 Db 763 CTGACTTCGGGCTCTCAACCTGTATACCAAGGCAAGTTCTTCCAGACATCTTGTGGGA 822
 QY 647 GCCTCTCTACGCTCGCCTGAGATAGTCAACGGGAGCGCTATGTGGGCGCAGAGGTGG 706
 Db 823 GCGGCTCTATGCTCGCAGAGATTGTCAATGGGAGCGCTTACACAGGCGCCAGAGGTGG 882
 QY 707 ACAGCTGGTCTCTGGGCGTTTCTCTGTACATCTCTGTGATGCGACCATGCCCCCTTTGACG 766
 Db 883 ACAGCTGGTCTCTGGGCGTTTCTCTGTACATCTCTGTGATGCGACCATGCCCCCTTTGATG 942
 QY 767 GGCGAGATCATAAAACTGGTGAAGCAAAATCAGTAAACGGGGCTTACCGTGAGCGGCCCA 826
 Db 943 GGCGATGACCAATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGGAGCGCACCTA 1002
 QY 827 AGCGGTCGCGCTGCTGGCGCTGATCCGCTGGCTGTTTATGGTGAACCCCAACCGCTCGG 886
 Db 1003 AACCTCTGATGCTGTGGCCTGATCCGGTGGCTGTGTGATGGTGAACCCCAACCGCTCGG 1062
 QY 887 CCACACTGGAGGATGTAGCCAGTCAATTGGTGGGTCAATTGGGTCACTACACCGGAGTCG 946

Db 260 GCTACGAGTTCCTGGAGACCCCTGGGCAAGGCACTACGGGAAGGTGAAGAAGCGCGGG 319
Qy 227 AGAGCTGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 286
Db 320 AGAGCTGGGGCGCTGGTGGCCATCAAGTCAATCCGGNAGGACAAATCAAGATGAGC 379
Qy 287 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACACCCCCACA 346
Db 380 AAGATCTGATGCACATACGGAGGAGATTGAGATCATGTCTCACTCAACACCCCTACA 439
Qy 347 TCATTGCCATCCATGAAGTGTTCGAGATAGCAGCAGATTGTGATGTCAATGAGATTG 406
Db 440 TCATTGCCATCCATGAAGTGTTCGAGAACACAGCAGATCGTATCGTCAATGAGATTG 499
Qy 407 CCAGCCGAGGCGATCTGTATGATTACATCAGTAGCGGCCACAGGCTCAGTGAGCGGACG 466
Db 500 CCAGCGGGCGACCTTTATGACTACATCAGGAGCGGCAGCAGCTCAGTGAGCGGAG 559
Qy 467 CCAGGCATTTCTCCGACAGATCGTGTCTGCCCTGCACTACTGCGCACAGAACCGGATCG 526
Db 560 CTAGGCATTTCTCCGGCAGATCGTCTCTGCGGTGCACTATTGCCATCAGAAACAGATTG 619
Qy 527 TTCACCGAGATCTCAAGCTGGAACATCTTCTAGATGCCAATGGAACATCAAGATTG 586
Db 620 TCCACCGGAGATCTCAAGCTGGAGAACATCTCTTTGGATGGCAATGGAATATCAAGATTG 679
Qy 587 CTGACTTTGGGCTCTCCAACTGTACACAAAGCAAGTTCTCTCAGACGTTCTGTGGGA 646
Db 680 CTGACTCGGTCTCTCCAACTGTACCATCAAGGCAAGTTCTCTGAGACATCTCTGGGA 739
Qy 647 GCCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTGG 706
Db 740 GCCCCCTCTATGCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCACAGGTGG 799
Qy 707 ACAGTGTCTCTGGCGTCTCTGTATCATCTCTGTGTCATGCGACCATGCCCTTTGACG 766
Db 800 ACAGCTGGTCTCGGTGTCTCTCTACATCTCTGGTGCATGGCACCATGCGCTTTGATG 859
Qy 767 GCGAGGATCAAAACACTGTGTGAAGCAATCAGTAAGCGGGCTTACCGTGAGCGGCCA 826
Db 860 GGCATGACCATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGGAGCCACTTA 919
Qy 827 AGCCGTCCGATGCTGTGGCTGATCCGGTGGCTGTTAATGGTGAACCCCAACCCGTCGGG 886
Db 920 AACCCTCTGATGCTGTGGCTGATCCGGTGGCTGTTGATGTGTGAACCCCAACCCGTCGGG 979
Qy 887 CCACACTGGAGATGTAGCCAGTCAATGTGGGTCAACTGGGGTTACACACCGGAGTCG 946
Db 980 CCACCTTGAGGATGTGGCCAGTCACTGTGGGTCAACTGGGGCTTACGCCACCCGAGTGG 1039
Qy 947 GGGAAACGGAAGCCCTGCTGAGGTGGGCAACCTAGTGTGACTTTGGCCGGGCTCCCA 1006
Db 1040 GAGAGAGAGGCTCCGATAGGGGTGGGCAACCTGGCAGTGAATCTGCCCGGCCCTCCA 1099
Qy 1007 TGGCGGACTGTTAGTCTGCTCTCGGCCCTCTCGGAGAAATGGAGCCAAAGGTGTGCA 1066
Db 1100 TGGCTGACTGCTCGGGGTTCTCTCCGCCCTCTCGGAGAAATGGGSCCAAGGTGTGCA 1159
Qy 1067 GCTTCTCAAGACGACGTGCGGAGGTGAAGCACTGTACCTGGGTGAGGCGGCAAC 1126
Db 1160 GCTTCTTCAAGCAGCATGACCTGTGGGGGAAGCACCCACCTGGCTGGGCGCCAGC 1219
Qy 1127 ATTCTCTTAAGAGTCCCGAAGAGAGATGACATGGCTCAAAATCTCAAGGTGACCCGG 1186
Db 1220 ATTGCTCAAGAGTCCCGAAGAGAGATGACATGGCCAGTCTCTCCACAGTGAACAGG 1279
Qy 1187 CTGAGGATACCTCTTCTCGCCCTGGCAGAGCAGCTTTAAGCTTCCGAAAGGCATTCTCA 1246
Db 1280 CTGATGACACTGCCCATGCCCTGGCAGAGCAACCTCAAGCTGCCAAGGSCATTCTCA 1339
Qy 1247 AGAAAAGTCTCTACTCTGTACGGGAGGTACAGGAGGACCTTCAGGAACTCAGACGGG 1306
Db 1340 AGAAGAGGTGTGACGCTCTGCAGAAAGGGGTACAGGAGGACCTTCGAGGCTCAGCCCAA 1399

Qy 1307 TGCTGTATCTCCAGGGCAGCCTGTCTGCTGTATCTCCCTGCTCCCAAGGAAAGGCATCC 1366
Db 1400 TCCCTGGAGCCCAAGGCGAGCTGCC-----CCCTGCTCCCAAGGCGCATTC 1450
Qy 1367 TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCCGAGGCTGTG 1426
Db 1451 TCAAGAAGCCCGACAGCGGAGTCTGGCTACTACTCTCTCCCGAGCCAGTGAATCTG 1510
Qy 1427 GGGAACTCTTAGACCGCAGTGATGTGTTGTAGTGGGACCCCGTGGAGCAGAGTCTC 1486
Db 1511 GGGAGCTCTTGGAGCGAGCGACGTGTTGTAGTGGGATCCCAAGAGCAGAGCCTC 1570
Qy 1487 CACAGGCTTCAGGGCTCTCTCCACCGCAAGGCAATTTCTCAAATCAATGGCAAGTTCT 1546
Db 1571 CGCAAGCTTCAGGGCTGCTCTCCATCGCAAGGCAATCTCTCAAATCAATGGCAAGTTCT 1630
Qy 1547 CCGCAGCAGCTTAGAAGGCACTACCCCTAGACCTTTGGCTCCCTGGACCAACTGGCCT 1606
Db 1631 CCAGAGCAGCTTGGAGCTCGCGGCCCCCAACCTTCGGCTCTCTGGATGAACTCGCCC 1690
Qy 1607 CTTCCCATCTGCAGCGCCGCCAGCGCCCTCAGGGGCTGTAGTGAGGACAGCATCC 1666
Db 1691 CACTCGCCCCCTGGGCCCGGCGCAGCGACCTCTAGGGGCTGTAGGAGGACAGCATCC 1750
Qy 1667 TGTCTCTCCGAGTCTTTGACCAATTTGGACTTGGCTTGAACTGCTTCCCGAAACCCCACTGA 1726
Db 1751 TGTCTCTGAGTCTTTGACCACTGGACTTGGCTTGAACTGCTTCCAGAGGCCCCCACTGC 1810
Qy 1727 GGGGCTGTGTGTCTGTGGACAACTCAGGGGGCTTGAAGAGCCTCCCTCAAGAG----- 1780
Db 1811 GGGGCTGTGTGTCTGTGGACAACTCAGGGGGCTTGAAGAGCCTCCCTCAGAGGGCCCCCTG 1870
Qy 1781 -----GTCTGAAGCAGATGGTGGCAGCAATCTTTGGGGGATAGCTGCTTTCTCTGACAG 1834
Db 1871 GAAGCTGCTCTGAGGCGCTGGCGGAGATCTTTTGGGGGAGACGTGCTTTTCTCTGACAG 1930
Qy 1835 ACTGCCAAAGAGGTGACTGACGCTTACAGCAAGCCCTTAGGAACTCTGCTCAAAGCTCAGC 1893
Db 1931 ACTGCCAAGAGGTGACAGGACCTACCGACAGGCACTGAGGGTCTGCTCAAAGCTCACC 1989

RESULT 11
ADM43851
ID ADM43851 standard; cDNA; 2501 BP.
XX
AC ADM43851;
XX
DT 03-JUN-2004 (first entry)
XX
DE Novel human arginine-rich protein cDNA #215.
XX
KW ss; gene; human; arginine-rich protein; cancer; inflammation;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN US2004053250-A1.
XX
PD 18-MAR-2004.
XX
PF 21-NOV-2002; 2002US-00302172.
PR 05-MAR-2001; 2001US-00799451.
PR 05-MAR-2002; 2002WO-US005095.
PR 20-AUG-2002; 2002US-00225251.
XX
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
XX Tang YT, Xue A, Drmanac RT;
XX

DR WPI; 2004-238579/22.
XX New isolated arginine-rich protein-like polynucleotides and polypeptides,
PT useful for diagnosing and/or treating conditions associated with aberrant
PT activity of the arginine-rich polypeptides, such as cancer and
XX inflammation.
XX
PS Disclosure; SEQ ID NO 215; 51pp; English.
XX
XX The invention relates to an isolated polynucleotide. The methods and
CC compositions of the present invention are useful for the diagnosis and/or
CC treatment of diseases or conditions associated with aberrant expression
CC or activity of the arginine-rich protein-like polypeptides, such as
CC cancer and inflammation. They can also be used in forensics, gene
CC mapping, identification of mutations responsible for genetic disorders,
CC and in assessing biodiversity. The present sequence represents a novel
XX human arginine-rich protein cDNA.
XX
SQ Sequence 2501 BP; 525 A; 788 C; 728 G; 460 T; 0 U; 0 Other;
Query Match 71.6%; Score 1355.4; DB 12; Length 2501;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;
47 CCTCCGCCCTCGGAGAGCGCCGCGCGCTGGCGGACGGCTCATCAAGTCGCCTA 106
140 CCACTCCCTCGCGCAGAGCTAGCCCGCGCGCTGGCGGAGGGCTGATCAAGTCGCCA 199
107 AACTCTGATGAAGAAGCAGCGGTGAAGCGGCAACCATCAAAACAACAACCTCGGCACC 166
200 AGCCCTTAATGAAGAAGCAGCGGTGAAGCGGCAACCAACCAAGCACAACCTCGGCACC 259
167 GCTACGAGTTCCTGGAGCCCTGGGCAAGGACCTAGCGGAAGGTGAAGAAGCAGAG 226
260 GCTACGAGTTCCTGGAGCCCTGGGCAAGGACCTAGCGGAAGGTGAAGAAGCGCGGG 319
227 AGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 286
320 AGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGGACAAATCAAGATGAGC 379
287 AGAGTCTGTCGACATACGGAAGGAGATTGAGATCATGTCTTCACTCAACACCCCA 346
380 AAGATCTGATGCAATACGGAAGGAGATTGAGATCATGTCTATCACTCAACACCCCTCA 439
347 TCATTGCCATCCATGAAGTGTTCAGAAATAGCAGCAAGATTGATGTGATGAGTATG 406
440 TCATTGCCATCCATGAAGTGTTCAGAAACAGCAGCAAGATCGTGATCGTATGAGTATG 499
407 CCAGCCGAGGCGATCTCTATGATTATCATCATGAGCGGCGCACCGCTGAGTGAGCGGACG 466
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467 CCAGGCAATTTCTCCGACAGATCGTGTCTGCGCTGCACTACTGCAACAGAGCGGATCG 526
560 CTAGGCAATTTCTCCGACAGATCGTGTCTGCGCTGCACTATTCGCAATCAGAAAGATTG 619
527 TTACACCGAGATCTCAAGCTGGAACATCTTCTAGATGCCAATGGAAATCATCAAGATTG 586
620 TCACCGAGATCTCAAGCTGGAACATCTTCTAGATGCCAATGGAAATCATCAAGATTG 679
587 CTGACTTTGGCCTCTCAACCTGTACCAAGGCAAGTTCTCTCAGACGTTCTGTGGGA 646
680 CTGACTTTGGCCTCTCAACCTGTACCAAGGCAAGTTCTCTCAGACATCTGTGGGA 739
647 GCCCTCTCTAGCCTCGCTGAGATGATGAACGGGAAGCCCTATGTGGGCCCAAGGTGG 706
740 GCCCCTCTATGCTCTGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCGCCAGAGTGG 799
707 ACAGCTGCTCTGTGGGGTGTCTCTCTGTACATCTCTGTGTGATGCAACCATCCCTTTGACG 766
800 ACAGCTGCTCTGTGGGGTGTCTCTCTGTACATCTCTGTGTGATGCAACCATCCCTTTGATG 859
767 GGCAGGATCAATAAACAACCTGGTGAAGCAATCAGTAAACGGGGCTTACCGTGAGCGGCCA 826

860 GGCAATGACCAATAGATCTTAGTGAACAGATCAGAACGGGGCTTACCGGAGCCACTA 919
827 AGCCGTCCGATGCTGTGGGCTGATCCGGTGGCTGTTAATGTGTGAACCCACCCGTCGGG 886
920 AACCTCTGATGCTGTGGGCTGATCCGGTGGCTGTTGATGTGTGAACCCACCCGCGGG 979
887 CCACACTGGAGGATGTAGCCAGTCAATTTGGTGGTCAACTGGGGTTTACACACCGGAGTCG 946
980 CCACCTCTGGAGGATGTGGCCAGTCACTGGTGGTCAACTGGGGCTTACGCCACCCGAGTGG 1039
947 GCGAACAAGGAGCCCTCGCTGAGGGTGGGCACCTAGTGTGACTTTGGCCGCGCTTCCA 1006
1040 GAGAGCAGAGGCTCCGCATGAGGGTGGGCACCTGTGCAGTGACTGTGCCCGCGCTTCCA 1099
1007 TGCGGAGATGTTTACGTGCTCTCGCGCCCTCTCTGGAGAAATGGAGCAAGGTGTGCA 1066
1100 TGGCTGACTGGCTCCGGGCTTCTCCCGCCCTCTCTGGAGAAATGGGCAAGGTGTGCA 1159
1067 GCTTCTTCAAGCAGAGTGGCGGAGGTGAAGCACTGTACTGGGCTGGAGCGGCAAC 1126
1160 GCTTCTTCAAGCAGAGTGGCACCTGTGGGGGAAGCAACCCCTGGCTGGAGCGCAGC 1219
1127 ATTCTCTTAAGAAAGTCCGAAAGAGATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1186
1220 ATTGCTCAAGAAATCCGCAAGAGAGATGACATGGCCAGTCTCTCCACAGTGAACGG 1279
1187 CTGAGGATACCTTTCTGCGCCCTGGCAAGAGCAGCTTAAAGCTTCGAAAGGATTTCTCA 1246
1280 CTGATGACATGTCCTGCTGGCAAGAGCAACCTCAAGCTGCAAGAGGATTTCTCA 1339
1247 AGAAAGTCTCTACCTGCTCAGGGAGGTACAGGAGACCTCAGGAATCTCAGACCGG 1306
1340 AGAAAGAGGTGTGAGCTCTGCAAGAGGGGTACAGGAGACCTCAGGAGCTCAGGCCAA 1399
1307 TGCTCTATCTCAGGCGCAGCTGTCTCTGCTGTATCTCTGCTTCCCAAGAAAGGATCTC 1366
1400 TCCTCGGAGCCAGGCGAGGTGCCCC-----CCCTGCTCCCAAGAGGATTC 1450
1367 TTAAGAAATCTCGACAGCGTGAATCTGGTTACTTCTCTCCAGAGCCAGCGATCTG 1426
1451 TCAAGAAAGCCCGACAGCGAGTCTGGCTACTTCTCTCCGAGCCAGTGAATCTG 1510
1427 GGAACCTCTTAGAGCGCAGTGTGTTGTGAGTGGGACCCCGTGGAGCAGAACTCTC 1486
1511 GGGAGCTCTTGAGCGCAGGCGAGGTGTTGTGAGTGGGATCCCAAGAGCAGAAAGCTC 1570
1487 CACAGCTTTCAGGGCTCTCTCCCTCCACCGCAAGGGCAATTCCTCAAACTCAATGGCAAGTCT 1546
1571 CGCAAGCTTTCAGGGCTCTCTCCCTCCATCGCAAGGCACTCTCAAACTCAATGGCAAGTCT 1630
1547 CCGGCAAGCTTTAGAGGCACTACCCCTAGACACTTTGGCTCCCTGGAGCAACTGGCCT 1606
1631 CCAGACAGCTTTGAGAGCTCGCGGCCCCCAACCTTCGGCTCCCTGGATGAATCGGCC 1690
1607 CTTCCCATCTTCAGCGCCCGCCAGCGCCCTCAGGGCTGTGAGTGGAGCAGATCC 1666
1691 CACTCGCCCCCTGGCCCCGGGCGAGCCCTCAGGGGCTGTGAGGAGCAGATCC 1750
1667 TGTCTCTCCAGTCTCTTTGACCAATTTGGAATTTGCACTTCTTCCCGGAAACCCCACTGA 1726
1751 TGTCTCTCTGAGTCTTTGACAGCTGGAATTTGCTGAAACGGCTCCAGAGCCCCCACTGC 1810
1727 GGGGCTGTGTGTGTGGAACAACCTGAGGGGCTTGAAGCAGCTCTTCCCGGAAACCCCACTGA 1780
1811 GGGGCTGTGTGTGTGGAACAACCTCAGGGGCTTGAAGGAGCCCCCTCAGAGGGGCCCTG 1870
1781 -----GTCTGAAGCGATGTTGGCAGAAATCTCTGGGGATAGTCTCTTTCTCAGCAG 1834
1871 GAAGCTGCTTGAAGCGCTGTGGCAGGATCTTTTGGGGAACAGCTGCTTTTCCCTGACAG 1930
1835 ACTGCCAAGAGGTGATGTCAGGCTTACAGAAAGCCCTAGGAATCTGCTCAAGCTCAGC 1893

Db 1931 ACTGCCAGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGTCTCAAAGCTCACC 1989

RESULT 12
ABX71420
ID ABX71420 standard; cDNA; 3443 BP.
XX AC ABX71420;
XX AC
XX AC
XX AC
DT 14-APR-2003 (first entry)
XX
XX Human cell cycle-associated cDNA from clone DKFZphtes3_7j3.
XX Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
XX Homo sapiens.
XX OS
XX PN WO200112659-A2.
XX
XX PD 22-FEB-2001.
XX PF 18-AUG-2000; 2000WO-IB001496.
XX PR 18-AUG-1999; 99US-0149499P.
XX PR 28-SEP-1999; 99US-0156503P.
XX
XX (GHEU-) GERMAN HUMAN GENOME PROJECT.
XX
XX WIemann S;
XX WPI; 2001-327840/34.
XX DR P-PSDB; ABUS3319.
XX
XX Nucleic acids having the sequences of clones isolated from libraries of
XX different human tissues, useful in recombinant DNA methodologies.
XX
XX Claim 1; Page 942-943; 1095pp; English.
XX
XX This invention describes novel polynucleotides and polypeptides isolated
XX from human cDNA libraries which can be used for gene therapy or in
XX vaccines. The polynucleotides of the invention and antibodies encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate polypeptide expression. The products of the
XX invention may also be used to identify modulators of expression and
XX activity and to down regulate expression and activity. The antibodies of
XX the invention may also be used as diagnostic agents for detecting the
XX presence of polypeptides in samples. This sequence encodes a polypeptide
XX described in the disclosure of the invention
XX
SQ Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;

Query Match 71.68; Score 1355.4; DB 5; Length 3443;
Best Local Similarity 84.08; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;

Qy 47 CCTCCGCCCTGGCCTCGAGAGCCCGCGCGCTGGCGGAGCGGCTCATCAAGTCGCCTA 106
Db 162 CCATCTCCTCGGCGAGAGCTAGCCCGCGCTGGCGGAGGCTGATCAAGTCGCCCA 221
Qy 107 AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCACCATCAAAACACAACCTGCGGCACC 166
Db 222 AGCCCTTAATGAAGAAGCAGCGGTGAAGCGGCACCATCAAAACACAACCTGCGGCACC 281
Qy 167 GCTACGAGTTCCTGGAGACCTGGGCAAGGCGACCTACGGGAGGTGAAGAGCAGAG 226
Db 282 GCTACGAGTTCCTGGAGACCTGGGCAAGGCGACCTACGGGAGGTGAAGAGGCGCGG 341
Qy 227 AGAGCTCGGGCGCTGCTGGTGGCCATCAAGTCCATCAGGAAGACAAAATCAAGATGAGC 286
Db 342 AGAGCTCGGGCGCTGCTGGTGGCCATCAAGTCCATCAGGAAGACAAAATCAAGATGAGC 401
Qy 287 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACACCCCCACA 346

Db 402 AAGATCTGATGTCATACATACGAGGGAGATTGAGATCATGTCTATCATCTCAACACCCCTCACA 461

Qy 347 TCATTGCCATCCATGAAGTCTTTGAGAAATAGCAGCAAGATTGTGATTGTCTATGAGTATG 406

Db 462 TCATTGCCATCCATGAAGTCTTTGAGAAATAGCAGCAAGATTGTGATTGTCTATGAGTATG 521

Qy 407 CCAGCCGAGCGGATCTGTATGATTATCATAGTGAAGCGCCACCGCTGAGTGAGCGGACG 466

Db 522 CCAGCCGAGCGGATCTGTATGATTATCATAGTGAAGCGCCACCGCTGAGTGAGCGGACG 581

Qy 467 CCAGGCATTTCTTCGACAGATCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 526

Db 582 CTAGGCATTTCTTCGCGCAGATCGTCTCTGCGTGCATCTATGCTGCTGCTGCTGCTGCTG 641

Qy 527 TTCAACGAGATCTCAAGCTGGAACATCTCTCTAGATGCAATGGAACCAATCAAGATTG 586

Db 642 TCACCGAGATCTCAAGCTGGAACATCTCTCTAGATGCAATGGAACCAATCAAGATTG 701

Qy 587 CTGACTTTGGCCTCTCCAACTGTACCAAGCAAGTTCTCTCCAGACGTTCTGTGGGA 646

Db 702 CTGACTTTGGCCTCTCCAACTGTACCAAGCAAGTTCTCTCCAGACGTTCTGTGGGA 761

Qy 647 GGCCTCTCTAGGCTCGCCTGAGATGATCAAGCGGAGCCCTATGTGGGCGCAGAGTGG 706

Db 762 GGCCTCTCTATGCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCGCCAGAGTGG 821

Qy 707 ACAGCTGCTCTCTGGGCGTTCTCTCTGATACATCTCTGATGCAACCATGCTGCTGCTG 766

Db 822 ACAGCTGCTCTCTGGGCGTTCTCTCTGATACATCTCTGATGCAACCATGCTGCTGCTG 881

Qy 767 GGCAGGATCAATAAACACTGCTGGAAGCAATCAGTAACGGGGCTTACCGTAGCGGCCA 826

Db 882 GGCATGACCAATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGTAGCGGCCA 941

Qy 827 AGCGCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886

Db 942 AACCCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1001

Qy 887 CCACACTGAGGAGTGTAGCCAGTCAATTTGGGGTCAACTGGGGTTACACCAACCGAGTGC 946

Db 1002 CCACCTTGGAGGATGTGGCCAGTCACTGCTGGGTCAACTGGGGTTACACCAACCGAGTGC 1061

Qy 947 GGAACAGGAGGCTCGCTGAGGGTGGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1006

Db 1062 GAGAGCAGGAGGCTCCGCTGAGGGTGGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1121

Qy 1007 TGGGAGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1066

Db 1122 TGGCTGACTGGCTCCGCGCTTCTCCGCGCCCTCTCTGGAGAAATGGGGGCCAAGGTGTGCA 1181

Qy 1067 GCTTCTTCAAGCAGCAGCTGCGCGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC 1126

Db 1182 GCTTCTTCAAGCAGCAGCTGCGCGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC 1241

Qy 1127 ATTCTCTTAAGAGTCCGGAAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1186

Db 1242 ATTCTCTTAAGAGTCCGGAAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1301

Qy 1187 CTGAGGATACCTCTTCTGCGCTGGCAAGAGAGCCCTTAAGCTTTCGAAAGGCAATCTCA 1246

Db 1302 CTGATGACACTGCGCCATCGCCCTGGCAAGAGCAACCTCAAGCTGCCAAGGCAATCTCA 1361

Qy 1247 AGAAAGTCTCTACTCTGCTGAGGGAGGTACAGGAGGACCTCAGGAACTCAGACCGG 1306

Db 1362 AGAAAGTCTCTACTCTGCTGAGGGAGGTACAGGAGGACCTCAGGAACTCAGACCGG 1421

Qy 1307 TGCTCTGATCTCCAGGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1366

Db 1422 TCCCTGCGAGCCCGAGGCGAGCTGCCCC-----CGCTGCTCCCCAAGAGGCGCATTC 1472

Qy 1367 TTAAGAGTCTGACAGCGTGAATCTGTTTACTCTCTCCAGAGCCCGAGGCTGCTG 1426

Db 1473 TCAAGAGCCCGAGCGGAGTCTGGCTACTCTCTCTCCGAGCCCGAGTGAATCTG 1532

QY 1427 GGGAACCTTTAGAGCCAGTGAATGTTGTTGAGTGGGACCCGCTGGAGCAGAGTCTC 1486
 Db 1533 GGAGAGCTTTTGGACGACAGGCGACGTGTTGTTGAGTGGGATCCCAAGGAGGAGCTC 1592
 QY 1487 CACAGGCTTCAGGCTCTCTCTCCACCGCAAGGCATCTCAAACTCAATGGCAAGTTCT 1546
 Db 1593 CGCAAGCTTCAGGCTCTCTCTCCATCGCAAGGCATCTCAAACTCAATGGCAAGTTCT 1652
 QY 1547 CCGGACAGGCTTTAGAGGCACTACCCCTAGACCTTTGGCTCCCTGGACAACTGGCCT 1606
 Db 1653 CCGGACAGGCTTTGGAGCTCGCGGCCCCACCACTTCGGCTCCCTGGATGAATCGGCC 1712
 QY 1607 CTTCCCATCTGACGCGCGGCCCGCCAGCCCTCAGGGGCTGTGAGTGAGACAGATCC 1666
 Db 1713 CACCTCGCCCTCGGCGCGGCCCGCCAGCCCTCAGGGGCTGTGAGTGAGACAGATCC 1772
 QY 1667 TGTCTCCGAGTCTTTGACCAATTTGACCTTGGCTGAACCTTTCGCCGAACCCCACTGA 1726
 Db 1773 TGTCTCTGAGTCTTTGACCAAGTGGACTTGTCTGAACGGCTCCAGAGCCCCCACTGC 1832
 QY 1727 GGGGCTGTGTCTGTGGACAACTGAGGGGCTTTGAGAGGCTTCCTCTCAAG- 1780
 Db 1833 GGGGCTGTGTCTGTGGACAACTGAGGGGCTTTGAGAGGCTTCCTCTCAAG- 1892
 QY 1781 -----GTCTGAAGCGATGTTGGCAGGAATCTTTGGGGGATAGTCTTTCTCTGACAG 1834
 Db 1893 GAGAGTCCCTGAGGCGCTGGCGGAGGATCTTTGGGGGAGACGTCTTTTCTCTGACAG 1952
 QY 1835 ACTGCCAAGAGGTGACTGACGCTTACAGACAGCCCTTAGGAATCTGCTCAAGCTCAGC 1893
 Db 1953 ACTGCCAAGAGGTGACAGGACCTTACCGACAGGCACTGAGGCTCTGCTCAAGCTCACC 2011

RESULT 13

AD76964
 ID AD76964 standard; cDNA; 3443 BP.

AC AD76964;

XX 26-FEB-2004 (first entry)

XX Novel human secreted and transmembrane protein cDNA Seqid 639.

XX human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.

XX Homo sapiens.

XX W02003072035-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005241.

XX 22-FEB-2002; 2002US-0359461P.

XX (GETH) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;

XX Williams PM, Wood WI, Wu TD;

XX WPI; 2003-721702/68.

XX P-PSDB; AD76965.

XX New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.

XX

PS Claim 2; SEQ ID NO 639; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neurotrophic factors and hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins,
 CC such as receptors or membrane bound proteins, are used as diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytostatic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC invention is a cDNA sequence which encodes a human PRO protein of the
 CC invention.

SQ Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;

Query Match 71.6%; Score 1355.4; DB 10; Length 3443;

Best Local Similarity 84.0%; Pred. No. 0;

Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;

QY 47 CTTCCGCTCTGGCTCGGAGAGCGCCGCGCTGGCGAGCGGCTCATCAAGTCGCGCTA 106

Db 162 CCACTCCCTCGCGCGGAGAGCTAGCCGCGCTGGCGAGGCTCATCAAGTCGCGCTA 221

QY 107 AACCTCTGATGAAGAAGCAGCGGCTGAAGCGGACCATCAACAAACAACTCGCGGACC 166

Db 222 AGCCCTTAATGAAGAAGCAGCGGCTGAAGCGGACCATCAACAAACAACTCGCGGACC 281

QY 167 GTTACAGATTCCTGGAGAGCGCTGGCGAAGGCGACCTACCGGAAGGTGAAGAAGCGAG 226

Db 282 GTTACAGATTCCTGGAGAGCGCTGGCGAAGGCGACCTACCGGAAGGTGAAGAAGCGAG 341

QY 227 AGAGCTCTGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGAACAATAAAGATGAGC 286

Db 342 AGAGCTCTGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGAACAATAAAGATGAGC 401

QY 287 AGGATCTGTGACATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACCA 346

Db 402 AGGATCTGTGACATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACCA 461

QY 347 TCATTGCCATCCATGAAGTGTGAGATAGCAGCAGAGATTGATGTTGTCATCGAGTATG 406

Db 462 TCATTGCCATCCATGAAGTGTGAGATAGCAGCAGAGATTGATGTTGTCATCGAGTATG 521

QY 407 CCAGCGGAGCGCATCTGTATGATTACATCAGTCCAGCGGCGCCAGTCCAGTCCAGCGGAGC 466

Db 522 CCAGCGGAGCGCATCTGTATGATTACATCAGTCCAGCGGCGCCAGTCCAGTCCAGCGGAGC 581

QY 467 CCAGGCAATTTTTCGACAGATCGTGTCTGCGCTGCACTACTCTCCACAGAGCGGATCG 526

Db 582 CTAGGCAATTTTTCGCGGAGATCGTCTCTGCGCTGCACTACTCTCCACAGAGCGGATCG 641

QY 527 TTCACCGAGATCTCAAGCTGGAAAAACATCTCTAGATGCCAATGAAACATCAAGATTG 586

Db 642 TCACCGAGATCTCAAGCTGGAAAAACATCTCTAGATGCCAATGAAACATCAAGATTG 701

QY 587 CTGACTTTGGGCTCTCCAACTGTATACCAAGGCGCAAGTTCTCTCCAGACGTTCTGTGGGA 646

Db 702 CTGACTTTGGGCTCTCCAACTGTATACCAAGGCGCAAGTTCTCTCCAGACGTTCTGTGGGA 761

QY 647 GCCTCTCTACGCTCGCTGAGATAGTCAACGGGAGGCGCTATGTGGGCGGAGGTTGG 706

Db 762 GCCTCTCTATGCTCTCGCAGAGATTGTCAATGGGAAGGCGCTACACAGGCGGAGGTTGG 821

Qy 707 ACAGTGGTCTCTGGGGTCTCTCTGTATCATCTCTGGTGCATGGCACCATTGCCCTTTGACG 766
Db 822 ACAGTGGTCTCTGGGTCTCTCTCTATCATCTCTGGTGCATGGCACCATTGCCCTTTGATG 881
Qy 767 GGCAGGATCAATAACACTGGTGAAGCAATCAGTAACGGGGCTTACCGTAGCGGCCCA 826
Db 882 GGCATGACCAATAAGATCTCTAGTAAACAGATCAGCAACGGGGCTTACCGGAGGACCACTA 941
Qy 827 AGCGGTCCGATGCTGTGGCTGTATCCGGTGGCTGTTAATGTCGAACCCACCCCGTGGG 886
Db 942 AACCTCTGATGCTGTGGCTGTATCCGGTGGCTGTTGATGTAACCCACCCCGCGGG 1001
Qy 887 CCACACTGGAGATGTAGCCAGTCAATTGGTGGGTCAACTGGGGTTACACCAACCGAGTGC 946
Db 1002 CCACCTGGAGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCTACGCCACCCGAGTGG 1061
Qy 947 GGGAAACAGGAGCCCTGGGTGAGGGTGGGCAACCTAGTGTGACTTTGGCCGGGCTTCCA 1006
Db 1062 GAGAGCAGGAGGCTCCGCATGAGGGTGGGCAACCTGGCAGTGACTCTGCCCGGCTTCCA 1121
Qy 1007 TGGCGGACTGTTACGTGCTCTCGCGCCCTCTGGAGAAATGGAGCCAAAGTGTGCA 1066
Db 1122 TGGGTGACTGCTCGGGTCTCTCCGCCCTCTCTGGAGAAATGGGCGCAAGGTGTGCA 1181
Qy 1067 GCTTCTTCAAGCAGCAGTGTCCGGGAGGTGGAAGCACTGTACTTGGGTGGAGCGGCAAC 1126
Db 1182 GCTTCTTCAAGCAGCAGTGTCTGGTGGGGAAGCACCACCCCTGGCTGGAGCGCCAGC 1241
Qy 1127 ATTCTCTTAAGAAGTCCGAAAGAGAAATGATGCTGAGTCTAAATCTGGAAGGTGACCCGG 1186
Db 1242 ATTCTCTTAAGAAGTCCGAAAGAGAAATGATGCTGAGTCTAAATCTGGAAGGTGACCCGG 1301
Qy 1187 CTGAGGATACCTCTCTCGCCCTCGCAAGAGCAGCCTTAAGCTTCCGAAGGCAATCTCA 1246
Db 1302 CTGATGACATGCCCCTCGCAAGAGCAACCTCAAGCTTCCGAAGGCAATCTCA 1361
Qy 1247 AGAAAGTCTCTTACCTCTGTCCGGGAGGTGACAGGAGCCCTCAGGAACTCAGACCGG 1306
Db 1362 AGAAAGTCTCTTACCTCTGTCCGGGAGGTGACAGGAGCCCTCAGGAACTCAGACCGG 1421
Qy 1307 TGCCTGATCTCAGGCGAGCTGTCTGCTGTATCTCTGCTCCCAAGGAAGGATCC 1366
Db 1422 TCCCTGGAGCCAGGCGAGCTGCC-----CGCTGCTCCCAAGGAAGGCAATC 1472
Qy 1367 TTAAGAAGTCTCAGCAGCTGAATCTGTTACTACTCTCTCCAGAGCCAGCAGTCTG 1426
Db 1473 TCAAGAAGCCCGAGCGAGTCTGCTACTACTCTCTCCGAGCCAGTGAATCTG 1532
Qy 1427 GGGAACTCTTAGACCGCAGTGTGTTGTGAGTGGGAGCCCGTGGAGCAGAAGTCTC 1486
Db 1533 GGGAGCTCTTGAGCGCAGGCGAGTGTGTTGTGAGTGGGATCCCAAGGAGCAGAAGCTC 1592
Qy 1487 CACAGGCTCAGGCTCTCTCTCAGCGAAGGCAATCTCAAACTCAATGGCAAGTTCT 1546
Db 1593 CGAAAGTCTCAGGCTCTCTCTCAGCGAAGGCAATCTCAAACTCAATGGCAAGTTCT 1652
Qy 1547 CCGCAGCAGCTTAGAGGCACTACCCCTAGCAGCTTTGGCTCCCTGACCACTGGCT 1606
Db 1653 CCGCAGCAGCTTAGAGGCTCGGCGCCCTCAGCAGCTTTGGCTCCCTGAGTGAATCGCCC 1712
Qy 1607 CCTCCCATCTTGACCGCGCCAGCGCCCTCAGGCGCTGTGAGTGAGCAGCAGCATCC 1666
Db 1713 CACCTCGCCCTTGCGCGCGGCGAGCGACCTCAGGCGCTGTGAGTGAGCAGCAGCATCC 1772
Qy 1667 TGTCTCCGAGTCTTTGACCAATTTGACTGTGCTGAACGTCTTCCGAAACCCCACTGA 1726
Db 1773 TGTCTCTGAGTCTTTGACCAATTTGACTGTGCTGAACGTCTTCCGAAACCCCACTGC 1832
Qy 1727 GGGGCTGTGTCTGTGGAACAACCTGAGGGGCTTTGAGCAGCTCTCTCTGAGG----- 1780
Db 1833 GGGGCTGTGTCTGTGGAACAACCTCAGGGGCTTTGAGGAGCGCCCTCAGAGGGCGCTG 1892

Qy 1781 -----GTCTGAAGCGATGGTGGCAGGAATCCTTTGGGGATAGTGTCTTCTCTGACG 1834
Db 1893 GAAGCTCCTTGAGCGCTGGCGGAGGATCCTTTGGGGGACAGTGTCTTTCCCTGACG 1952
Qy 1835 ACTGCCAAGAGGTGACTGAGCCTTACAGACAGCCCTTAGGAATCTGTCAAAGTCTCAG 1893
Db 1953 ACTGCCAAGAGGTGAGCAGCCTTACCGACAGGCACTGAGGGTCTGTCAAAGTCTCAG 2011
RESULT 14
ADF81952
ID ADF81952 standard; DNA; 3443 BP.
XX
XX ADF81952;
XX AC
XX AC
XX 26-FEB-2004 (first entry)
DT
XX Leukaemia-related DNA sequence #2508.
DE
XX Cytostatic; Gene therapy; leukaemia; ss.
XX
XX Unidentified.
XX OS
XX PN W02003039443-A2.
XX PD 15-MAY-2003.
XX PF 04-NOV-2002; 2002WO-EP012303.
XX PR 05-NOV-2001; 2001EP-00126244.
XX PR 30-APR-2002; 2002EP-00009758.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (JYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE//) HAERLACH T.
PA (SCHO//) SCHOCH C.
PA (KERN//) KERN W.
XX
XX Haerlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugae M;
PI Eils R, Brors B, Mergenthaler S;
XX WPI; 2003-505037/47.
XX
XX Determining the subtype of leukemia cells and whether a patient sample
contains leukemia cells or other cells useful for treating leukemia,
PT comprises determining the expression profile of a group of markers in a
PT patient sample.
XX
XX Disclosure; SEQ ID NO 2508; 2938pp; English.
XX
XX The present invention relates to a method (M1) for determining the
CC subtype of leukaemia cells and whether a patient sample contains
CC leukaemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukaemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukaemia.
XX
XX Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;
SQ
Query Match 71.6%; Score 1355.4; DB 10; Length 3443;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;
Qy 47 CCTCGCCCTGGCTCGGAGAGCGCCGCGCTGGCGAGCGGCTCATCAAGTCGCCTA 106
Db 162 CCATCTCCCTCGCGCAGAGCTAGCCGCGCTGGCGAAGGGCTGATCAAGTCGCCCA 221
Qy 107 AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCAACCATCAACAACAACTCTGGGACCC 166
Db 222 AGCCCTTATGAAGAAGCAGCGGTGAAGCGGCAACCATCAACAACAACTCTGGGACCC 281
Qy 167 GCTACGAGTTCTTGAGAGCCTCGGCAAGGGCACTACGGGAAGGTGAAGAAGCAGCAG 226
|||||

Db 282 GCTACGAGTTCTCGGACACCTGGGCAAGGCACTACGGGAAGGTGAAGAGCGCGG 341
Qy 227 AGAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGAGCAAAATCAAGATGAGC 286
Db 342 AGAGCTCGGGCGCTGGTGGCCATCAAGTCAATCCGGAAGGACAAATCAAGATGAGC 401
Qy 287 AGAGTCTGCTGCACATACGAGGAGAGATTGAGATCATGTCTTCACTCAACCCACCCACCA 346
Db 402 AAGATCTGATGCATACGAGGAGAGATTGAGATCATGTCTTCACTCAACCCACCCACCA 461
Qy 347 TCATTGCCATCCATGAAGTGTTCAGAAATAGCAGCAAGATTGTGATTGTATGATGATG 406
Db 462 TCATTGCCATCCATGAAGTGTTCAGAAACAGCAGCAAGATCGTATCGTATGAGTATG 521
Qy 407 CCAGCCAGGCGATCTGTATGATTACATCAGTGAAGCGGCCACCGCTGAGTGAAGCGGACG 466
Db 522 CCAGCCGGGGCGACCTTTATGACTACATCAGCAGAGCGGCGAGCAGCTCAGTGAGCGCAAG 581
Qy 467 CCAGGCAATTTCTCCGACAGATCGTGTCTGCCCTGCCTACTGCGCCACAGAAAGCGATCG 526
Db 582 CTAGGCAATTTCTCCGCGAGATCGTCTCGCGGTGCACTATTGCCATCAGAAAGATTG 641
Qy 527 TTCAACGAGATCTCAAGCTGGAACATCTCTTCTAGATGCCAATGGAACATCAAGATTG 586
Db 642 TCCACCGAGATCTCAAGCTGGAGAACATCTCTTTGGATGCCAATGGGAATATCAAGATTG 701
Qy 587 CTGACTTTGGCTCTCAACCTGTACCAAGCAAGTAAGTTCTCTCAGACGTTCTGTGGGA 646
Db 702 CTGACTTTGGCTCTCAACCTGTACCAATCAAGCAAGTAAGTTCTCTCAGACATTTCTGTGGGA 761
Qy 647 GCCCTCTCTAGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTGG 706
Db 762 GCCCTCTCTAGCCTCGCAGAGATTGTCAATGGGAAGCCCTACAGAGCCAGAGGTGG 821
Qy 707 ACAGCTGGTCTGTGGCGTTCTCTCTGTACATCTCTGTGTGATGCAACCATGCTTTGACG 766
Db 822 ACAGCTGGTCTGTGGCGTTCTCTCTGTACATCTCTGTGTGATGCAACCATGCTTTGATG 881
Qy 767 GGCAGGATCATAAACACTGGTGAAGCAATCAGTGAAGGGCTTACGGTGAAGCGGCCCA 826
Db 882 GGCATGACCATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGGAGGCCACTA 941
Qy 827 AGCGCTCCGATGCTGTGGCTGATCGGTGGCTGTTAATGGTGAACCCACCGCTCGGG 886
Db 942 AACCTCTGATGCTGTGGCTGATCGGTGGCTGTTGATGGTGAACCCACCGCTCGGG 1001
Qy 887 CCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAACTGGGGTTACACCAACCGAGTCG 946
Db 1002 CCACCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCTACGCCACCGAGTGG 1061
Qy 947 GGGNACAGGAAGCCCTGGGTGAGGGTGGGACCCCTAGTGTGACTTTGGCGGGCTCCA 1006
Db 1062 GAGAGCAGGAGGCTCCGCATGAGGGTGGGACCCCTGGCAGTGAATCTGCCCGGCTCCA 1121
Qy 1007 TGGCGGACTGGTACGTGCTCTCTCGGCCCTCTCTGGAGAAATGGAGCAAGGTGTGCA 1066
Db 1122 TGGCTGACTGGCTCGGGCTCTCTCGGCCCTCTCTGGAGAAATGGGCGCAAGGTGTGCA 1181
Qy 1067 GCTTCTTCAAGCAGCAGCTGCGGGAGGTGGAAGCACTGTACTGGGTGAGAGCGGCAAC 1126
Db 1182 GCTTCTTCAAGCAGCAGCTGCGGGAGGTGGAAGCAACCCCTGGCTGGAGCGCCAGC 1241
Qy 1127 ATTCTCTTAAGAGTCCGGAAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1186
Db 1242 ATTGCTCTAAGAGTCCGGAAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACACGG 1301
Qy 1187 CTGAGGATACCTCTCTCGCCCTGGCAAGAGCAGCTTAAAGTTCGGAAGGCAATTCCTCA 1246
Db 1302 CTGATGACATGCCCCCTGGCAAGAGCAACCTCAAGTCTGCCAAGGCAATTCCTCA 1361
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Db 1533 GGGAGCTCTTGGACGCGAGCGAGTGTGTGTAGTGGGATCCCAAGGAGCAGAAAGCTC 1592
Qy 1487 CACAGGCTTCAGGCTCTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGCAAGTCT 1546
Db 1593 CGCAAGCTTCAGGGCTGCTCTCTCATCGCAAGGCAATCTCAAACTCAATGGCAAGTCT 1652
Qy 1547 CCGCGACAGCTTTAGAAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGAGCAAACTGGCCT 1606
Db 1653 CCAGACAGCTTTGGAGCTCGCGGCCCCACACCTTCGGCTCCCTGGATGAATCGCCC 1712
Qy 1607 CTCCCATCTGACGCGCGGCCCGAGCGGCCCTCAGGGGCTGTGAGTGAGGACAGCAATCC 1666
Db 1713 CACCTCGCCCTCGCGGCCCGAGCGCACCTCAGGGGCTGTGAGCGAGGACAGCAATCC 1772
Qy 1667 TGTCTCCGAGTCTTTGACCAATTTGGACTTGGCTGNAAGTCTTCCGGAACCCCACTGA 1726
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Db 1833 GGGGCTGTGTGTCTGTGGCAACCTCAGGGGGCTTGAAGCAGCTCCCTCAGAGGGCCCTG 1892
Qy 1781 -----GTCTGAAGCGATGGTGCAGGAATCTTGGGGGATAGTGTCTTTCTGTGACAG 1834
Db 1893 GAAGCTGCCTGAGCGCTGGCGGCGAGGATCTTTTGGGGGACAGCTGCTTTTCCCTGACAG 1952
Qy 1835 ACTGCCAAGAGGTGACTGCGAGCCTCAGACAAGCCCTAGGAATCTGCTCAAGCTCAGC 1893
Db 1953 ACTGCCAAGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCAAGCTCACC 2011

RESULT 15

ADO20171
ID ADO20171 standard; cDNA; 3443 BP.

XX AC ADO20171;

XX XX
DT 12-AUG-2004 (first entry)XX XX
DE Human PRO polynucleotide #540.

XX XX
KW Human; PRO; gene; ss; immune related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW renal disease; demyelinating disease; central nervous system;
KW peripheral nervous system; demyelinating polyneuropathy;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.

OS Homo sapiens.

XX XX
PN WO2004043361-A2.XX XX
PD 27-MAY-2004.XX XX
PF 06-NOV-2003; 2003WO-US035268.XX XX
PR 08-NOV-2002; 2002US-0425235P.XX XX
PA (GETH) GENENTECH INC.

XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX P-PSDB; ADO20172.
XX WPI; 2004-420067/39.
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX spondyloarthritis.
XX Claim 1; SEQ ID NO 1136; 1731pp; English.
XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polynucleotide of
XX the invention.
XX SQ Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;

Query Match 71.6%; Score 1355.4; DB 12; Length 3443;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 276; Indels 21; Gaps 2;

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287 AGGATCTGCTGCATACGAGGAGAGATTGAGATCATGTTCTCACTCAACCCGCCACA 346
402 AAGATCTGATGCATACGAGGAGAGATTGAGATCATGTTCTCACTCAACCCGCCACA 461
347 TCATTGGCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATGATGATG 406
462 TCATTGGCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATGATGATG 521
407 CCAGCGAGGCGATCTGATGATTAATCATCAGTGAAGCGGCGAGCTGAGTGAAGGAGC 466
522 CCAGCGGCGGCGATCTTATGATTAATCATCAGTGAAGCGGCGAGCTGAGTGAAGGAGC 581
467 CCAGCGATTTCTCCGACAGATCTGTCTGCGCTGCACTACTGCGCACAGAAAGCGGATCG 526
582 CTAGGCAATTTCTCCGCGAGATCTGTCTGCGCGTGCATATTGCCATCAGAACAGATTG 641
527 TTCAACGAGATCTCAAGCTGGAACATCTCTTCTAGATGCCAATGGAACATCAAGATTG 586
642 TCCACCGAGATCTCAAGCTGGAACATCTCTTCTTGGATGCCAATGGAATATCAAGATTG 701
587 CTGACTTTGGCTCTCCAACTGTACCAAGCAAGTTCCTCCAGACGTTCTGTGGGA 646
702 CTGACTTTGGCTCTCCAACTGTACCAAGCAAGTTCCTCCAGACATTCCTGTGGGA 761

Qy 647 GCCCTCTCTAGCGCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGGTGG 706
Db 762 GCCCTCTCTAGCGCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGGTGG 821
Qy 707 ACAGCTGGTCTCTGGGGTCTCTCTGTACATCTGTGTGATGCGACCATGCGCTTTGACG 766
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Qy 1427 GGAATCTTTAGAGCGCAGT 1486
Db 1533 GGGAGCTCTTGGAGCGAGCGAGT 1592
Qy 1487 CAGAGCTTCAAGGCTCTCTCTCCAGCGCAAGGCAATCTCAAACTCAATGGCAAGTCT 1546
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Job time : 883.636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 14:50:33 ; Search time 7944.68 Seconds
(without alignments)
11267.845 Million cell updates/sec

Title: US-09-980-464-4_COPY_123_2015

Perfect score: 1893
Sequence: 1 atggagtcggtggccttact.....gaatctgctcaagtcagc 1893

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

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11: gb_sts.*

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13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1893	100.0	2902	6	AR279568 Sequence
2	1888.2	99.7	2027	6	AX381046 Sequence
3	1872.2	98.9	2917	10	BC033302 Mus muscu
4	1859	98.2	2938	10	BC046833 Mus muscu
5	1683.4	88.9	2026	6	AX380986 Sequence
6	1683.4	88.9	2929	6	AX380960 Sequence
7	1528.4	80.7	291762	2	AC125887 Sequence
8	1360.2	71.9	1884	6	AX407118 Sequence
9	1360.2	71.9	3353	6	AX407116 Sequence
10	1357.6	71.7	3360	6	AX642961 Sequence
11	1357	71.7	1887	6	CQ714327 Sequence
12	1357	71.7	3395	6	CQ782778 Sequence
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22	943.4	49.8	1186	6	AX381029 Sequence
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ALIGNMENTS

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LOCUS	AR279568					
DEFINITION	Sequence 4 from patent US 6514719.					
ACCESSION	AR279568					
VERSION	AR279568.1	GI:29714427				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 2902)					
AUTHORS	Bird,T.A., Virca,G.D., Martin,U. and Anderson,D.M.					
TITLE	Methods for identifying compounds that alter kinase activity					
JOURNAL	Patent: US 6514719-A 4 04-FEB-2003;					
FEATURES	Location/Qualifiers					
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ORIGIN						

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QY	121	AAGCAGCGGTGAGCGGACCATCAACACAACTCGGCGACCGCTACGAGTTCCTG	180	
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QY	181	GAGACCTCGGCAAGGCGACCTACGGAAGGTGAAGAAGCAGCAGAGAGCTCGGGCGGT	240	
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RESULT 2

AX381046
LOCUS AX381046 2027 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 87 from Patent WO0212456.
ACCESSION AX381046
VERSION AX381046.1 GI:19575868
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Drucker, D.J., Rosen, C.F. and Lefebvre, D.L.
TITLE Ampk-related serine/threonine kinase, designated snark
JOURNAL Patent: WO 0212456-A 87 14-FEB-2002;
1149336 ONTARIO INC. (CA)
FEATURES
source
1. .2027
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"

ORIGIN

Query Match 99.7%; Score 1888.2; DB 6; Length 2027;
Best Local Similarity 99.8%; Pred. No 0;
Matches 1890; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 135 TCGGAGAGCGCCCGGCTGGGAGCGGCTCATCAGTCCGCTTAAACCTCTGATGAG 194

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)

2388257
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 2917)
Direct Submission
Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 40 Row: d Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
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VERSION
BC046833.1
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MGC.
SOURCE
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ORGANISM
Mus musculus
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Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Strausberg, R.
Direct Submission
Submitted (13-FEB-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
Web site: <http://genome.uiowa.edu>
Contact: bento-soares@uiowa.edu
Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fisher, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
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ACCESSION AX380986
VERSION AX380986.1 GI:19575826
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ORGANISM Rattus sp.
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Rattus.
REFERENCE 1
AUTHORS Drucker, D.J., Rosen, C.F. and Lefebvre, D.L.
TITLE Ampk-related serine/threonine kinase, designated snark
JOURNAL Patent: WO 0212456-A 27 14-FEB-2002;
1149336 ONTARIO INC. (CA)
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RESULT 6
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LOCUS      2929 bp      DNA      linear      PAT 18-MAR-2002
DEFINITION Sequence 1 from Patent WO0212456.
ACCESSION AX380960
VERSION    AX380960.1 GI:19575800
KEYWORDS
SOURCE
ORGANISM   Rattus sp.
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            Rattus.
REFERENCE 1
AUTHORS   Drucker,D.J., Rosen,C.F. and Lefebvre,D.L.
TITLE     Ampk-related serine/threonine kinase, designated snark
JOURNAL   Patent: WO 0212456-A 1 14-FEB-2002;
          1149336 ONTARIO INC. (CA)
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ORIGIN

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Best Local Similarity 93.4%; Pred. No. 0;
Matches 1769; Conservative 0; Mismatches 121; Indels 3; Gaps 1;

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Qy      61  TCGGAGAGCCCGCGCTGGGAGCAGGGGCTCATCAAGTGCCTAAACCTCTGATGAAG 120

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Qy      121  AAGCAGCGGTGAAGCGGCAACCATCAAAACACAACCTCGGGCACCGCTACGAGTTCCTG 180
Db      203  AAGCAGCGGTGAAGCGGCAACCATCAAAACACAACCTGAGGCACCGCTACGAGTTCCTG 262
Qy      181  GAGACGCTGGGCAAGGCACTTACGGGAAGGTGAAGAGGCAAGAGAGCTCGGGCGGT 240
Db      263  GAGACGCTGGGCAAGGCACTTACGGGAAGGTGAAGAGGCAAGAGAGCTCGGGACGC 322
Qy      241  CTGCTGGCCATCAAGTCCATCAGGAAGACAAAATCAAGATGAGCAGGATCTCTGCAC 300
Db      323  CTGCTGGCCATCAAGTCTATCAGGAAGGACAAAATCAAGATGAGCAGGATCTCTGCAC 382
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Db      383  ATAAGGAGGAGATCGAGATCATGTCTTCACTCAACACCCCAACATCATTTGCCATCAT 442
Qy      361  GAAGTGTTCAGAAATAGCAGCAAGATTTGTGTCATGAGTATGCGAGCGAGGCGAT 420
Db      443  GAAGTGTTCAGAAATAGCAGCAAGATTTGTGTCATGAGTATGCGAGCGAGGCGAT 502
Qy      421  CTGTATGATTACATCAGTGAGCGGCGCACCGCTGAGTGAGCGGAGCGGACGAGCATTTCTTC 480
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Qy      481  CGACAGATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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Db 1463 CAGCGTGAATCTGTTACTACTCTCTCTCCAGAGCCCGAGTCTGGGGAATCTTAGAC 1522
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RESULT 7
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DEFINITION Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS
***, 13 unordered pieces.
AC125887
VERSION AC125887.3 GI:25008671
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 291762)

Worley,K.C.

Direct Submission

Submitted (02-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 291762)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23269681.

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

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----- Project Information
Center project name: GWLD
Center clone name: CH230-274J3
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 226053 bases at least Q40
Consensus quality: 230853 bases at least Q30
Consensus quality: 233437 bases at least Q20
Estimated insert size: 233445; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
      (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1 70277: contig of 70277 bp in length
* 70278 70377: gap of unknown length
* 95031: contig of 24654 bp in length
* 95032 95131: gap of unknown length
* 108956: contig of 13825 bp in length
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* 271698 271797: gap of unknown length
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* 273027 273126: gap of unknown length
* 273127 274531: contig of 1405 bp in length
* 274532 274631: gap of unknown length
* 274632 276287: contig of 1656 bp in length
* 276288 276387: gap of unknown length
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RESULT 8
AX407118
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DEFINITION Sequence 3 from Patent WO224921.
ACCESSION AX407118
VERSION AX407118.1 GI:21439883
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Curtis, R.A. and Galvin, K.M.
TITLE 3700, a novel human protein kinase and uses therefor
JOURNAL Patent: WO 0224921-A 3 28-MAR-2002;
Millennium Pharmaceuticals, Inc. (US)
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Best Local Similarity 84.2%; Pred. No. 0;
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VERSION AX407116.1 GI:21439882
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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AUTHORS Curtis,R.A. and Galvin,K.M.
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LOCUS Sequence 38 from Patent WO01096547.
ACCESSION AX642961

VERSION AX642961.1 GI:28550104

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

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Yue, H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y.,
Gandhi, A. R., Triboulet, C. M., Walla, N., Yao, M. G., Lu, D. A.,
Greenwald, S. R., Rankumar, J., Griffin, J. A., Kearney, L., Burford, N.,
Nguyen, D. B., Tang, Y. T., Baughn, M. R., He, A., Thornton, M.,
Hafalia, A., Patterson, C., Gururajan, R., Lo, T. P., Khan, F.,
Recipon, S. A., Asimail, Y., Policky, J. L., Ding, L., Grether, M.,
Elliott, V. S., Thangavelu, K., Batra, S. and Ison, C. H.

Humain kinases

Patent: WO 01096547-A 38 20-DEC-2001;

Incyte Genomics, Inc. (US)

location/Qualifiers

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VERSION CQ714327.1 GI:42275184
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REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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thereof
JOURNAL Patent: WO 02068579-A 261 06-SEP-2002;
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ACCESSION BD127309
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REFERENCE 1 (bases 1 to 3395)
AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
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SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
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ACCESSION BC017306.2 GI:33878200

VERSION MGC.

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AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Aitschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E.,

Schmerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

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Strausberg, R.

Direct Submission

Submitted (05-NOV-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Aug 19, 2003 this sequence version replaced gi:16878205.

Contact: MGC help desk

Email: cgaps-remail.nih.gov

Tissue Procurement: Lou Straudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nigr.nih.gov

Akhter, N., Ayele, K., Beckett-Sternberg, S.M., Benjamin, B.,

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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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 SKLT"

gene

CDS

ORIGIN

Query Match 71.7%; Score 1357; DB 9; Length 3402;
 Best Local Similarity 84.1%; Pred. No. 0;
 Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;
 Qy 47 CTTCCGCGCTTGGCCTCGGAGAGCGCCGCGCTGGCGGACGGCTCATCAAGTCGCTTA 106
 Db 134 CCACTCCCTCGCGCGCAGAGCTAGCCGCGCTGGCGGAGGCTCATCAAGTCGCTTA 193
 Qy 107 AACCTCTGATGAAGAAGCAGCGCGGTGAAGCGGCACCATCAACAACAACTCGGCACC 166
 Db 194 AGCCCTTAATGAAGAAGCAGCGCGGTGAAGCGGCACCATCAACAACAACTCGGCACC 253
 Qy 167 GTTACAGATTCTCTGGAGAGCCTCGGCAAGGCGACCTACGCGGAAGGTGAAGAAGCAG 226
 Db 254 GCTACAGATTCTCTGGAGACCTCTGGCNAAGGCACCTACGCGAAGGTGAAGAAGCAG 313
 Qy 227 AGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGAACAATAAATCAAGATGAGC 286
 Db 314 AGAGCTCGGGCGCTCTGGTGGCCATCAAGTCAATCGGAAGGACAAAATCAAGATGAGC 373
 Qy 287 AGATCTGTGCATACACGAGGAGATTGAGATCATGTCTTCTCCTCAACACCCCCACA 346
 Db 374 AGATCTGTGTGCATACACGAGGAGATTGAGATCATGTCTTCTCCTCAACACCCCTACA 433
 Qy 347 TCATTGCGATCCATGAAGTGTGTTGAGATAGCAGCAAGATTGTGATTGTCTATGAGTATG 406
 Db 434 TCATTGCGATCCATGAAGTGTGTTGAGATAGCAGCAAGATTGTGATTGTCTATGAGTATG 493
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Db 494 CCAGCCGGCGACCTTTATGACTACATCAGGAGCGGACGAGCTCAGTGAGCGCGAAG 553
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Db 554 CTAGGCATTTCTCCGCGAGATCGTCTCGCGTGCACATATTGCCATCAGAACAGAGTTG 613
Qy 527 TTCAACGAGATCTCAAGCTGGAACATCTCTTAGATGCCAATGGAACATCAAGATTG 586
Db 614 TCCACCGAGATCTCAAGCTGGAGAACATCTCTTGGATGCCATGGGAATATCAAGATTG 673
Qy 587 CTGACTTTGGCTCTCCAACTGTACCAAGCAAGTTCTCTCCAGACGTTCTGTGGGA 646
Db 674 CTGACTTCCGCTCTCCAACTGTACCAATCAAGCAAGTTCTCTCCAGACATTTCTGTGGGA 733
Qy 647 GCCTCTCTACGCTCGCTGAGATAGTCAACGGAAGCCCTATGTGGGCCAGAGGTGG 706
Db 734 GCGCCCTCTATGCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCCCAGAGGTGG 793
Qy 707 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCTCTGGTGCATGGCACCATGCCCTTTTCACG 766
Db 794 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCTCTGGTGCATGGCACCATGCCCTTTTCATG 853
Qy 767 GGCAGGATCAATAACACTGTGTGAAGCAAAATCAGTAAACGGGGCTTACCGTGAGCCGCCA 826
Db 854 GGCATGACCATAGATCTTAGTGAACACAGATCAGCAACGGGGCCCTACCGGAGCCACTA 913
Qy 827 AGCGTCCGATGCTGTGGCTGTATCGGTGGCTTTAATGGTGAACCCACCCGTCGGG 886
Db 914 AACCTCTGATGCTGTGGCTGTATCGGTGGCTTTAATGGTGAACCCACCCGTCGGG 973
Qy 887 CCACACTGGAGGATGTAGCCAGTCAATTGGTGGGTCAACTGGGGTTACACACCAGGAGTCG 946
Db 974 CCACCTTGGAGGATGTGGCCAGTCACTGGTGGGTCACTGGGGTACGCCACCCGAGTGG 1033
Qy 947 GGGAAAGGAAGCCCTCGGTGAGGGTGGGCAACCTAGTGTGACTTTTGGCGGGCCCTCCA 1006
Db 1034 GAGAGCAGGAGGCTCCGATGAGGGTGGGCAACCTGGCAGTACTCTGCCGCGCCCTCCA 1093
Qy 1007 TGGGGAGTGGTTACGTTCCTCGCGCCCTCTCGCGCCCTCTCTGGAGATGGAGCCAGGTGCA 1066
Db 1094 TGGCTGACTGGCTCCGGCTTCCTCCCGCCCTCTCTGGAGATGGGGCCCAAGGTGTGCA 1153
Qy 1067 GCTTCTTCAAGCAGCAGTGCAGGAGGTGGAAGCAGTGTACTCGGGCTGGAGCGGCAAC 1126
Db 1154 GCTTCTTCAAGCAGCAGTGCACCTGGTGGGGAAGCAACACCCCTGGCTGGAGCGCCAGC 1213
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Qy 1187 CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCAGCCCTTAGCTTCGGAAGGCATTTCTCA 1246
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Qy 1247 AGAAAAAGTCTCTTACCTCTGTCAGGGAGGTACAGGAGGACCCCTCAGGAACTCAGACCGG 1306
Db 1334 AGAAGAGGTCTCAGCTCTCGAAGAGGGGTACAGGAGGACCCCTCCGAGCTCAGCCCAA 1393
Qy 1307 TGCTGTATATCCAGGGAGCCTGTCTGCTGTATCCCTGCTCCCAAGGAAGGCATCC 1366
Db 1394 TCCCTGGAGCCCAAGGGCAGGCTGCC-----CCCTGCTCCCAAGAGGGCATTC 1444
Qy 1367 TTAGAGAGTCTCGACAGGTGAATCTGTTACTACTCTCTCCAGAGCCGAGCTCTG 1426
Db 1445 TCAAGAAAGCCCGACAGCGGAGTCTGGCTACTACTCTCTCCGAGCCGAGTGAATCTG 1504
Qy 1427 GGGAACTCTTAGAGCGCAGTGTATGTTGTAGTGGGGACCCCGTGGAGCAGAGTCTC 1486
Db 1505 GGGAGCTCTTGGAGCGCAGCGACGTGTTGTAGTGGGATCCCAAGGAGCAGAGCCTC 1564
Qy 1487 CACAGGCTCAGGGCTCTCTCTCAACCGAAGGCAATCTCAAACTCAATGGCAAGTTCT 1546
Db 1565 CGAAGCTTCAGGGCTCTCTCTCAATCGCAAGGCATCTCTCAAACTCAATGGCAAGTTCT 1624

Qy 1547 CCGGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT 1606
Db 1625 CCAGACAGCCTTTGGAGCTCGCGGCCCCCACCACCTTTGGCTCCCTGGATGAATCGCCC 1684
Qy 1607 CTTCCCATCTCGACGCCCGGCCAGCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1666
Db 1685 CACCTCGCCCTCGGCCCGGCCAGCGGACCCCTCAGGGGCTGTGAGCGAGGACAGCATCC 1744
Qy 1667 TGTCTCCGAGTCTTTTGACCAATTGGAATTGACTTTGCTGAACTCTTCCGAAACCCCACTGA 1726
Db 1745 TGTCTCTGAGTCTTTTGACCAAGTGGACTTGGCTGAAACGGCTCCCAAGAGCCCCCACTGC 1804
Qy 1727 GGGGCTGTGTCTGTGGCAACCTCAGGGGGCTTGAGCAGCCTCCCTCAGAAG----- 1780
Db 1805 GGGGCTGTGTGTCTGTGGCAACCTCAGGGGGCTTGAGGAGCCCCCTCAGAGGGCCCTG 1864
Qy 1781 -----GTCTGAAAGCGATGGTGCAGGAATCTTTGGGGATAGCTGTTTTCTCTGACAG 1834
Db 1865 GAAGCTGCCTGAGCGCTGGCGGAGGATCCTTTGGGGACAGCTGCTTTTCCCTGACAG 1924
Qy 1835 ACTGCCAAGAGGTGACTGACAGCCTACAGACAAGCCCTTAGGAATCTGCTCAAAGTCAAGC 1893
Db 1925 ACTGCCAAGAGGTGACAGCAGCCTACCGACAGGCACTGAGGGTCTGCTCAAAGTCAAGC 1983

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 16:12:33 ; Search time 353.728 Seconds
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Perfect score: 1893

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493.6	26.1	4933	1 PCT-US04-14421-36	Sequence 36, Appl
2	493.6	26.1	4933	7 US-10-840-512-36	Sequence 36, Appl
3	400.2	21.1	477	7 US-10-948-737-10961	Sequence 10961, A
4	221	11.7	944	7 US-10-487-901-6208	Sequence 6208, Ap
5	197.4	10.4	4094	1 PCT-US04-14421-37	Sequence 37, Appl
6	197.4	10.4	4094	7 US-10-840-512-37	Sequence 37, Appl
7	191.4	10.1	2107	7 US-10-998-525-5	Sequence 5, Appli
8	186	9.8	1512	9 US-60-638-099-231	Sequence 231, App
9	180.2	9.5	1518	9 US-60-638-099-214	Sequence 214, App
10	179.6	9.5	2006	7 US-10-998-525-21	Sequence 21, Appl
11	179.4	9.5	3394	7 US-10-995-561-364	Sequence 364, App
12	179.4	9.5	3442	7 US-10-995-561-361	Sequence 361, App
13	179.4	9.5	3466	7 US-10-995-561-363	Sequence 363, App
14	179.4	9.5	3487	7 US-10-995-561-359	Sequence 359, App
15	179.4	9.5	3514	7 US-10-995-561-360	Sequence 360, App
16	179	9.5	2123	7 US-10-998-525-11	Sequence 11, Appl
17	176.4	9.3	2179	7 US-10-956-157-4597	Sequence 4597, Ap
18	176.4	9.3	4919	7 US-10-956-157-4596	Sequence 4596, Ap
19	176.4	9.3	5074	7 US-10-990-328-3866	Sequence 3866, Ap
20	171.2	9.0	1735	1 PCT-US04-14421-15	Sequence 15, Appl
21	171.2	9.0	1735	7 US-10-840-512-15	Sequence 15, Appl
22	166.2	8.8	1527	9 US-60-638-099-106	Sequence 106, App
23	166.2	8.8	1530	9 US-60-638-099-232	Sequence 232, App
24	166.2	8.8	1948	7 US-10-998-525-3	Sequence 3, Appli

Sequence 15, Appl
Sequence 224, App
Sequence 228, App
Sequence 47, Appl
Sequence 49, Appl
Sequence 49, Appl
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Sequence 55, Appl
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Sequence 215, App
Sequence 3, Appli
Sequence 5, Appli
Sequence 221, App
Sequence 19, Appl
Sequence 23, Appl
Sequence 225, App

ALIGNMENTS

RESULT 1

PCT-US04-14421-36
; Sequence 36, Application PC/TUS0414421
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; APPLICANT: CAENRPEEL, SEAN
; APPLICANT: MANNING, GERARD
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: HIGORIEV, IGOR
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-1454
; CURRENT APPLICATION NUMBER: PCT/US04/14421
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469,014
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 4933
; TYPE: DNA
; ORGANISM: Mus musculus
; PCT-US04-14421-36

Query Match 26.1%; Score 493.6; DB 1; Length 4933;
Best Local Similarity 66.6%; Pred.No. 1.1e-97;
Matches 766; Conservative 0; Mismatches 354; Indels 30; Gaps 3;

Qy 71 CCGGGCGCTGGCGGACGGGCTCATCAAGTCGCTAAACCTCTGATGAAGAAGCAGCGG 130
Db CGCTGGAGGGGTCGGCGGGGCTGTCAGCCCGGAGCCGAGGAGCCGACGCGG 127

Qy 131 TGAAGCGGACCATCAACAACAACTGGCGGACCGCTACGAGTTCCTGGAGACGCTGG 190
Db 128 TGAAGCGGACATCAACCAACAACTTGAAGCATCGCTATGAGCTGCAAGAGACCCCTGG 187

Qy 191 GCAAGGGCACCTACGGGAAGGTGAAGAAGCCAGAGAGAG--CTCGGGCGCTCTGGTGG 247
Db 188 GCAAGGTACTACGGCAAGTCAAGAGAGCCACCGAGAGGTTTCAGGCCGAGTGGTTG 247

Qy 248 CCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCAGGATCTGCTGCACATACGGA 307
Db 248 CTATAAATCCATCCGTAAGGACAAATTAAGGACGAGCTAGACATGTTTCACATCAGAC 307

Qy 308 GGAGATTTGAGATCATGTCTTCTACTCAACACCCCAACATCATGTCATCATCAAGTGT 367
Db 308 GAGAGATTGAGATCATGTCTTCTACTCAACACCCCAACATCATGTCATCATCAAGTGT 367

Db 119 CCGCAAACTCTGGCAATGGATCTTTGGCAAGTGAAGATCGCGGAGCATATACAC 178
Qy 234 GGGGGTCTGGTGGCCATCAAGTCAATCAGGAAGACAAATCAAGATGAGGATCT 293
Db 179 CGGGCACAAGTTCGGATCAAGATCTCTCAACCGCAGGAAGATCAAGCCATGGAATGA 238
Qy 294 GCTGCACATACGGAGGAGATTTAGATCATGTCTTCACTCAACACCCACATCATTC 353
Db 239 AGAGAAAGTTCGAGAGAGATTAATCTGAGGTTGTTATGATCCACACATCATTAAG 298
Qy 354 CATCATGAAGTGTGAGATAGCAGCAAGATTTGATTTGATGAGTATGCCAGCG 413
Db 299 GTTGTATGAAGTGTGGAGACGAGCACAGACATTTACGTGTGATGAGTACGCAAGTC 358
Qy 414 AGGGATCTGTATGATACATCAGTACGAGCGCCACGGCTGAGTACGAGGAGCGCAGCA 473
Db 359 GGGAGAGCTCTTCGACTACATTTGTTGGAATGGTGGGCTTCAAGATCAAGCTCGACG 418
Qy 474 TTTCTTCGACAGATCGTGTCTGCCCTGCATCTACTGCCACAGAGCGGATCGTTACCG 533
Db 419 TTTCTTCGACAGATATATCAGGGTGCAGTACTGCCATAGAAACATGTTAGTTATCG 478
Qy 534 AGATCTCAAGCTGGAAACATCTCTTATAGTGCATAGCAATGGAACATCAAGATTTGCTGACTT 593
Db 479 TGATCTCAAGCGGAAATCTGCTCTCGACTCTCAATGGAACGTTAAAGATTTGGGACTT 538
Qy 594 TGGCTCTCCAACTGTACCAAGCAAGTCTCTCCAGAGTCTGTGGGAGCCCTCT 653
Db 539 TGGCTTAAAGCAACATTTAGCAGAGCGGACATTTCTTAAACATAGCTGTGGAAGTCCAAA 598
Qy 654 CTACGCTCGCTCGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTTGACAGCTG 713
Db 599 CTATGCTCTCAGAGGTTATCTCTGGCAAGCTCTATGCTGGAACAGGTTGACGTATG 658
Qy 714 GTCTCTGGGCTTCTCTGTACATCTCTGTGATGCAATGGAACATGCTTTGACGGGAGGA 773
Db 659 GAGTTGGGGCTTATTTGATGACATCTCTTTGGGAGCGCTTCAATTTGACGATGAAA 718
Qy 774 TCATAAACAATGCTGAGCAATCAAGTAAAGGAGGCTTACCGTACGCGCCCAAGC---C 830
Db 719 CATTCAAAACCTTTTCAAGAAATTAAGGAGGAGCTTACATCTACCAAGTCTATCTC 778
Qy 831 GTCCGATGCTGTGGCTGTATCCGCTGATCCGCTGCTTAAATGATGAACCCACCGCTCGGGCAC 890
Db 779 TGCCGGTGCAAAAGATTTAATCCCGGTATGCTAGTGGTTCATCCATGAACGATGAC 838
Qy 891 ACTGGAGATGTAGCCAGTCAATTTGGTGGTCAA 923
Db 839 TATAGCGAGATTCGTGAGCATCCTTGGTTCCA 871

RESULT 5

PCT-US04-14421-37

; Sequence 37, Application PC/TUS0414421

; GENERAL INFORMATION:

; APPLICANT: SUGEN, INC.

; APPLICANT: CAENEPEEL, SEAN

; APPLICANT: MANNING, GERARD

; APPLICANT: CHARYDCZAK, GLEN

; APPLICANT: GRIGORIEV, IGOR

; TITLE OF INVENTION: NOVEL KINASES

; FILE REFERENCE: 034536-1454

; CURRENT APPLICATION NUMBER: PCT/US04/14421

; PRIOR FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: 60/469,014

; NUMBER OF SEQ ID NOS: 239

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37

; LENGTH: 4094

; TYPE: DNA

; ORGANISM: Mus musculus

PCT-US04-14421-37

Query Match 10.4%; Score 197.4; DB 1; Length 4094;

Best Local Similarity 54.7%; Pred. No. 1.9e-33;

Matches 415; Conservative 0; Mismatches 341; Indels 3; Gaps 1;

Qy 168 CTAGGAGTCTCTGGAGACGCTGGCGAGGACCTACCGGAAGTGAAGAGCCACGAGA 227
Db 158 CTAGGAGATCGACCGCACCAATCGCGAAGGCAATCTTCGTGTGTCGAAGCGGCCACGCA 217
Qy 228 GAGTCGCGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATAGCA 287
Db 218 CCTCGTCACCAAGGCCAAGGTTCGCTATTAATCATAGATAAGCCAGCTGGATGAAGA 277
Qy 288 GGATCTCTGCACATACGAGGAGGATGAGATCATGTCTTCACTCAACACCCCCACAT 347
Db 278 AAACTTGAAGAAGATTTTCGGGAGGTTTCAGATAATGAAGATGCTTTGCCATCCACAT 337
Qy 348 CATTGCCATCCATCAAGTGTTCGAGATAGCAGCAAGATTTGATTTGTCTCATGGAGTATGC 407
Db 338 CATCAGACTCTACAGGTATGAGACAGAGCGCATGATTTACTGTGTGACAGATACGC 397
Qy 408 CAGCCGAGGCGATCTGTATGATTAATCATCATAGTACGCGCCACCGCTGAGTACGCGGAGC 467
Db 398 TAGCGAGGGGAGATATTTGACCACTTGGTAGCCCATGGAAGATGCGAGAGAAGGAGC 457
Qy 468 CAGGCATTTCTCGGACAGATCTGTCTGCCCTGCATCTGCGCATCCAGAACCGGATCGT 527
Db 458 TCAGCGGAAGTTCAAAACAGATCGTCAAGCGGTGTATTTTGTCTCTCGGAATATCGT 517
Qy 528 TCACCGAGATCTCAAGCTGGAAACATCTTCTTAGATGCCAATGGAACATCAAGATTGC 587
Db 518 TCATCTGATTTAAAGCCGAAACCTTACTTCTGGAGCCCATCTGAAATATCAAAATAGC 577
Qy 588 TGACTTTGGCTCTCCAACTGTACCAAGCAAGTTCCTCCAGACGTTCTGTGGGAG 647
Db 578 AGACTTTGGCTCAGCAACCTCTTCACTCCAGGGCAGCTGCTGAAGACGTTGGTGGCAG 637
Qy 648 CCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGAGTGA 707
Db 638 CCTCTCTATGCGCCCGCCAGAGCTTTCGAAGGAAGGAATATGATGGGCCCAAGTGA 697
Qy 708 CAGCTGTCTCTGGGGTCTCTCTGTACATCTCTGTGTCATGGCACCATGCTTTCACGG 767
Db 698 CATATGAGCTTGGAGTTGCTCTCTATGTGTGTGTGTGGCGCTTCCCGTTTATGG 757
Qy 768 GCAGGATCATAAACAATCTGTGGAAGCAATCAGTAAACGGGGCTTACCGTACGCGCCAA 827
Db 758 GAGCACACTGCAGATCTGCGGGCCGCGTGTGAGTGGCAAGTTCGCGATCCCGTTCTT 817
Qy 828 GCGTCCGATGCTGTG---GCTGATCGGTGGCTGTTAATGCTGAACCCACCCGCTG 884
Db 818 TATGTCCAGAGTGTGAGCACTTGATCCGCCACATGCTGTGTGTAGATCCAAATAGCG 877
Qy 885 GGCACACTGGAGATGTAGCCAGTCAATTTGGTGGGTCAA 923
Db 878 CCTCTCAATGAACACATCTGAGGACCAAGTGGATGAA 916

RESULT 6

US-10-840-512-37

; Sequence 37, Application US/10840512

; GENERAL INFORMATION:

; APPLICANT: CAENEPEEL, SEAN

; APPLICANT: MANNING, GERARD

; APPLICANT: CHARYDCZAK, GLEN

; APPLICANT: GRIGORIEV, IGOR

; TITLE OF INVENTION: NOVEL KINASES

; FILE REFERENCE: 034536-1455

; CURRENT APPLICATION NUMBER: US/10/840,512

; CURRENT FILING DATE: 2004-05-07

; PRIOR APPLICATION NUMBER: 60/469,014

; PRIOR FILING DATE: 2003-05-09

QY 731 TGTATCTCTGGTGCATGCCACCATGCTTTGAGCGGACGATCATATAACACTGGTGA 790
Db |||||
QY 834 TTTATGCTCTCTTTGTGGCACTCTCCCATTTGAGATGAGATATCCAAACCTTTTCA 893
Db |||||
QY 791 AGCAAAATCA 799
Db |||||
QY 894 AGAAATAA 902
Db |||||

RESULT 8

US-60-638-099-231
; Sequence 231, Application US/60638099
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic Phenotypes
; FILE REFERENCE: 38-21(53720)
; CURRENT APPLICATION NUMBER: US/60/638,099
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 48056
; SEQ ID NO 231
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Zea mays
US-60-638-099-231

Query Match 9.8%; Score 186; DB 9; Length 1512;
Best Local Similarity 56.5%; Pred. No. 4.6e-31;
Matches 367; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

QY 153 CAACCTGGGACCGCTACGAGTTCTTGGAGACGCTGGGCAAGGCGACCTACGGGAAGGT 212
Db |||||
QY 24 CAACCTTTGGGCGTTTACCGAATTTGCCAAACCTTAGGAATTTGGTTCGTTNAAGT 83
Db |||||
QY 213 GAAGAACGCGACGAGAGCT---CGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGA 269
Db |||||
QY 84 GAAGATCGCGAACATATATTGACTGGCCATAAGGTGGCAATCAAGATCTCTCAATCGCCG 143
Db |||||
QY 270 CAAAATCAAGATGAGCAGGATCTGTGCACATACGAGGAGAGATTCAGATCATGTCTTC 329
Db |||||
QY 144 TAAGTCAAGAGCATGGAATGGAAGAGAAAGTGAAGAGAAATCAAGATCTGAGATT 203
Db |||||
QY 330 ACTCAACACCCCAATCATTTGCCATTCATGAAGTGTGTTGAGAAATAGCAGCAAGATTGT 389
Db |||||
QY 204 ATTTATGATCTCTCATATACGCTTTATGAGGTGATAGATACACCTGCTGATATTA 263
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QY 390 GATTGTATGAGTATGCCAGCGAGGATCTGTATGATATCATAGTGAAGCGCCACG 449
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QY 264 TGTGTTATGAGTATGTTAAATCTGGAGAGTTGTTTGAATACATTTGTTGAGAGGGAAG 323
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QY 450 GCTGAGTGAGCGGACCGCAGGCAATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTG 509
Db |||||
QY 324 ACTACATGAAGAGAACCGCGCTTTTTCAGCAGATCATATCTGTTGATATTTG 383
Db |||||
QY 510 CCACAGAACGGGATCGTTTCAACGAGATCTCAAGCTGGAATAACATCTTCTAGATGCCAA 569
Db |||||
QY 384 CCATAGGAACATGTTGCTCACCGTGATTTAAAGCCAGAGAAATCTCTTTTGGATTGAA 443
Db |||||
QY 570 TGGAAACATCAAGATTGCTGACTTTGGCTCTCAACCTGTACCAACAAGCAAGTTCTCT 629
Db |||||
QY 444 ATGCAACATTAAGATTTGCTGATTTTGGCTTAAGTAATGTTATGCGTGTGATGCTCACTTCT 503
Db |||||
QY 630 CCAGACCTTTCTGTTGGAGCCCTCTCTACGCTCGCCCTGAGATAGTCAACGGGAAGCCCTA 689
Db |||||
QY 504 TAAGACGAGTTGTTGTTAGCCCGAATTTATGAGCAGCTGAGGTCTATCTGTTAACTATA 563
Db |||||
QY 690 TGTGGGCGCCAGAGTGGACAGCTGGTCTCTGGGGTTCCTCTGTACATCTCTGTGCAATGG 749
Db |||||
QY 564 TGTGTTCTCTGAAGTTGATGTTGGAGCTGGGCGTTATTTCTTATGCTCTCTCTTTTGGG 623
Db |||||
QY 750 CACCATGCCCTTTGACGGGAGGATCATAAACACTGGTGAAGCAATCA 799
Db |||||
QY 624 CACTCTCCATTTGACGATGAGAAATTTCTAAACCTTTTAAAGAAATAA 673
Db |||||

RESULT 9

US-60-638-099-214
; Sequence 214, Application US/60638099
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic Phenotypes
; FILE REFERENCE: 38-21(53720)
; CURRENT APPLICATION NUMBER: US/60/638,099
; CURRENT FILING DATE: 2004-12-21
; NUMBER OF SEQ ID NOS: 48056
; SEQ ID NO 214
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Oryza sativa
US-60-638-099-214

Query Match 9.5%; Score 180.2; DB 9; Length 1518;
Best Local Similarity 55.9%; Pred. No. 8.4e-30;
Matches 363; Conservative 0; Mismatches 283; Indels 3; Gaps 1;

QY 154 AACCTGGGACCGCTACGAGTTCTTGGAGACGCTGGGCAAGGCGACCTACGGGAAGGTG 213
Db |||||
QY 25 AACCTCTTTGGCGTTTACCGGATTTGCCAAACCTTAGGATTGGGTCAATTTGGCAAGTG 84
Db |||||
QY 214 AAGAACGCGACGAGAGAGCT---CGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGAC 270
Db |||||
QY 85 AAGATCGCGGAGCATATATTGACTGGTCAAGGTGGCAATCAAGATCTCTCAATCCCGT 144
Db |||||
QY 271 AAAATCAAGATGAGCAGGATCTGTGCACATACGAGGAGAGATTCAGATCATGTCTTCA 330
Db |||||
QY 145 AAGATCAAGAGCATGAGATGGAAGAGAAAGTTAAAGAGAAATCAAGATCTAGATT 204
Db |||||
QY 331 CTCAACACCCCAATCATTTGCCATTCATGAAGTGTGTTGAGAAATAGCAGCAAGATTGTG 390
Db |||||
QY 205 TTTATGACCCCAATCATTTCCCTTTATGAGTGTAGACACCCAGCTGATATTTAT 264
Db |||||
QY 391 ATTGTCTGAGTATCCGAGCGGAGTCTGTATGATTACATCAGTGAAGCGCCACGG 450
Db |||||
QY 265 GTTGTATTGAGTATGTCAAACTGGAGAGTTGTTTGAATACATCGTTGAGAGGGAAGA 324
Db |||||
QY 451 CTGAGTGAGCGGACCGCAGGCAATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGC 510
Db |||||
QY 325 CTGCAAGAGAGAGAAAGCTCGACGCTTTTCCAGCAGATCATATCTGGTGTGATATTCG 384
Db |||||
QY 511 CACAGAGAGGAGATCGTTTCAACGAGATCTCAAGCTGGAATAACATCTTCTTAGATGCCAAT 570
Db |||||
QY 385 CATAGAAACATGTTGTTGTTTCTATCGTGATCTTAAGCCAGAGAACCTTCTTTTGGACTCCAA 444
Db |||||
QY 571 GGAACATCAAGATTCGCTGACTTTGGCTCTCCAACTGTACCAACAAGCAAGTTCTTC 630
Db |||||
QY 445 TGCAATGTTAAGATTCAGACATTTGGCTTGAGTAATGTTATGCGTGTGATGCTCTTCTG 504
Db |||||
QY 631 CAGACGCTTTCTGTTGGAGCCCTCTCTACGCTCGCCCTGAGATAGTCAACGGGAAGCCCTAT 690
Db |||||
QY 505 AAGACAAGTTGTTGTTAGCCCAATTTATGAGCAGCACTGAGGTGATATCTGTTAACTATAT 564
Db |||||
QY 691 GTGGGCGCCAGAGTGGACAGCTGGTCTCTGGGGGTTCTCTGTACATCTCTGTGTCATGGC 750
Db |||||
QY 565 GCTGGGCGCTGAAGTTGATGTTGGAGTTGTTGGTGTGTTATTTCTTTATGCTCTCTTTTGGT 624
Db |||||
QY 751 ACCATGCCCTTTGACGGGAGGATCATAAACACTGGTGAAGCAATCA 799
Db |||||
QY 625 ACCCTTCCATTTGATGACGAGAAATATCCCAACCTTTTAAAGAAATAA 673
Db |||||

RESULT 10

US-10-998-525-21
; Sequence 21, Application US/10998525
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen
; APPLICANT: Heppard, Elmer
; APPLICANT: Sakai, Hajime


```
RESULT 12
US-10-995-561-361
; Sequence 361, Application US/10995561
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 2004-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 3442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-361

Query Match          9.5%; Score 179.4; DB 7; Length 3442;
Best Local Similarity 53.1%; Pred. No. 1.5e-29;
Matches 403; Conservative 1; Mismatches 352; Indels 3; Gaps 1;

QY 168 CTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACCGGAAGGTGAAGAGGCACGAGA 227
DB 813 CTACAGACTGTTGAAACAATCGCAAGGGGAATTTGCAAAAGTAAATTTGGCAGACA 872
QY 228 GAGTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCA 287
DB 873 TATCCTTTACAGGCGAGAGGTTGCAATAAAATAATTTGCAAAATCAAGTGAATCCAAC 932
QY 288 GGATCTGCTGCACATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACACAT 347
DB 933 AAGTCTCAAAAGCTCTTCAGAGAGTAAAGATTAATGAAGATTTTAATCATCCCAATAT 992
QY 348 CATTGCCATCCATGAAGTGTGTTGAGAAATAGCAGCAAGATTTGATGTGTCATGAGTATGC 407
DB 1053 AAGTGGAGGTGAAGTATTTGACTATTTGGTTGACATGCGAGGATGAAGGAAAAAGAAC 1112
QY 468 CAGCCAGCGCATCTGTATGATTACATCAGTGAAGCGGCCACGCTCAGTGAAGCGGACGC 527
DB 1113 AAGATCTAAATTTAGACAGATTGTGTCTGCAGTTCAATCTGCCATCAGAAACGGATCGT 1172
QY 528 TCACCGAGATCTCAAGCTGGAACCAATCCTCTTAGATGCAATGGAATGGAACATCAAGATTGC 587
DB 1233 AGATTTCGGTTTACGCAATGAAATTTACTGTTGGCGGTAAACTCGACACGTTTGTGGCAG 1292
QY 648 CCCTCTACGCTCGCTCCCAACTGTACCAAGCAAGTTCCTCCACAGCTTCTGTGGAG 647
DB 1293 TCCTCCATACGACGACCTGAGCTCTTCAGGGCAAGAAATATGACGGGCCAGAGTGA 1352
QY 708 CAGCTGGTCTCTGGGGCTTCTCTGTACATCTCTGTGTCATCTGGGCAATGAGCATGCGCCCA 767
DB 1353 TGTGTGGAGTCTGGGGGTCAATTTATACACACTAGTCACTGCTCACTTCCCTTGTATGG 1412
QY 768 GCAGGATCATAAACACTGTGTAAGCAATCAGTAACGGGGCTTACCGTGAGCGGCCAA 827
DB 1413 GCAAAACCTTAAGGAACCTGAGAGAGAGATTTAAGAGGGAATACAGAAATCCCTTCTA 1472
QY 828 GCCGTCCGATCGCTGTG---GCCTGATCGGTGGCTGTTAATGGTGAAACCCACCGCTCG 884
DB 1473 CATGCTACAGACTGTGAAACCTTCTCAACGCTTTCCTGGTGTAAATCCAATTAACG 1532
QY 885 GGCCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAA 923

Db 1533 CGGCACCTAGACAAATCATGAGGACAGCGTGGATCAA 1571

RESULT 13
US-10-995-561-363
; Sequence 363, Application US/10995561
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF SEQ ID NOS: 2004-11-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 363
; LENGTH: 3466
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-363

Query Match          9.5%; Score 179.4; DB 7; Length 3466;
Best Local Similarity 53.1%; Pred. No. 1.5e-29;
Matches 403; Conservative 1; Mismatches 352; Indels 3; Gaps 1;

QY 168 CTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACCGGAAGGTGAAGAGGCACGAGA 227
DB 813 CTACAGACTGTTGAAACAATCGCAAGGGGAATTTGCAAAAGTAAATTTGGCAGACA 872
QY 228 GAGTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCA 287
DB 873 TATCCTTTACAGGCGAGAGGTTGCAATAAAATAATTTGCAAAATCAAGTGAATCCAAC 932
QY 288 GGATCTGCTGCACATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACACAT 347
DB 933 AAGTCTCAAAAGCTCTTCAGAGAGTAAAGATTAATGAAGATTTTAATCATCCCAATAT 992
QY 348 CATTGCCATCCATGAAGTGTGTTGAGAAATAGCAGCAAGATTTGATGTGTCATGAGTATGC 407
DB 993 AGTGAAGTATTTGCGAGTCAATTTGAAACTGAAAAACACTTACCTAATCATGGAATATGC 1052
QY 408 CAGCCAGCGCATCTGTATGATTACATCAGTGAAGCGGCCACGCTCAGTGAAGCGGACGC 467
DB 1053 AAGTGGAGGTGAAGTATTTGACTATTTGGTTGACATGCGAGGATGAAGGAAAAAGAAC 1112
QY 468 CAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAAGCGGATCGT 527
DB 1113 AAGATCTAAATTTAGACAGATTGTGTCTGCAGTTCAATCTGCCATCAGAAACGGATCGT 1172
QY 528 TCACCGAGATCTCAAGCTGGAACCAATCCTCTTAGATGCAATGGAATGGAACATCAAGATTGC 587
DB 1173 ACATCGAGACCTCAAGGCTGAAATCTATTGTTAGATGCGGATGAACTTAATTAATAGC 1232
QY 588 TGACTTTGGCTCTCCCAACTGTACCAAGCAAGTTCCTCCACAGCTTCTGTGGAG 647
DB 1233 AGATTTCGGTTTACGCAATGAAATTTACTGTTGGCGGTAAACTCGACACGTTTGTGGCAG 1292
QY 648 CCCTCTACGCTCGCTCCCAACTGTACCAAGCAAGTTCCTCCACAGCTTCTGTGGAG 707
DB 1293 TCCTCCATACGACGACCTGAGCTCTTCAGGGCAAGAAATATGACGGGCCAGAGTGA 1352
QY 708 CAGCTGGTCTCTGGGGCTTCTCTGTACATCTCTGGTGCATGCGCACCATGCGCTTGTGACGG 767
DB 1353 TGTGTGGAGTCTGGGGGTCAATTTATACACACTAGTCACTGCTCACTTCCCTTGTATGG 1412
QY 768 GCAGGATCATAAACACTGTGTAAGCAATCAGTAACGGGGCTTACCGTGAGCGGCCAA 827
DB 1413 GCAAAACCTTAAGGAACCTGAGAGAGAGATTTAAGAGGGAATACAGAAATCCCTTCTA 1472
QY 828 GCCGTCCGATCGCTGTG---GCCTGATCGGTGGCTGTTAATGGTGAAACCCACCGCTCG 884
DB 1473 CATGCTACAGACTGTGAAACCTTCTCAACGCTTTCCTGGTGTAAATCCAATTAACG 1532
QY 885 GGCCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAA 923
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Db 1473 CATGTTACAGACTGTGAAACCTTCTCAACAGCTTCTCGTGTCTAAATCAATTAACG 1532
QY 885 GGCCACACTGGAGGATGAGCAGTCAATGTTGGTCAA 923
Db 1533 CGGCACCTTAGACCAATCATGAGGACAGGTGGATCAA 1571

RESULT 14

US-10-995-561-359
; Sequence 359, Application US/10995561
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 3487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-359

Query Match 9.5%; Score 179.4; DB 7; Length 3487;
Best Local Similarity 53.1%; Pred. No. 1.5e-29;
Matches 403; Conservative 1; Mismatches 352; Indels 3; Gaps 1;

QY 168 CTACGAGTTCCTGGAGACGCTGGCAAGCGCACCTACGGGAAGGTGAAGAGGCACGAGA 227
Db 813 CTACAGACTGTTGAAACAATCGCAAGGGGAATTTTGCACAAAGTAAATTTGCAAGACA 872
QY 228 GAGCTCGGGCGTCTGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCA 287
Db 873 TATCTTTACAGGAGAGAGTTGCAATAAATAATTTGACAAATCACTGATGAATCAAC 932
QY 288 GGATCTGCTGCACATACGGAGGAGATTGAGATCATGCTTCACTCAACCCACCCACAT 347
Db 933 AAGTCTACAAAGCTCTTCAGAGAGTAAGAATAATGAAGATTTAAATCATCCCAATAT 992
QY 348 CATGGCCATCCATGAAGTGTGGAGATAGCAGCAAGATTGTGATGTCTATGAGTATGC 407
Db 993 AGTGAAGTTATTCGAGTCAATGAACTGAAAAACACTCTACTAATCATGGAATATGC 1052
QY 408 CAGCCGAGGCGATCTGTATGATTTACATCAGTGAAGCGCCACCGCTCAGTGAAGCGGACGC 467
Db 1053 AAGTGAAGTGAAGTATTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAGAGC 1112
QY 528 TCACCGAGATCTCAAGCTGGAAACATCTCTTAGATGCCAATGGAAATCAAGATTGC 587
Db 1173 ACATCGAGACCTCAAGGCTGAAAATCTATTGTTAGATGCCGATGAACATTAATAATGC 1232
QY 588 TGACTTTGGCCTCTCCACCTGATAGTCAACCGGAAGCCCTATGTGGGCCACAGGATGGA 647
Db 1233 AGATTTGGGTTTATGCAATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAG 1292
QY 648 CCCTCTACGCTCGCTCAGATAGTCAACCGGAAGCCCTATGTGGGCCACAGGATGGA 707
Db 1293 TCCTCCATAGCAGACCTGAGCTCTTCAGGGCAGAAATATGACGGGCACAGATGGA 1352
QY 708 CAGCTGGTCTCTGGGCGTCTCTCTGTACATCTCTGGTGCATGGCACCATGCCCTTTGACGG 767
Db 1353 TGTGTGGAGTCTGGGGTCAATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGG 1412
QY 768 GCAGGATCATAAACACTGTGTGAAGCAATCAGTAACGGGGCTTACGGTAGCGGCCCAA 827
Db 1413 GCAAAACCTTAAGGAACCTGAGAGAGAGAGTATTTAAGAGGGGAAATACAGAAATCCCTTCTA 1472

QY 828 GCGTCCGATCCCTGTG---GCCTGATCCGGTGGCTGTTAATGTTGAACCCACCCGTCG 884
Db 1473 CATGTTACAGACTGTGAAACCTTCTCAACGCTTCTCGTGTCTAAATCAATTAACG 1532
QY 885 GGCCACACTGGAGGATGTAGCCAGTCAATGTTGGTCAA 923
Db 1533 CGGCACCTTAGACCAATCATGAGGACAGGTGGATCAA 1571

RESULT 15

US-10-995-561-360
; Sequence 360, Application US/10995561
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 360
; LENGTH: 3514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-360

Query Match 9.5%; Score 179.4; DB 7; Length 3514;
Best Local Similarity 53.1%; Pred. No. 1.5e-29;
Matches 403; Conservative 1; Mismatches 352; Indels 3; Gaps 1;

QY 168 CTACGAGTTCCTGGAGACGCTGGCAAGCGCACCTACGGGAAGGTGAAGAGGCACGAGA 227
Db 813 CTACAGACTGTTGAAACAATCGCAAGGGGAATTTTGCACAAAGTAAATTTGCAAGACA 872
QY 228 GAGCTCGGGCGTCTGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCA 287
Db 873 TATCTTTACAGGAGAGAGTTGCAATAAATAATTTGACAAATCACTGATGAATCAAC 932
QY 288 GGATCTGCTGCACATACGGAGGAGATTGAGATCATGCTTCACTCAACCCACCCACAT 347
Db 933 AAGTCTACAAAGCTCTTCAGAGAGTAAGAATAATGAAGATTTAAATCATCCCAATAT 992
QY 348 CATGGCCATCCATGAAGTGTGGAGATAGCAGCAAGATTGTGATGTCTATGAGTATGC 407
Db 993 AGTGAAGTTATTCGAGTCAATGAACTGAAAAACACTCTACTAATCATGGAATATGC 1052
QY 408 CAGCCGAGGCGATCTGTATGATTTACATCAGTGAAGCGCCACCGCTCAGTGAAGCGGACGC 467
Db 1053 AAGTGAAGTGAAGTATTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAGAGC 1112
QY 468 CAGGCAATTTCTCCGACAGATCGTGTCTGCTGCACTACTGCCACAGAACCGGATCGT 527
Db 1113 AAGATCTAAATTTAGACAGATTGTCTGCACTTCAATCTGCATCAGAAACCGATCGT 1172
QY 528 TCACCGAGATCTCAAGCTGGAAACATCTCTTAGATGCCAATGGAAATCAAGATTGC 587
Db 1173 ACATCGAGACCTCAAGGCTGAAAATCTATTGTTAGATGCCGATGAACATTAATAATGC 1232
QY 588 TGACTTTGGCCTCTCCACCTGATAGTCAACCGGAAGCCCTATGTGGGCCACAGGATGGA 647
Db 1233 AGATTTGGGTTTATGCAATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAG 1292
QY 648 CCCTCTACGCTCGCTCAGATAGTCAACCGGAAGCCCTATGTGGGCCACAGGATGGA 707
Db 1293 TCCTCCATAGCAGACCTGAGCTCTTCAGGGCAGAAATATGACGGGCACAGATGGA 1352
QY 708 CAGCTGGTCTCTGGGCGTCTCTCTGTACATCTCTGGTGCATGGCACCATGCCCTTTGACGG 767
Db 1353 TGTGTGGAGTCTGGGGTCAATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGG 1412
QY 768 GCAGGATCATAAACACTGTGTGAAGCAATCAGTAACGGGGCTTACGGTAGCGGCCCAA 827
Db 1353 TGTGTGGAGTCTGGGGGTCAATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGG 1412

Qy	768	GCAGGATCATAAACACTGGTGAAGCAATCAGTAACGGGGCTTACCGTGAGCGCCCAA	827
Db	1413	GCATAACCTAAAGGAACCTGAGAGAGAGAGTATTAGAGGGGAAATACAGAAATCCCTTCTA	1472
Qy	828	GCCGTCGGATGCCCTGTG---GCCTGATCCGGTGGCTTTAATGGTGAACCCACCCGTCG	884
Db	1473	CATGCTACACAGCTGTGAACCTTCTCAACGTTTCCTGGTGTAAATCCAATTAAACG	1532
Qy	885	GGCCACACTGGAGGATGTAGCCAGTCATTGGTGGTCAA	923
Db	1533	CGGCACCTCTAGAGCAAAATCATGAAGGACAGGTGGATCAA	1571

Search completed: January 25, 2005, 07:13:05
 Job time : 357.728 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 14:56:28 ; Search time 235.428 Seconds
(without alignments)
8761.524 Million cell updates/sec

Title: US-09-980-464-4

Perfect score: 2902

Sequence: 1 cactagtgtatccaagaat.....aaaaaaaaaaaaaaaaaaaaa 2902

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*
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6: /cgn2_6/prodata/1/ina/backfileseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2902	100.0	2902	4	US-10-355-975A-4	Sequence 4, Appli	
3	1372.2	47.3	2501	4	US-09-799-451-215	Sequence 215, App	
4	202.6	7.0	2175	4	US-09-984-890-1	Sequence 1, Appli	
5	202.6	7.0	2175	4	US-10-274-194-1	Sequence 1, Appli	
C	6	189.2	6.5	484	4	US-09-270-767-1257	Sequence 1257, Ap
C	7	189.2	6.5	484	4	US-09-270-767-16539	Sequence 16539, A
8	186.4	6.4	2908	4	US-09-930-181-1	Sequence 1, Appli	
9	182.4	6.3	2652	3	US-08-557-006C-39	Sequence 39, Appl	
10	182.4	6.3	2761	3	US-08-557-006C-24	Sequence 24, Appl	
11	181.2	6.2	1742	3	US-08-557-006C-38	Sequence 38, Appl	
12	179.8	6.2	2698	2	US-08-677-298-1	Sequence 1, Appli	
13	176.4	6.1	2899	4	US-09-774-528-112	Sequence 112, App	
14	174	6.0	3364	4	US-09-930-181-3	Sequence 3, Appli	
15	173	6.0	2334	4	US-10-003-690-3	Sequence 3, Appli	
16	173	6.0	2337	4	US-10-116-326-1	Sequence 1, Appli	
17	173	6.0	2980	4	US-10-003-690-1	Sequence 1, Appli	
18	172.2	5.9	1539	4	US-09-633-328B-1	Sequence 1, Appli	
19	172	5.9	3609	4	US-09-799-875-6	Sequence 6, Appli	
20	172	5.9	5983	4	US-09-799-875-4	Sequence 4, Appli	
21	171.4	5.9	1647	3	US-09-101-146-44	Sequence 44, Appl	
22	165.6	5.7	1929	3	US-09-359-161-4	Sequence 4, Appli	
23	163.6	5.6	1747	3	US-08-557-006C-44	Sequence 44, Appl	
24	160.4	5.5	1507	4	US-09-523-849-4	Sequence 4, Appli	
25	160.4	5.5	1544	4	US-09-734-673-1	Sequence 1, Appli	
26	160.4	5.5	2060	4	US-09-523-849-1	Sequence 1, Appli	
27	158	5.4	1736	3	US-08-557-006C-37	Sequence 37, Appl	

28	158	5.4	1783	3	US-08-557-006C-36	Sequence 36, Appli
29	155.6	5.4	1051	4	US-09-523-849-3	Sequence 3, Appli
30	154	5.3	2112	4	US-10-116-326-5	Sequence 5, Appli
31	149.4	5.1	1599	3	US-09-256-465-1	Sequence 1, Appli
32	149.4	5.1	1599	3	US-09-167-322-3	Sequence 3, Appli
33	149.4	5.1	1599	3	US-09-023-655-1004	Sequence 1004, Ap
34	147.8	5.1	1254	4	US-09-590-740-3	Sequence 3, Appli
35	144.4	5.0	2181	4	US-09-417-197-70	Sequence 70, Appli
36	144.4	5.0	2184	4	US-09-417-197-138	Sequence 138, App
37	144.4	5.0	2610	2	US-09-212-771-1	Sequence 1, Appli
38	144.4	5.0	2610	3	US-09-091-058-1	Sequence 1, Appli
39	144.4	5.0	2610	4	US-09-023-655-1206	Sequence 1206, Ap
40	144.4	5.0	2610	4	US-09-590-740-1	Sequence 1, Appli
41	143.6	4.9	546	4	US-09-523-849-20	Sequence 20, Appli
42	143	4.9	488	4	US-09-523-849-24	Sequence 24, Appli
43	137.6	4.7	2738	4	US-09-554-726A-9	Sequence 9, Appli
44	136.2	4.7	1480	4	US-09-016-434-1454	Sequence 1454, Ap
45	134.6	4.6	2626	4	US-09-590-740-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-579-664B-4
; Sequence 4, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-579-664B-4

Query Match		100.0%;	Score 2902;	DB 4;	Length 2902;	
Best Local Similarity		100.0%;	Pred. No. 0;			
Matches 2902;		Conservative	0;	Mismatches	0;	Indels
						Gaps
						0;
Qy	1	CAC TAGTGGATCCAAAGAAATTCGGCACGAGGCGTGTCTCGGGTGGCGGTGTGACCTCTTGAG	60			
Db	1	CAC TAGTGGATCCAAAGAAATTCGGCACGAGGCGTGTCTCGGGTGGCGGTGTGACCTCTTGAG	60			
Qy	61	CCCGCGGCTCAGCGCGCTGTCTACTGTGTCGCCAGCCCACTCCACTCCGCGGTCCCGCA	120			
Db	61	CCCGCGGCTCAGCGCGCTGTCTACTGTGTCGCCAGCCCACTCCACTCCGCGGTCCCGCA	120			
Qy	121	CCATGAGTGGTGGGCTTACTCCAGCGCGCGGCGGCTCCCTCGGCTCCGCGCTGG	180			
Db	121	CCATGAGTGGTGGGCTTACTCCAGCGCGCGGCGGCTCCCTCGGCTCCGCGCTGG	180			
Qy	181	CCTCGGAGAGCGCCCGCGCGCTGGCGGAGCGGGCTCATCAAGTCGCTTAAACCTCTGATGA	240			
Db	181	CCTCGGAGAGCGCCCGCGCGCTGGCGGAGCGGGCTCATCAAGTCGCTTAAACCTCTGATGA	240			
Qy	241	AGAAGCAGCGGTGAAGCGGCAACCATCAAAACAACTTCGCGGCAACCGCTACGAGTTCC	300			
Db	241	AGAAGCAGCGGTGAAGCGGCAACCATCAAAACAACTTCGCGGCAACCGCTACGAGTTCC	300			
Qy	301	TGGAGACGCTGGCAGGGGCACTACGGGAGGTGAAGAGGACGAGAGAGTTCGGGGC	360			
Db	301	TGGAGACGCTGGCAGGGGCACTACGGGAGGTGAAGAGGACGAGAGAGTTCGGGGC	360			

Db 1381 CTACCTCGTCAGGGAGGTACAGGAGGACCTCAGGAACCTCAGACCGGTGCTGATCTC 1440
Qy 1441 CAGGGAGCCCTGTCCTGCTGTATCCCTGCTCCCAAGAAAGGATCCTTAAAGTCTC 1500
Db 1441 CAGGGAGCCCTGTCCTGCTGTATCCCTGCTCCCAAGAAAGGATCCTTAAAGTCTC 1500
Qy 1501 GACAGCGTGAATCTGCTTACTACTCTCTCCAGAGCCAGGAGCTCTGGGGAACCTCTAG 1560
Db 1501 GACAGCGTGAATCTGCTTACTACTCTCTCCAGAGCCAGGAGCTCTGGGGAACCTCTAG 1560
Qy 1561 AGCCAGTGTATGTTTGTAGTGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTTCAG 1620
Db 1561 AGCCAGTGTATGTTTGTAGTGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTTCAG 1620
Qy 1621 GGCTCCTCTCCACCGCAAGGGCAATCTCAAACTCAATGCGAAGTCTCCCGCACAGCCT 1680
Db 1621 GGCTCCTCTCCACCGCAAGGGCAATCTCAAACTCAATGCGAAGTCTCCCGCACAGCCT 1680
Qy 1681 TAGAAGGCACCTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCCTCTCCCATCTG 1740
Db 1681 TAGAAGGCACCTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCCTCTCCCATCTG 1740
Qy 1741 CAGCCCGGCCAGCCGCTCAGGGGCTGTGAGTGAGGACAGCATCTGTCTCCGAGT 1800
Db 1741 CAGCCCGGCCAGCCGCTCAGGGGCTGTGAGTGAGGACAGCATCTGTCTCCGAGT 1800
Qy 1801 CCTTTGACCAATTTGGACTTGGCTGAACTCTTCCGAAACCCCACTGAGGGGCTGTGTGT 1860
Db 1801 CCTTTGACCAATTTGGACTTGGCTGAACTCTTCCGAAACCCCACTGAGGGGCTGTGTGT 1860
Qy 1861 CTGTGGAACACCTGAGGGGCTTGCAGCAGCTCTCCTCAGAAAGTCTGAAGCGATGGTGGC 1920
Db 1861 CTGTGGAACACCTGAGGGGCTTGCAGCAGCTCTCCTCAGAAAGTCTGAAGCGATGGTGGC 1920
Qy 1921 AGGAATCTTTGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGTGAAGTGCAGCCT 1980
Db 1921 AGGAATCTTTGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGTGAAGTGCAGCCT 1980
Qy 1981 ACAGACAAGCCCTAGGAATCTGCTCAAGCTCAGCTAGGAGGAGATGGTCCCTAGT 2040
Db 1981 ACAGACAAGCCCTAGGAATCTGCTCAAGCTCAGCTAGGAGGAGATGGTCCCTAGT 2040
Qy 2041 ATGGGTAGGCTCTGAGAGGTTTGCAGAGAACCTTGGCTGGATTCCTCCAGTGAATA 2100
Db 2041 ATGGGTAGGCTCTGAGAGGTTTGCAGAGAACCTTGGCTGGATTCCTCCAGTGAATA 2100
Qy 2101 GAGTACATCAAGGCTCTAGCTCTGACGCTGACTGAACCTGAAGATGAGAGAAATCGC 2160
Db 2101 GAGTACATCAAGGCTCTAGCTCTGACGCTGACTGAACCTGAAGATGAGAGAAATCGC 2160
Qy 2161 ATTGATGTGAAAGGAATGGAAACCTTGTGCTCCGAGTCTTATAGTGGGTGGCCCTGAA 2220
Db 2161 ATTGATGTGAAAGGAATGGAAACCTTGTGCTCCGAGTCTTATAGTGGGTGGCCCTGAA 2220
Qy 2221 GGTGCTTACCTCTTTGTGCTAGTGTGACCATGACATTTCCACCCCTGTTCTCTGG 2280
Db 2221 GGTGCTTACCTCTTTGTGCTAGTGTGACCATGACATTTCCACCCCTGTTCTCTGG 2280
Qy 2281 CTGCACTTCAATAGTCTTGTGCTTCCATCAACCCAGGCTTGAACCCCTGACTTCCT 2340
Db 2281 CTGCACTTCAATAGTCTTGTGCTTCCATCAACCCAGGCTTGAACCCCTGACTTCCT 2340
Qy 2341 GGGAGGTAATGTGTAGTGTGCTGCTTATTTAGAGGAACAGCCTCTGTTTCCATCT 2400
Db 2341 GGGAGGTAATGTGTAGTGTGCTGCTTATTTAGAGGAACAGCCTCTGTTTCCATCT 2400
Qy 2401 CTGCTGTGTGATCTCAAAAGACCTGGGAAAGACTCGGACCGCTGTTGACTTCAATCAA 2460
Db 2401 CTGCTGTGTGATCTCAAAAGACCTGGGAAAGACTCGGACCGCTGTTGACTTCAATCAA 2460
Qy 2461 GGGGACAGATGCCCCTGGACCCCATCTTATGATCTCAGAGCTTGAACCTTGAAGCTGTT 2520

Db 2461 GGGGACAGATGCCCCTGGACCCCATCTTATGATCTCAGAGCTTGAACCTTGAAGCTGTT 2520
Qy 2521 CCTAGTACCCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAATGTC 2580
Db 2521 CCTAGTACCCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAATGTC 2580
Qy 2581 TGACTTATTTATTTTGTGATTTCTCAGTCTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 2640
Db 2581 TGACTTATTTATTTTGTGATTTCTCAGTCTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 2640
Qy 2641 TTTTGTGTTTAAAGTGAATTTTCTGCTTTTCAATAATGTGAATCTGTTTCTGGGGAAC 2700
Db 2641 TTTTGTGTTTAAAGTGAATTTTCTGCTTTTCAATAATGTGAATCTGTTTCTGGGGAAC 2700
Qy 2701 TCCACTGTGCCACTGAAGTTTATGTACAGAAAGTATTTGGCAATGATGTCCCTCTATTTC 2760
Db 2701 TCCACTGTGCCACTGAAGTTTATGTACAGAAAGTATTTGGCAATGATGTCCCTCTATTTC 2760
Qy 2761 AAGGGGGTGGGGGCGTTTTTCAAAATGTATGTTGAGCACTGCTGGATTGAGTCTCCA 2820
Db 2761 AAGGGGGTGGGGGCGTTTTTCAAAATGTATGTTGAGCACTGCTGGATTGAGTCTCCA 2820
Qy 2821 GTCCCTTCACACCACCAAGGCTGGCCACCCTCCCTCATCTTCATCTGTGGCCAAAAA 2880
Db 2821 GTCCCTTCACACCACCAAGGCTGGCCACCCTCCCTCATCTTCATCTGTGGCCAAAAA 2880
Qy 2881 AAAAAAAAAAAAAAAAAAAAAA 2902
Db 2881 AAAAAAAAAAAAAAAAAAAAAA 2902

RESULT 3

US-09-799-451-215
; Sequence 215, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Aeundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aiding J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 215
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(1989)
US-09-799-451-215

Query Match 47.3%; Score 1372.2; DB 4; Length 2501;
Best Local Similarity .81.6%; Pred. No. 0;
Matches 1649; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

QY 82 CTACTGCTGCGCCGACCACTCCACTCGCGGTCCCGCACCACCATGAGTGGTGGCTTAC 141
DB 65 CTATTGATTCCTTGCCTGCGCCCTTGTCTCACTCTCTGCTCGCATGAGTGGTGGTTCG 124
QY 142 TCAGAGCCCGCAGCCAGGCTCCTTCGAGCTTCGCGCTCGGCTCGGAGAGCGCCCGCGC 201
DB 125 CGCGGCGCTCGCGCCCTCACTCCCTTCGCGCCGAGAGCTA-----GCCCGCGC 172
QY 202 TGGCGGAGCGGCTCATCAAGTCGCTAAACCTCTGATGAAGAAGCAGCGGTGAAGCGC 261
DB 173 TGGCGGAAGGCTGATCAAGTCGCGCCCAAGCCCTAATGAAGAAGCAGCGGTGAAGCGC 232
QY 262 ACCATCAAAACAAACCTTCGCGCACCGCTACGAGTTCCTTGAGACGCTGGCGAAGGGCA 321
DB 233 ACCACCAAAAGCAACCTTCGCGCACCGCTACGAGTTCCTTGAGACGCTGGCGAAGGGCA 292
QY 322 CTTACGGGAAGGTGAAGAAGCAGCAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCA 381
DB 293 CTTACGGGAAGGTGAAGAAGCAGCAGAGAGCTCGGGGCGCTGGTGGCCATCAAGTCAA 352
QY 382 TCAGGAAGCAAAATCAAAAGATGAGCAGGATCTGTGCACATACGAGGAGGATTCAGA 441
DB 353 TCGGAAGGCAAAATCAAAAGATGAGCAGGATCTGTGCACATACGAGGAGGATTCAGA 412
QY 442 TCATGCTTCACTCAACCCACCCACATCAATTCGCATCCATGAAGTGTTCGAGAATAGCA 501
DB 413 TCATGCTCACTCAACCCACCCACATCAATTCGCATCCATGAAGTGTTCGAGAATAGCA 472
QY 502 GCAAGATTGATTGTCATGAGATGATGCGAGGATGTCAGCGAGGCGATCTGTATGATTAATCAGTG 561
DB 473 GCAAGATCGTGATCGTATGAGATGATGCGAGGATGTCAGCGAGGCGACCTTTATGACTACATCAGCG 532
QY 562 AGCGGCCACGGCTGAGTGAGCGGAGCGCAGGCAATTCCTCCGACAGATCGTGTCTGCC 621
DB 533 AGCGGCAGAGCTCAGTGAGCGGAGCGGAGCTAGGCAATTCCTCCGCGAGATCGTCTCTGCC 592
QY 622 TGCACTACTGCCACCAAGCGGATCGTTCCAGCGAGATCTCAAGCTGGAAAAATCCTTC 681
DB 593 TGCACTATTGCCATCAGAACAGAGTGTTCACCGAGATCTCAAGCTGGAGAACATCTCT 652
QY 682 TAGATGCAATGGAACATCAAGATTGCTGACTTTGGCTCTCCAACTGTACACAAAG 741
DB 653 TGGATGCAATGGAATATCAAGATTGCTGACTTGGTCTCTCAACTCTACCATCAAG 712
QY 742 GCAAGTTCCTCCAGAGCTTCTGTGGAGCCCTCTACGCTCGCTGAGATAGTCAAG 801
DB 713 GCAAGTTCCTCCAGAGCTTCTGTGGAGCCCTCTATGCTCGCCAGAGATTGTCAATG 772
QY 802 GGAAGCCCTATGTGGGCCAGAGGTGACAGTGGTCTCTGGGCGTTCTCTGTATATCC 861
DB 773 GGAAGCCCTACACAGGCCAGAGGTGACAGTGGTCCCTGGGTGTCTCTCTACATCC 832
QY 862 TGTGATGTCACATGCCCTTTGACGGGAGGATCATAAACAATGTTGGAAGCAATCA 921
DB 833 TGTGATGTCACATGCCCTTTGATGGGATGATCAACATAAGATCTTAGTGAACACAGATCA 892
QY 922 GTAAACGGGCTTACCGTGAGCGGCCCAAGCGCTCCGATGCTGTGGCTGATCGGTGGC 981
DB 893 GCAACGGGCTTACCGGGAGCCCACTAAACCTCTGATGCTGTGGCTGATCGGTGGC 952
QY 982 TGTTAATGTGTAACCCCGCTCGGSCACACTTGGAGGATGTAGCCAGTCAATTTGGTGGG 1041
DB 953 TGTGATGTGTAACCCCGCGCGGCCCACTTGGAGGATGTGGCCAGTCACTTGTGGG 1012
QY 1042 TCAACTGGGTTTACCAACCGGAGTCGGGAAACAGGAAGCCCTCGGTGAGGGTGGGCACC 1101
DB 1013 TCAACTGGGCTACGCCACCGAGTGGAGAGCAGGAGGCTCCGATGAGGGTGGGCACC 1072
QY 1102 CTAGTGTGACTTTGGCCGGCTCCATGCGGAGTGGTTACGTGGCTCTCGCGGCCCC 1161
DB 1073 CTGGAGTGAATCTGCCCCGCGCTTCAATGCTGACTGGCTCCGCGGTTCCTCCCGCCCC 1132

QY 1162 TCCTGGAGAAATGAGGCAAGGTGTGACAGTCTTCTCAAGCAGCAGCTGCCGGAGGTGAA 1221
DB 1133 TCCTGGAGAAATGAGGCAAGGTGTGACAGTCTTCTCAAGCAGCAGTGCACCTTGGTGGGAA 1192
QY 1222 GCACTGTACCTGGGCTGGAGCGGCAATTTCTTTAAGAGTCCGAAAGAGAGATGACA 1281
DB 1193 GCACCACTTGGCTGGAGCGGCAATTTCTCGTCAAGAAAGTCCCGAAGAGAGATGACA 1252
QY 1282 TGGCTCAAAATCTGCAAGGTGAGCCGGCTGAGGATACCTCTTCTCGGCCCTGGCAAGAGCA 1341
DB 1253 TGGCCAGTCTCTCCACAGTGAACGGCTGATGACACTCGCCCTCGCCCTGGCAAGAGCA 1312
QY 1342 GCCTTAAGCTTCCGAAGAGCAATTTCTCAAGAAAAGTCTCTACTCTCTCGTCAAGGAGAGTAC 1401
DB 1313 ACCTAAGCTGCCAAAGGGCAATTTCTCAAGAAAGGTTGTCAGCTCTCTGCAAGAGGGTAC 1372
QY 1402 AGAGGACCTTCAGGAACCTCAGACCGGTGCTGATCTCTCAGGGCAGCTGTCCCTGCTG 1461
DB 1373 AGAGGACCTTCGGAGCTCAGCCCAATCTCTCGAGCCCGAGGCGAGGCTGCC----- 1426
QY 1462 TATCTCTGCCAAGGAAAGGCAATCTTAAAGAGTCTCGACAGCGTGAATCTGTTTACT 1521
DB 1427 ---CCCTGCTCCCAAGAGGGCAATTTCTCAAGAAAGCCCGCAGCGGAGTCTGGCTACT 1483
QY 1522 ACTCTCTCCAGACCCAGCGAGTCTGGGAACTCTTAGACGCGAGTGTGTTTGTGA 1581
DB 1484 ACTCTCTCCGAGCCAGTGAATCTGGGAGCTCTTGGAGCGAGCGAGCTGTTTGTGA 1543
QY 1582 GTGGGACCCCGTGGAGCAGAGTCTCCACAGGCTTCAGGGCTCTCTCTCACCGCAAGG 1641
DB 1544 GTGGGATCCCAAGGAGCAGAGCTCCGCAAGCTTCAGGGCTCTCTCTCATCGCAAG 1603
QY 1642 GCATCTCAAACTCAATGGCAAGTCTCCGCGACAGCTTTAGAGGCACTACCCCTAGCA 1701
DB 1604 GCATCTCAAACTCAATGGCAAGTCTCTCCAGACAGCTTTGGAGCTCGCGGCCCCACCA 1663
QY 1702 CTTTGGCTCCCTGGACCAACTGGCTCTCTCCATCTCGCAGCGCCGCGCCAGCGCCCT 1761
DB 1664 CTTTGGCTCCCTGGATGAATCTGCCCCACCTCGCCCCCTGGCCCGGCGCAGCGCCCT 1723
QY 1762 CAGGGCTGTGAGTGAGGACAGCATCTGTCTCTCGAGTCTTTGACAAATTTGACTTGC 1821
DB 1724 CAGGGCTGTGAGTGAGGACAGCATCTGTCTCTCTGAGTCTTTGACAGCTGACTTGC 1783
QY 1822 CTCAAGCTCTTCCGAAACCCCACTGAGGGCTGTGTCTGTGGCAACCTGAGGGGC 1881
DB 1784 CTCAAGCGCTCCAGAGCCCCCACTCGGGGCTGTGTCTGTGGCAACCTCAGGGGC 1843
QY 1882 TTGAGCAGCTCCCTCAGAAAG-----GTCTGAAGCGATGGTGGCAGGAATCCT 1929
DB 1844 TTGAGGAGCCCCCTCAGAGGGCCCTGGAGCTGCCTGAGCGCTGGCGCAGGATCCTT 1903
QY 1930 TGGGGATAGCTCCTTTCTTCTGACAGATGCGCAAGAGGTGACTGACGCTTACAGCAAG 1989
DB 1904 TGGGGACAGCTCCTTTCTTCTGACAGCTGCGCAGGAGGTGACAGCGACCTTACGACAG 1963
QY 1990 CCTAGATCTCTCAAGCTCAGCTGAGGAAGGAGATGGTGGCTTAGTATGGGCTAG 2049
DB 1964 CACTGAGGGTCTGCTCAAAAGCTCACCTGAGTGGAGTAGGCAATTTGCCCCAG-CCCGGTGAG 2022
QY 2050 GCTCTGAGAGGGTTTGAGAGGAACCTCGGCTCGGATTCCT 2090
DB 2023 GCTCTGAGTGCAGCTGGTTGACCCCGGAGGAGATGCTT 2063

RESULT 4

US-09-984-890-1

; Sequence 1, Application US/09984890

; Patent No. 6492156

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-890-1

Query Match 7.0%; Score 202.6; DB 4; Length 2175;
Best Local Similarity 54.9%; Pred. No. 4e-42;
Matches 422; Conservative 0; Mismatches 344; Indels 3; Gaps 1;
QY 290 CTACGAGTTCCTGGAGAGCGTGGGCAAGGCGACCTACGGAAGGTGAAGAGGCACGAGA 349
DB 156 CTACCGGCTCCTCAAGACCATTTGGCAAGGTAAATTTTGGCAAGGTGAAGTTGGCCCGACA 215
QY 350 GAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGAAAGACAAATCAAGATGAGCA 409
DB 216 CATCTGACTGGGAAAGAGTAGCTGTGAAGATCATTTGCAAGACTCAACTGAATCCTC 275
QY 410 GGATCTGTCACATACGAGGAGGATTTGAGATCATGCTTCACTCAACCAACCCACAT 469
DB 276 CAGCTCCAGAACTATTCCGGAAGTAAGAAATTAAGAGTTTGAATCATCCCAACAT 335
QY 470 CATTTGCCATCCATGAAGTGTGGAGATAGCAGCAAGATTTGTATGTCTATGGAGTATGC 529
DB 336 AGTTAAATATTATTTGAAGTATTGAGACTTGAGAAACCGCTCTACCTTGTCTATGGATGCG 395
QY 530 CAGCCGAGGAGTCTGTCGAGAGTATGAGATCATGATGAGCGCCACGCTGAGTGGGAGCG 589
DB 396 TAGTGGCGGAGAGTATTTGAATTAACCTAGTGGCTCATGGCAGGATGAAGAAAAAGGCG 455
QY 590 CAGGCATTTCTCCGACAGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
DB 456 TCAGGCCAATTTCCGCGAGGTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515
QY 650 TCACCGAGATCTCAAGCTGGAAACATCTCTTCTAGATGCAATGGAAACATCAAGATTGC 709
DB 516 CCATAGAGACTTAAAGGCGAAGAAACCTGCTCTTGGATGCTGATGAAATCAAGATTGC 575
QY 710 TGACTTTGGCTTCCAGCTGGAACATCTCTTCTAGATGCAATGGAAACATCAAGATTGC 769
DB 576 AGACTTTGGCTTCCAGCTGGAACATCTCTTCTAGATGCAATGGAAACATCAAGATTGC 635
QY 770 CCCTCTCTACGCTTCGCTCAGATAGTCAACGGGAGCCCTATGTTGGGCCAGAGGTGGA 829
DB 636 TCCCTCTTATGCTGCTCCAGAACTCTTCCAGGGCAAAATATGATGGACCCGAGGTGGA 695
QY 830 CAGCTGGTCTCTGGGCGTCTCTCTGTACATCTCTGTGTCATGGCAACCATGCTTGAACGG 889
DB 696 TGTGTGGAGCTAGGAGTATCTCTATACACTGGTCAGCGGATCCCTGCTTTGATGG 755
QY 890 GCAGGATCAAAACACTGTGTGAGCAATCAGTAAAGGAGTACCGTGGAGCCGCGCA 949
DB 756 ACAGAACCTCAAGAGCTGCGGAAACGGGTACTGAGGGGAAATATCCGTATTCATCTTA 815
QY 950 GCCGTCCGATGCTGTG---GCCTGATCCGGTGGCTTAAATGGTGAACCCCGCTCG 1006
DB 816 CATGTCCAGGACTGTGAAACCTGCTTAAGAAATTTCTCATTTCTTAATCCGAGCAAG 875
QY 1007 GGCCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAACTGGGGTTAC 1055
DB 876 AGGCACTTTAGACAAATCATGAAGATCGATGGATGAATGTGGGTAC 924

RESULT 5

US-10-274-194-1

; Sequence 1, Application US/10274194

; Patent No. 6706511

; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-274-194-1

Query Match 7.0%; Score 202.6; DB 4; Length 2175;
Best Local Similarity 54.9%; Pred. No. 4e-42;
Matches 422; Conservative 0; Mismatches 344; Indels 3; Gaps 1;
QY 290 CTACGAGTTCCTGGAGAGCGTGGGCAAGGCGACCTACGGAAGGTGAAGAGGCACGAGA 349
DB 156 CTACCGGCTCCTCAAGACCATTTGGCAAGGTAAATTTTGGCAAGGTGAAGTTGGCCCGACA 215
QY 350 GAGCTCGGGCGTCTGGTGGCCATCAAGTCCATCAGAAAGACAAATCAAGATGAGCA 409
DB 216 CATCTGACTGGGAAAGAGTAGCTGTGAAGATCATTTGCAAGACTCAACTGAATCCTC 275
QY 410 GGATCTGTCACATACGAGGAGGATTTGAGATCATGCTTCACTCAACCAACCCACAT 469
DB 276 CAGCTCCAGAACTATTCCGGAAGTAAGAAATTAAGAGTTTGAATCATCCCAACAT 335
QY 470 CATTTGCCATCCATGAAGTGTGGAGATAGCAGCAAGATTTGTATGTCTATGGAGTATGC 529
DB 336 AGTTAAATATTATTTGAAGTATTGAGACTTGAGAAACCGCTCTACCTTGTCTATGGATGCG 395
QY 530 CAGCCGAGGAGTCTGTCGAGAGTATGAGATCATGATGAGCGCCACGCTGAGTGGGAGCG 589
DB 396 TAGTGGCGGAGAGTATTTGAATTAACCTAGTGGCTCATGGCAGGATGAAGAAAAAGGCG 455
QY 590 CAGGCATTTCTCCGACAGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
DB 456 TCAGGCCAATTTCCGCGAGGTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515
QY 650 TCACCGAGATCTCAAGCTGGAAACATCTCTTCTAGATGCAATGGAAACATCAAGATTGC 709
DB 516 CCATAGAGACTTAAAGGCGAAGAAACCTGCTCTTGGATGCTGATGAAATCAAGATTGC 575
QY 710 TGACTTTGGCTTCCAGCTGGAACATCTCTTCTAGATGCAATGGAAACATCAAGATTGC 769
DB 576 AGACTTTGGCTTCCAGCTGGAACATCTCTTCTAGATGCAATGGAAACATCAAGATTGC 635
QY 770 CCCTCTCTACGCTTCGCTCAGATAGTCAACGGGAGCCCTATGTTGGGCCAGAGGTGGA 829
DB 636 TCCCTCTTATGCTGCTCCAGAACTCTTCCAGGGCAAAATATGATGGACCCGAGGTGGA 695
QY 830 CAGCTGGTCTCTGGGCGTCTCTCTGTACATCTCTGTGTCATGGCAACCATGCTTGAACGG 889
DB 696 TGTGTGGAGCTAGGAGTATCTCTATACACTGGTCAGCGGATCCCTGCTTTGATGG 755
QY 890 GCAGGATCAAAACACTGTGTGAGCAATCAGTAAAGGAGTACCGTGGAGCCGCGCA 949
DB 756 ACAGAACCTCAAGAGCTGCGGAAACGGGTACTGAGGGGAAATATCCGTATTCATCTTA 815
QY 950 GCCGTCCGATGCTGTG---GCCTGATCCGGTGGCTTAAATGGTGAACCCCGCTCG 1006
DB 816 CATGTCCAGGACTGTGAAACCTGCTTAAGAAATTTCTCATTTCTTAATCCGAGCAAG 875
QY 1007 GGCCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAACTGGGGTTAC 1055
DB 876 AGGCACTTTAGACAAATCATGAAGATCGATGGATGAATGTGGGTAC 924

RESULT 6

US-09-270-767-1257/c
; Sequence 1257, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1257
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-1257

Query Match 6.5%; Score 189.2; DB 4; Length 484;
Best Local Similarity 64.3%; Pred. No. 5.2e-39;
Matches 284; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY	355	CGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGCAAAATCAAGATGAGCAGGATC	414
DB	442	CGGGCAGGAGTGGCTATCAAAACCATCAAGAAAGTCAAGATCGAGGCGCGGATT	383
QY	415	TGCTGCACATACGAGGAGATTGAGATCATGTCTTCACTCAACCCACCCACATCATTTG	474
DB	382	TGTTGGCATCCGTGGGAGTGCAGATTATGAGTCAATGTCATGTCATCCAAATATCC	323
QY	475	CCATCATGAAGTGTGGAATAGCAGCAAGATTGTGATTGTTCATGAGTATGCCAGCC	534
DB	322	ACATCTACGAAGTATTGAGAATCGTGAGAAATGGTGTAGTCATGGAATTTGCCCGTG	263
QY	535	GAGCGATCTGTATGATTACATCAGTGAGCGGCACGGCTGAGTGAGCGGAGCCAGGC	594
DB	262	CGGGCAGCTCTACGACTATCTCTGTAAGGAAGGTTCTCCAGGAGGAGCGAGAC	203
QY	595	ATTCTTCCGACAGATCGTCTGCCCTGCCTGCTACTGTCACCAAGACGGATGTTCCACC	654
DB	202	GCATCTTCCGCCAGGTGGCCCGCTTACTACTGTCAAGCAACAAGATCTGCCATC	143
QY	655	GAGATCTCAAGCTGGAAAACATCTTCTAGATGCCAATGGAACATCAAGATTGCTGACT	714
DB	142	GCATCTCAAGCTGGAGACATCTCTGTCGACGAGGAGGCAATGCTAAGATTGCTGATT	83
QY	715	TTGGCTCTCCAACTGTATACCAAAAGGCAAGTTCTTCCAGAGCTTCTGTGGGAGCCCTC	774
DB	82	TTGGGTTGTGAATGTGTTTGTATGACCGACGCTGCTGGGCACCTTTTGGGGTTCCCCAC	23
QY	775	TCTACGCTCGCTGAGATAGT	796
DB	22	TCTATGCTCGCCGGAATTTGT	1

RESULT 7

US-09-270-767-16539/c
; Sequence 16539, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16539
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-16539

Query Match 6.4%; Score 186.4; DB 4; Length 2908;
Best Local Similarity 53.5%; Pred. No. 7.2e-38;
Matches 413; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY	288	CGCTACGAGTCTCTGGAGACGCTGGGCAAGGCGCACCTACGGGAAGGTGAAGAGGCACGA	347
DB	157	CCCTACCGGTGGAGAAGACGCTGGGCAAGGCGCACAGGTCTGGTGAAGCTGGGGGTT	216
QY	348	GAGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGACAAAATCAAGATGAG	407
DB	217	CACTGGTCACTCGCCAGAGGTGGCCATCAAGATGTCACCGTGAGAGCTCAGCGAG	276
QY	408	CAGGATCTGTGCACATACGAGGAGATTGAGATCATGTCTTCACTCAACACCCCCAC	467
DB	277	TCGGTCTGATGAAGGTGGAGCGGAGATCGCGATCTCTGAAGCTCATTTGAGCAGCCCCAC	336

Query Match

6.5%; Score 189.2; DB 4; Length 484;
Best Local Similarity 64.3%; Pred. No. 5.2e-39;
Matches 284; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY	355	CGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGCAAAATCAAGATGAGCAGGATC	414
DB	442	CGGGCAGGAGTGGCTATCAAAACCATCAAGAAAGTCAAGATCGAGGCGCGGATT	383
QY	415	TGCTGCACATACGAGGAGATTGAGATCATGTCTTCACTCAACCCACCCACATCATTTG	474
DB	382	TGTTGGCATCCGTGGGAGTGCAGATTATGAGTCAATGTCATGTCATCCAAATATCC	323
QY	475	CCATCATGAAGTGTGGAATAGCAGCAAGATTGTGATTGTTCATGAGTATGCCAGCC	534
DB	322	ACATCTACGAAGTATTGAGAATCGTGAGAAATGGTGTAGTCATGGAATTTGCCCGTG	263
QY	535	GAGCGATCTGTATGATTACATCAGTGAGCGGCACGGCTGAGTGAGCGGAGCCAGGC	594
DB	262	CGGGCAGCTCTACGACTATCTCTGTAAGGAAGGTTCTCCAGGAGGAGCGAGAC	203
QY	595	ATTCTTCCGACAGATCGTCTGCCCTGCCTGCTACTGTCACCAAGACGGATGTTCCACC	654
DB	202	GCATCTTCCGCCAGGTGGCCCGCTTACTACTGTCAAGCAACAAGATCTGCCATC	143
QY	655	GAGATCTCAAGCTGGAAAACATCTTCTAGATGCCAATGGAACATCAAGATTGCTGACT	714
DB	142	GCATCTCAAGCTGGAGACATCTCTGTCGACGAGGAGGCAATGCTAAGATTGCTGATT	83
QY	715	TTGGCTCTCCAACTGTATACCAAAAGGCAAGTTCTTCCAGAGCTTCTGTGGGAGCCCTC	774
DB	82	TTGGGTTGTGAATGTGTTTGTATGACCGACGCTGCTGGGCACCTTTTGGGGTTCCCCAC	23
QY	775	TCTACGCTCGCTGAGATAGT	796
DB	22	TCTATGCTCGCCGGAATTTGT	1

RESULT 8

US-09-930-181-1
; Sequence 1, Application US/09930181
; Patent No. 6455292

GENERAL INFORMATION:

; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2908
; TYPE: DNA
; ORGANISM: *Homo sapiens*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(2112)
US-09-930-181-1

Query Match

6.4%; Score 186.4; DB 4; Length 2908;
Best Local Similarity 53.5%; Pred. No. 7.2e-38;
Matches 413; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY 468 ATCAATGCCATCATGAAGTGTGTAATAGCAGCAAGTGTGATGTGATGAGTAT 527
Db 337 GTCTAAAGCTGCACGACGTTTATGAAAACAAAATAATTTGTACCTGTGTGATGAGAACAC 396
QY 528 GCCAGCGGAGCGCATCTGTATGATTAATCATCAGTGAAGCGGCCACCGCTGAGTGAGCGGAC 587
Db 397 GTGTCAAGGTGGTGAAGTCTTCGACTACCTGGTGAAGAGGGGAGGCTGACGCCCTAAGGAG 456
QY 588 GCCAGGCAATTTCTTCGACAGATCGTGTCTGCCCTGCACCTACTGACCAACGAGAAACCGGATC 647
Db 457 GCTCGGAAGTCTTCGCGCAGATCATCTCTGCGCTGGACTTCTGCCACAGCCACTCCATA 516
QY 648 GTTACCGGAGATCTCAAGCTGGAAGAAACATCTCTCTAGATGCCAATGGAACATCAAGATT 707
Db 517 TGGCACAGGGATCTGAACCTGAAACCTCTCTGCGACGAGAAGAACAAACATCCGCATC 576
QY 708 GCTGACTTTGCGCTCTCCAACTGTACCAAAAGGCAAGTTCTCTCAGACGTTCTGTGGG 767
Db 577 GCAGACTTTGGCATGGGCTCCCTGCAGGTTGGCGACAGCCTGTTGGACAGCTGTGGG 636
QY 768 AGCCCTCTCAAGCCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTG 827
Db 637 TCCCCCACTAGCCTGCCCGAGGTGATCCGGGGGAGAAGTATGACGGCCCGGAAGGCG 696
QY 828 GACAGCTGTCTCTGGCGCTTCTCTGTACATCTCTGTGTCATGGCACCATTGCCCTTTGAC 887
Db 697 GAGCTGTGAGCTGCGCGCTCATCTCTTCCCTTGTCTGTGGGGGCTCTGCGCTTCGAC 756
QY 888 GGGCAGGATCATAAACACTGGTGAAGCAAAATCAGTAAACGGGGTTACCGTGAAGCGGCC 947
Db 757 GATGACAACTTGGACAGCTGCTGGAGAAGGTGAAGCGGGGCTGTTCCACATGCCGCAC 816
QY 948 ---AAGCCGCTCGATGCTGTGGCCTGATCCGCTGTGCTGTAATGTGAACCCACCCGT 1004
Db 817 TTTATCCCGCGACTGCCAGAGTCTGCTACGGGGCATGATCGAGGTGGAACGCGCACGC 876
QY 1005 CGGCGCACACTGGAGGATGACGAGTCAATGTGGGTCACTGGGGTTACA 1056
Db 877 CGCCTCAGCTAGAGCACATTCAGAAAACACATATGGTATATAGGGGGCAAGA 928

RESULT 9

US-08-557-006C-39
; Sequence 39, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forster, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIORITY APPLICATION NUMBER: PCT/GB94/01093
; PRIORITY FILING DATE: 1994-05-20
; PRIORITY APPLICATION NUMBER: GB 9310489.1
; PRIORITY FILING DATE: 1993-05-21
; PRIORITY APPLICATION NUMBER: GB 9318010.7
; PRIORITY FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 2652
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1) .. (1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-39

Query Match 6.3%; Score 182.4; DB 3; Length 2652;
Best Local Similarity 53.0%; Pred. No. 7.4e-37;
Matches 437; Conservative 0; Mismatches 381; Indels 6; Gaps 2;
QY 242 GAAGCAGGCGGTGAAGCGGCACCATCAAAAACAAACCTGCGGCACCGCTACGAGTTCT 301
Db 4 GAACATGGCTGAGAGAGCAGAGCAGCGGGCGTGTGAAGATCGGACACTACGTGCTGGG 63
QY 302 GGAGACGCTGGGCAAGGGCACTTACGGGAAGGTGAAGAGGACGAGAGAGTCG---GG 358
Db 64 GGACACCCCTGGGCGTCGGCACCTTCGGCAAGTGAAGATTGGAGAACAATCAATTGACAGG 123
QY 359 GGGTCTGTGGCCATCAAGTCCATCAGGAACACAAAAATCAAAAGATGACGAGATCTGCT 418
Db 124 CCATTAAGTGGCAGTTAAGATCTTAATAGACAGAAGATTCGAGTTTAGATGTTGTTGG 183
QY 419 GCACATACGAGGAGATTGAGATCATGTCTTCACTCAACCAACCCCAACATCATTTGCCAT 478
Db 184 AAAAATAAAACAGAAAAATTTCAAAATCTTAAACTCTTCGTCATCTCTCATATTATCAAACT 243
QY 479 CCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATTGTTCATGGAGTATGCCAGCGGAG 538
Db 244 CTACCAAGTGTACGACACTCCAAACAGACTTTTATGGAATGGAATATGTGTGGAGG, 303
QY 539 CGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAGCGGAGCGCCAGGCAATTT 598
Db 304 TGATTTGTCGACTACATCTGTAAACACGGGAGGTTGAAGAGGTGGAAGCTCGCCGGCT 363
QY 599 CTTCCGACAGATCGTGTGCTGCTGACATCTAGTCCCAACAGAAACGGGATCGTTTACCCGAG 558
Db 364 CTTCCAGCAGATTCGTCTGCGCTGACTACTGTACAGGACATGTTGTTGCCACAGGGA 423
QY 659 TCTCAAGCTGGAAGAACATCTTCTAGTCCCAATGGAACATCAAGATTGCTGACTTTGG 718
Db 424 CTTGAAGCCAGAGAACGTTGCTGAGCACCAGATGAATGCTAAGATAGCTGACTTTCGG 483
QY 719 CTTCTCAACCTGTACCAAAAGGCAAGTTCTCTCCAGACGTTCTGTGGGAGCGCTCTCTA 778
Db 484 ACTCTCTAATATGATGTGAGTGGTGAATTTCTACGAATAGCTGTGGATCGCAAAATTA 543
QY 779 CGCCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTGAGAGCTGGTC 838
Db 544 TGCAGCACCGGAGGTCACTCAGGAAGGCTGTATGCGGGTCTCTGAGGTTGATATCTGGAG 603
QY 839 TCTGGGGGTTCTCTGTACATCTGTGTCATGSCACCATGCCCTTTTGAACGGGAGGATCA 898
Db 604 CTGTGGTGTATCTCTGTATGCCCTTCTGTGGCACCCCTCCCTTTCGACGATGAGCACGT 663
QY 899 TAAACACACTGGTGAAGCAAAATCAGTAACCGGGGCTTACCGTGAAGCCGCCAACCGTCCGA 958
Db 664 GCCTACGCTCTTTAAGAGATCCGAGGGGTGTGTTCTACATCCCGAGTATCTCAACCG 723
QY 959 TGCTGTGGC---CTGATCCGGTGGCTGTGTAATGTGGGAACCCCAACCCGCTGGCCACAT 1015
Db 724 TTCTATTGCCACTCTCTGTATGCACATGCTGCAAGTGGAGCCCTTGAAGCGAGCAACTAT 783
QY 1016 GGAGGATGAGCCAGTCAATGTGGGTCAACTGGGGTTACACCA 1059
Db 784 CAAAGACATACGAGAGCATGAATGGTTTAAACAGGATTTGCCCA 827

RESULT 10

US-08-557-006C-24
; Sequence 24, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forster, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C

Db 543 ACCGGAGGTCTCTCAGGAAGGCTGTATCGGGTCTCTGAGTGTATCTGGAGCTGTGG 602
QY 845 CGTTCCTCTACATCTCTGTGTGATGCGACCATGCCCTTTGACGGGAGGATCATATAAC 904
Db 603 TGTATCTCTGTATGCCCTTCTCTGTGGCACCCCTCCCGTTGACGATGAGCACGTCGCTAC 662
QY 905 ACTGGTGAAGCAATCAGTAAGCGGGCTTACCGGTGAGCGCCGCCAAGCGTCCGATGCGTG 964
Db 663 GCTCTTTAAGAGATCCGAGGGGTGTGTTCTATCATCCGGAGTATCTCAACGGTTCAT 722
QY 965 TGSC---CTGATCCGGTGGCTGTAAATGSGTGAACCCACCCCGTGGGCCACACTGGAGGA 1021
Db 723 TGCACACTCTGCTGATGCACATGCTGCAGGTGGACCCCTTGAAGCGAGCACTATCAAGA 782
QY 1022 TGTAGCCAGTCANTGTGGGTCAACTGGGGTTACACCA 1059
Db 783 CATACGAGCATGAATGGTGTAAACAGGATTTGCCCA 820

RESULT 12

US-08-677-298-1

; Sequence 1, Application US/08677298

; Patent No. 5863729

; GENERAL INFORMATION:

; APPLICANT: Pivnicka-Worms, Helen

; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1

; TITLE OF INVENTION: KINASE

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle, Suite 201

; CITY: Boulder

; STATE: CO

; COUNTRY: USA

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 09-JUL-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Caruthers, Jennie M.

; REGISTRATION NUMBER: 34,464

; REFERENCE/DOCKET NUMBER: 9-96

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 499-8080

; TELEFAX: (303) 499-8089

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2698 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: not relevant

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 376..2565

US-08-677-298-1

Query Match

Best Local Similarity 6.2%; Score 179.8; DB 2; Length 2698;

Matches 404; Conservative 0; Mismatches 352; Indels 3; Gaps 1;

QY 290 CTACGAGTCTCTGAGACGCTGGCAAGGCGACCTACCGGAAGGTGAAGAGGCGACAGA 349

Db 540 CTACAGACTGTTGAAACAATCGCAAGGGGAATTTTGCAAAAGTAAATTTGGCAAGACA 599

QY 350 GAGCTCGGGGCGTCTGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCA 409
Db 600 TATCTTTAAGGAGAGAGGTTCGAATAAATAAATTAATGACAAACTCAGTTGAATCCAAC 659
QY 410 GATCTGCTGCACATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACCCACAT 469
Db 660 AAGTCTACAAAAGCTCTTCAGAGAAGTAAAGATTAATGAAGATTTTAAATCATCCCAATAT 719
QY 470 CATTCGCATCCATGAAGTGTTCAGAAATAGCAGCAAGATTGTGATTCATGAGATATGC 529
Db 720 AGTGAAGTATTTCGAAGTCAATTCGAAACTGAAAAACACTCTACCTAATCATGGAATATGC 779
QY 530 CAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACCGCTGAGTCAGCGGGACGC 589
Db 780 AAGTGGAGGTGAAGTATTTGACTATTTGGTTGCACATGGCAGGATGAAGAAAAAGAAC 839
QY 590 CAGGCATTTCTCCGACAGATCGTGTCTGCCCTGCACACTCTGCCACACAGAACGGGATCGT 649
Db 840 AAGATCTAAATTTAGACAGATTGTGTCTGCAGTTCAATCTGCCATCAGAAACGGATCGT 899
QY 650 TCACCGAGATCTCAAGCTGGAAAAACATCCTTTAGATGCCAATGGAACATCAAGATTGC 709
Db 900 ACATCGAGACCTCAAGGCTGAAAAATCTATTGTTAGATGCCGATGAACATTAATAATAGC 959
QY 710 TGACTTTGGCTCTCTCAACCTGTACCAAAAGGCAAGTTCTCCAGACGTTCTGTGGGAG 769
Db 960 AGATTTCCGTTTGTAGCAATGAATTTACTGTTGGCGGTAAACTCGACACGTTTGTGGCAG 1019
QY 770 CCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCACAGAGTGA 829
Db 1020 TCCTCCATACGACGACCTGAGCTCTTCAGGGGCAAGAAATATGACGGGCCAGAGTGA 1079
QY 830 CAGCTGCTCTCGGGGCTTCTCCTGTACATCTCTGTGTCATGCGCACCATGCCCCCTTTGACGG 889
Db 1080 TGTGTGGAGTCTGGGGTCAATTTTATACACACTAGTCAGTGGGCTCACTTCCCTTTGATGG 1139
QY 890 GCAGGATCATAAACACTGTGTGAAGCAAAATCAGTAACGGGGCTTACCGTGAGCGGCCAA 949
Db 1140 GCAAAACCTTAAGAACTGAGAGAGAGATTAAGAGGGAATACAGAATTCCTCTTA 1199
QY 950 GCGTCCGATGCTCTGTG---GCCTGATCCGGTGGCTGTTAATGGTGAACCCACCCCGTCG 1006
Db 1200 CATGCTCTACAGACTGTGAAAAACCTTCTCAACCGTTTCTGGTGTCTAAATCCAATTAACG 1259
QY 1007 GGCACACTGGAGGATGACCGAGTCAATTTGGTGGTCAA 1045
Db 1260 CGGCACTCTAGACAAATCATGAAGGACAGGTGGATCAA 1298

RESULT 13

US-09-774-528-112

; Sequence 112, Application US/09774528

; Patent No. 6743619

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhang, Jie

; APPLICANT: Zhao, Qing A.

; APPLICANT: Yang, Yonghong

; APPLICANT: Xue, Aildong J.

; APPLICANT: Wehrman, Tom

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Dunrui

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6743619el Nucleic Acids and

; FILE REFERENCES: Polypeptides

; CURRENT APPLICATION NUMBER: US/09/774,528

; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 112
; LENGTH: 2899
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)..(2899)
US-09-774-528-112

Query Match 6.1%; Score 176.4; DB 4; Length 2899;

Best Local Similarity 52.4%; Pred. No. 2.7e-35;
Matches 412; Conservative 0; Mismatches 371; Indels 3; Gaps 1;
QY 235 TGATGAGAGCAGCGGTGAAGCGGCACCTACGGAAGGTGAAGAGCGACGAGAGCT 354
DB 120 TGGTCATGGCGGATGGCCCGAGGCACTTGCAGCGCGCGCGTCCGGGTGGGGTTCTACG 179
QY 295 AGTTCTCGAGAGCGCTGGGCAAGGGCACCTACGGAAGGTGAAGAGCGACGAGAGCT 354
DB 180 ACATCGAGGCGACGCTGGGCAAGGGCACTTCGCTGTGTGAAGCTGGGCGGCGACCGGA 239
QY 355 CGGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGAACAATAAATCAAAAGATGAGCAGGATC 414
DB 240 TCACCAAGACGGAGGTGGCAATAAATAATCGATAAGTCTCAGCTGGATGCAGTGAAC 299
QY 415 TGCTGCACATACGAGGAGATGAGATCATGTCTTCACTCAACCAACCCACATCATTTG 474
DB 300 TTGAGAAATCTACCGGAGAGTACAAATAATGAATAATGTTAGACCAACCCCTCACATATCA 359
QY 475 CCATCCATGAAGTGTGGAAATAGCAGCAAGATTGTGATTGTTCATGGAGTATGCCAGCC 534
DB 360 AACTTATCAGGTAAATGAGACCAAAATGATGTGTACCTTGTGACAGAAATATGCCAAA 419
QY 535 GAGCGCATCTGTATGATTAATCAGTGAAGCGGCACCGCTGAGTGAGCGGCGACGCCAGGC 594
DB 420 ATGGAGAAATTTTGAATCTTGTCTAATCATGCGCGGTTAAATGATCTGAAGCCAGGC 479
QY 595 ATTTCTCCAGAGATCGTGTGCTGCTGCACTACTGCCACCAAGACGGGATCGTTCAAC 654
DB 480 GAAAAATCTGGCAAAATCTGCTGCTGTGTTGATTAATGTCATGCTGCGAAGATTGTGCACC 539
QY 655 GAGATCTCAAGCTGGAAGACATCTCTAGATGCAATGGAACATCAAGATTGCTGACT 714
DB 540 GTGACCTCAAGCTGAAATATCTCTGCTGGATTAACATGAATATCAAAATAGCAGATT 599
QY 715 TTGGCCTCTCAACCTGTACCAAGGCAAGTTCTCTCCAGAGCTTCTGTGGGAGCCCTC 774
DB 600 TCGGTTTTGGAAATTTCTTTAAAGTGTGAATCTGCTGGCAACATGGTGTGGCAGCCCC 659
QY 775 TCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCGAGAGGTGACAGCT 834
DB 660 CTTATGAGCCCGCAGAGTCTTTGAAGGCGCAGAGTATGAAGGACCAACAGCTGGAATCT 719
QY 835 GGTCTCTGGCGCTTCTCTGTACATCTGTGTGATGCAATGCAATGCTTTGAGCGGCGAG 894
DB 720 GGAGTATGGGAGTGTCTTTATGTCTGTGTGTGAGCTGTGCCCCCTTTGATGGACCGA 779
QY 895 ATCAAAACACCTGGTGAAGCAATACAGTAACCGGGGCTTACCGTGAAGCCGCCCAAGCCGT 954
DB 780 CTCTTCCAAATTTGAGGCGAGAGGTTCTGGAAGGAAGATTCCGGATTCCGATTTCATGT 839
QY 955 CCGATGCTGTG---GCCTGATCGGTGGCTGTGTTAATGGTGAACCCCAACCCCGTGGGCCA 1011
DB 840 CAGAAGATTGCGACACCTTATCCGAAGGATGTGTGCTCTAGACCCATCAAAACGGCTAA 899
QY 1012 CACTGG 1017
DB 900 CCATAG 905

RESULT 14

US-09-930-181-3
; Sequence 3, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3

Query Match 6.0%; Score 174; DB 4; Length 3364;

Best Local Similarity 53.4%; Pred. No. 1.2e-34;
Matches 414; Conservative 0; Mismatches 355; Indels 7; Gaps 2;
QY 288 CGCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGAAGGTGAAGAGGCAACGA 347
DB 280 CCCTACCGCTGGAGAGAGCGCTGGGCAAGGGCGACAGAGTCTGGTGAAGCTGGGGGTT 339
QY 348 GAGAGCTCGGGGCGTCTGTGGCCATCAAGTCCATCAGGAAGACAAAATCAAAAGATGAG 407
DB 340 CACTGGCTCACCTGCCAGAAAGTGGCCATCAAGATCGTCAACCGTGAAGAGCTCAGCGAG 399
QY 408 CAGGATCTCTGCACATACGAGGAGATGAGATCATGCTTCACTCAACCAACCCAC 467
DB 400 TCGGTCTGATGAAGTGGAGCGGAGATCGCATCTCTGAAGCTCATTTGAGCAACCCAC 459
QY 468 ATCATTTGCCATCCATCAAGTGTGTGAAATAGCAGCAAGATTCTGATT----GTCAATGGA 523
DB 460 GTCTAAAGCTGCACAGCTTTATGAACAAAATAATTTGTAGGTACCTGGTGTGCTAGA 519
QY 524 GTATGCCAGCCGAGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAGCG 583
DB 520 ACAGTGTGAGGTGTGAGCTCTTCGACTACCTGGTGAAGAGGGGAGGTGACGCGCTAA 579
QY 584 GGAGCGCAGCATTTCTTCGACAGATCGTGTCTGCCCTGCATCTGCTCCACCAAGACGG 643
DB 580 GGAGGCTCGGAAGTTCTTCGCGCAGATCATCTCTGCGCTGGACTTCTGCCCACAGCCACTC 639
QY 644 GATCGTTTCAACGAGATCTCAAGCTGGAATAACATCTTCTAGATGCCAATGGAATAACATCA 703
DB 640 CATATGCCACAGGATCTGAACTGAAACCTCTCTGCTGGACGAGAGAAACATATCCG 699
QY 704 GATTGTGATTTTGGCTCTCCAACTGTACCAAGCAAGTTCCTCCAGAGCTTCTG 763
DB 700 CATCGCAGACTTTGGCATGGCGTCCCTGCAAGTGTGGCAGCAGCTGTTGGAGACCACTG 759
QY 764 TGGAGCCCTCTCTAGCCCTCGCTGAGATAGTCAACGGAAGCCCTATGTGGGCCCCAGA 823
DB 760 TGGGTCCCCCACTACGCCCTGCGGAGGTGATCCGGGGGGGAAGATATGACGCGCGGAA 819
QY 824 GGTGGAGCAGCTGTCTCTGGCGCTTCTCTGTATCATCTCTGTGATGCGGACCATGCCCC 883
DB 820 GCGGAGCTGTGAGCTGCGGCGCTCATCTGTTGCGCTTGTCTGTTGGGGCTCTGCGCTT 879
QY 884 TGACGGCGAGGATCATAAACACTGTGTGAAGCAAAATCAGTAAACGGGGCTTACCGTGAGCC 943
DB 880 CGACGATGACAACTTGGCAGCAGCTGTGGAGAGGTGAAGCGGGGCGTGTTCACATGCC 939
QY 944 GCCC---AAGCCGTCCGATGCTGGCCCTGATCCGGTGGCTGTTAATGTGTGAACCCAC 1000
DB 940 GCACCTTTATCCCGCCGACTGCGCAGAGTCTGCTACGGGGGATGATCGAGTGGACGCCG 999

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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 20:17:54 ; Search time 1516.67 Seconds
(without alignments)
10994.228 Million cell updates/sec

Title: US-09-980-464-4
Perfect score: 2902
Sequence: 1 cactagtggatccaaagaat.....aaaaaaaaaaaaaaaaaaaaa 2902

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2902	100.0	2902	15	US-10-355-975-4
2	2863.4	98.7	3073	17	US-10-322-281-22
3	2066.8	71.2	2929	17	US-10-343-514-1
4	2022.2	69.7	2027	17	US-10-343-514-87
5	1938.8	66.8	37278	17	US-10-322-281-21
6	1771.4	47.5	2026	17	US-10-343-514-27
7	1379	47.5	3353	9	US-09-963-159-1
8	1379	47.5	3353	16	US-10-423-543-43
9	1375.8	47.4	3404	17	US-10-322-281-25
10	1374.2	47.4	3443	18	US-10-370-715B-639
11	1374.2	47.4	3463	18	US-10-618-941-11
12	1372.2	47.3	2501	16	US-10-302-172-215
					Sequence 4, Appli
					Sequence 22, Appl
					Sequence 1, Appli
					Sequence 87, Appl
					Sequence 21, Appl
					Sequence 27, Appl
					Sequence 1, Appli
					Sequence 43, Appl
					Sequence 25, Appl
					Sequence 639, App
					Sequence 11, Appl
					Sequence 215, App

13	1370.6	47.2	3360	16	US-10-311-034-38	Sequence 38, Appl
14	1360.2	46.9	1884	9	US-09-963-159-3	Sequence 3, Appli
15	1360.2	46.9	1884	16	US-10-423-543-45	Sequence 45, Appl
16	1071.4	36.9	1186	17	US-10-343-514-13	Sequence 13, Appl
17	943.4	32.5	1186	17	US-10-343-514-70	Sequence 70, Appl
18	849.2	29.3	2616	17	US-10-363-829-151	Sequence 151, App
19	849.2	29.3	2619	17	US-10-363-829-250	Sequence 250, App
20	732	25.2	39699	17	US-10-322-281-24	Sequence 24, Appl
21	675.4	23.3	741	17	US-10-343-514-32	Sequence 32, Appl
22	648	22.3	707	17	US-10-343-514-91	Sequence 91, Appl
23	648	22.3	712	17	US-10-343-514-31	Sequence 31, Appl
24	644.2	22.2	661	17	US-10-343-514-93	Sequence 93, Appl
25	643	22.2	734	17	US-10-343-514-92	Sequence 92, Appl
26	583.2	20.1	588	17	US-10-343-514-97	Sequence 97, Appl
27	557.4	19.2	660	17	US-10-343-514-33	Sequence 33, Appl
28	534	18.4	578	17	US-10-343-514-95	Sequence 95, Appl
29	515	17.7	548	17	US-10-343-514-96	Sequence 96, Appl
30	513	17.7	521	17	US-10-343-514-94	Sequence 94, Appl
31	511.6	17.6	579	17	US-10-343-514-35	Sequence 35, Appl
32	507.6	17.5	6828	9	US-09-780-949-1	Sequence 1, Appli
33	507.6	17.5	6828	15	US-10-354-358-81	Sequence 81, Appl
34	507.6	17.5	6828	15	US-10-172-118-1541	Sequence 1541, Ap
35	507.6	17.5	6828	16	US-10-342-887-1541	Sequence 1541, Ap
36	507.6	17.5	6828	18	US-10-723-860-2552	Sequence 2552, Ap
37	507.6	17.5	6854	18	US-10-723-860-6703	Sequence 6703, Ap
38	506.4	17.5	1886	9	US-09-780-949-3	Sequence 3, Appli
39	506.4	17.5	2884	9	US-09-780-949-5	Sequence 5, Appli
40	493.6	17.0	585	17	US-10-343-514-37	Sequence 37, Appl
41	483.8	16.7	548	17	US-10-343-514-36	Sequence 36, Appl
42	474.6	16.4	521	17	US-10-343-514-34	Sequence 34, Appl
43	383.4	13.2	439	17	US-10-343-514-10	Sequence 10, Appl
44	381.4	13.1	436	17	US-10-343-514-14	Sequence 14, Appl
45	365.6	12.6	421	17	US-10-343-514-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-10-355-975-4
; Sequence 4, Application US/10355975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/579,664B
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-355-975-4

Query Match	100.0%	Score 2902;	DB 15;	Length 2902;
Best Local Similarity	100.0%	Pred. No. 0;		
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Db 2521 CCTAGTACCCAGATGTGGATGGATGCTCTGTTCTCAGGCAACGGGACCTAGAAATGTC 2580
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US-10-322-281-22
; Sequence 22, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945201000
; CURRENT APPLICATION NUMBER: US/10/322,281
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-281-22
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Query Match 98.7%; Score 2863.4; DB 17; Length 3073;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2864; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1052 TTACACACCGGAGTGGGGGAAACAGGAAGCCCTGCTGAGGGTGGGCAACCCCTAGTGGTGA 1111
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Db 1861 TCCTCAGAAAGTCTGAAGCGATGGTGGCAGGAATCTTGGGGATAGCTGCTTTCTCT 1920
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QY 2432 ACTCGGACCGCTGTTTGTGACTTCAATCTCAAGGGGACAGATGCCCTCGGACCCCATCTTAG 2491
Db 2401 ACTCGGACCGCTGTTTGTGACTTCAATCTCAAGGGGACAGATGCCCTCGGACCCCATCTTAG 2460
QY 2492 ATCTCAGAGACTTGAACCTTGAAGCTTCTTAGTACCCAGATGTGGATGGATGCTCTGT 2551
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QY 2552 TTCTCAGGCGCAACGGGACCTAGAAATGTGCTGACTTATTTATTTTGTGATTTCTCACTT 2611
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RESULT 3

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US-10-343-514-1
; Sequence 1, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; APPLICANT: LEFEBVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2929
; TYPE: DNA
; ORGANISM: RAT
US-10-343-514-1
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Query Match 71.2%; Score 2066.8; DB 17; Length 2929;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 2488; Conservative 0; Mismatches 277; Indels 115; Gaps 14;

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QY 109 GCGGTCCCGCGCACCATGGAGTGGTGGCTTACTTCAGCGCGCGAGCGAGCGCTCCCTCGG 168
Db 69 GCGGTCCCGCGCACCATGGAGTGGTGGCTTACTTCAGCGCGCGAGCGAGCGCTCCCTCGG 128
QY 169 CTTCCGCGCTCGGCTCGGAGAGCGCGCGCTGCGGCGGCTCATCAAGTGGCTTA 228
Db 129 CTTCCGCGCTGBCACAGAGAGCGCGCGCTGCGGCGGCTCATCAAGTGGCTTA 188
QY 229 AACCTCTGATGAAGAACGAGCGCGGTGAAGCGCACCATCAAAACAACCTCGGCGACC 288
Db 189 AACCTCTGATGAAGAACGAGCGCGGTGAAGCGCACCATCAAAACAACCTCGGCGACC 248
QY 289 GCTACAGATTTCTGGAGACGCTGGGCAAGGCGCCTACGGGAAGGTGAAGAAAGCACGAG 348
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QY 529 CCAGCGAGGCGATCTGTATGATTACATCAGTGAAGGCGCACGCTGAGTGAGCGGAGC 588
Db 489 CCAGCGAGGCGATCTGTATGATTACATCAGTGAAGGCGCACGCTGAGTGAGCGGAGC 548
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Db 1089 TGGCGGACTGTTTACGTGCTCTCTCCGCGCGCTCTCTGAGGAATGGAGCCAAAGTGTGA 1148
QY 1189 GCTTCTTCAAGCAGCAGCTGCGGAGGTGGAAGCACTGTACTTGGGCTGAGCGGCAAC 1248
Db 1149 GCTTCTTCAAGCAGCAGCTGCGGAGGTGGAAGCACTGCGGCGCTGAGCGGCAAC 1208
QY 1249 ATTCTCTTAAAGAGTCCCGAAAGAGAAATGACATGGCTCAAAATCTGCAAGGTTGACCCGG 1308
Db 1209 ATTCTCTTAAAGAGTCCCGCAGAGGAAATGACATGGCTCAGACTCTGCAAGTACCCAG 1268
QY 1309 CTGAGGATACCTTCTCGCCCTGGCAAGAGCAGCCTTAAAGCTTCGAAAGGCAATTCTCA 1368
Db 1269 TTGAAGATATCTCTCTCGCCCTGGCAAGAAACAGCCTCAAGCTTCGAAAGGTATCTCA 1328
QY 1369 AGAAAGAGTCTCTACTCTCGTCAAGGAGGTACAGGAGGACCTCTCAGGAATCTCAGACCG 1428
Db 1329 AGAAAGAGTCTCTCTCTCTCATCGGGGAGGTACAGGAGGCGCTCTCAGGAATCTCAGACCG 1388
QY 1429 TGCTGATACTCCAGGCGAGCTGTCTCTGCTGTATCCCTGCTCCCAAGGAAAGGCAATCC 1488
Db 1389 TGTCCATATACCCAGGCGAGCTGTCTCTGCTATACCCCTGCTCCCAAGGAGGCAATTC 1448
QY 1489 TTAAGAGTCTCGACAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCCGTGGAGCAGAGTCTG 1548
Db 1449 TTAAGAGTCTCGGCAAGCGTGAATCTGGTTACTACTCTCTCCAGAGCCCGTGGAGTCTG 1508
QY 1549 GGGAACTCTTAGACCGCAGTGTGTGTGAGTGGGAGCCCGTGGAGCAGAGTCTC 1608
Db 1509 GGGAACTCTTAGACCGCAGTGTGTGTGAGTGGGAGCCCGTGGAGCAGAGTCTC 1568
QY 1609 CACAGGCTTCAGGCGCTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGCAAGTTCT 1668
Db 1569 CACAGGCTTCAGGCGCTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGCAAGTTCT 1625
QY 1669 CCAGCAAGCTTTAGAGGCACTACCCCTAGCAGCTTTGGCTCCCTGGAGCAACTGGCCT 1728
Db 1626 CCAGCAAGCTTTAGAGGCACTACCCCTAGCAGCTTTGGCTCCCTAGACCAACTGGCCT 1685
QY 1729 CTTCCATCTCTGAGCGCGCGCCCGCGGCGCTCAGGGGCTGTGAGTGAGGACAGCATCC 1788
Db 1686 CTTCCATCTCTGAGCGCGCGCGCGCGGCGCTCAGGGGCTGTGAGTGAGGACAGCATCC 1745
QY 1789 TGTCTCTCCAGTCTTTGACCAATTTGAGCTTTGCTGAACTCTTCCGAAACCCCACTGA 1848
Db 1746 TGTCTCTCCAGTCTTTGACCAATTTGAGCTTTGCTGAACTCTTCCGAAACCCCACTGA 1805
QY 1849 GGGGCTGTGTCTGTGGAACAACCTGAGGGGCTTGAAGCAGCTCCCTCAGAAAGTCTGA 1908
Db 1806 GGAGCTGTGTCTGTGGAACAACCTGAGGAGGCTTGAAGCAGCTCCCTCAGAAAGGCTAA 1865
QY 1909 AGCGATGGTGGCAGGAATCTTTGGGGGATGAGTCTTTCTCTGACAGACTGCGCAAGG 1968
Db 1866 AACGATGGTGGCAGGAATCTTTGGGGGATGAGTCTTTCTCTGACAGACTGCGCAAGG 1925
QY 1969 TGACTGAGCTTACAGCAAGCCCTAGGAATCTGCTCAAAAGCTCAGCTGAGGAGGAGGA 2028
Db 1926 TGACAGAGCTTACAGCAAGCCCTAGGAATCTGCTGAAAGCTCAGCTGAGGAGGAGG 1985
QY 2029 TGGTGGCTTAGT-ATGGGGTAGGCTCTGAGAGGGTTTGCAGAGGAACCCCTGGGTGGGATT 2087
Db 1986 CAGTGGCTTAGTGGGTAGACTCTTAGAGGGGTTTGCAGAGGAACCTGGGT-AGATT 2044
QY 2088 CTTCCAGTGAATAGATACATCAAG---GGCTCTAGTCTGAGCAGCTGAGTGAACCTGA 2143
Db 2045 CCCAGGGTTGTAGATACATCAAGAACTCTCTCTCTGCTCTGAGCTGAGTGAACCTGG 2104
QY 2144 AAGTGAAGAAATCCGATTTGATGGAAGGAATGGGAACCTTGTGCTGCCAGTGTGA 2203
Db 2105 AGCTGAAGAAATAGCAGAGATATGGAAGGACTGACCTACAGAGTCTGAGTGAAGATG 2164
QY 2204 TAGTGGGGT---GGCCTGAAGGTGCTCTCTCTTTGTGCTATGAGTGTCAACCATGACA 2260

Db 2165 TGAGCGGCACAGAGACTGAAAGTGCCTACCTCTTTATGC--TGAGTGTACCCATGGCA 2222
Qy 2261 TTTCCCAACCTGTCTCTGGCTGACC-----TTCAATATAGTTTCTGTTTCCATCA 2312
Db 2223 TCTCCC--CCCTGCTCTCTGCCAGTGTACCCAGGTGTACCCATAGTTTCTGTTCCGATCG 2281
Qy 2313 ACCACAGGTTAGAACCTCTGACTTCTCTGGGAGTAAATGTAGTACTGCCATTATTTA 2372
Db 2282 ACCACAGGTTAGAACCTCTGACTTCTCTGGGAGTAAATGTAGTACTGCCATTATTTA 2341
Qy 2373 GAGAGAAACAGCCTCTGTTTCCATCTCTGCTCTCTGCTCTGCTATCTCAAGACCTGGGAAGA 2432
Db 2342 AAGAGAAACAGCCTCTGTTTCCATCTCTGCTCTCTGCTATCTCAAGACCTAGAAAGA 2401
Qy 2433 CTGGACCGCTGTTGACTTCTATCTCAAGGGACAGATGCCCTCGACCCCATCTTAGA 2492
Db 2402 CTC--AATGCTGTTTCACTTCTATCTCAAGGGAC----- 2434
Qy 2493 TCTCAGAGACTTGAACCTTGAAGCTGTTCTTAGTACCAGATGTGGATGGAT--GCTCTGT 2551
Db 2435 -CTCAGAGACTGAGCCTTGAAGCTGTTCTGTATACAGACTATGATGATATGTTCTGT 2493
Qy 2552 TTCTCAGGCCAACGGGACCTAGAAATGTCTGACTTATTTATTTTGTGATTTCTCACTT 2611
Db 2494 TTCTCAGGCCAACGGGACCTAGAAATGTCTGACTTATTTA--TTTTTGTGATTTCTCACTT 2551
Qy 2612 CTGTTTTTGGTT----- 2624
Db 2552 CTGGTTCTGTTCGTTTTTTTGTGTTGTTTTGTTGTTGTTGTTGTTGTTTCTTGTGTTTTT 2611
Qy 2625 -----TTTGTGTTGTTGTTGTTGTTTAAAGTGAATTTTGTCTGCTTTTCAATAATG 2678
Db 2612 TGTGTTGTTGTTGTTGTTGTTTAAAGTGAATTTTGTCTGCTTTGCTTTGCTTAATG 2671
Qy 2679 TGAATGCTGTGTTCTGGGAACTCCACTGTGCCACTGAAGTTTAAATGATGATGTTCTGAG 2738
Db 2672 TGAATGCTGTGTTCTGGGAAAGCCACTGTGTCATTGAAGTGTGTGTACAGAGAATATT 2731
Qy 2739 TGGCAATGATGTCCTCTATCAAGGGGGTGGGGGGTTTTTCAATGATGTTCTTTGAG 2798
Db 2732 TGGCAGTGAATCTCTTAAT-----GGGGGGTGGGCTTTTCAAGATGATGTTCTTTGAG 2783
Qy 2799 CACTGTCTGATGAGTCTCCAGTCCCTTCAAGCCCAAGGCTGGCCACCTCCCTCACT 2858
Db 2784 CACTGTCTGATGGGTCTCTCTGCTCCCTCACACCAGAGCTGTCCACCTCCCTCACT 2843

RESULT 4

US-10-343-514-87
; Sequence 87, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKEN, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCES: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 2027
; TYPE: DNA
; ORGANISM: MOUSE

US-10-343-514-87

Query Match 69.7%; Score 2022.2; DB 17; Length 2027;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2024; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 49 GTGACCTCTGAGCGCGGGCTCAGCGCGGCTGCTACTGCTCCGACCCCACTCCACCTC 108
Db 1 GTGACCTCTGAGCGCGGGCTCAGCGCGGCTGCTACTGCTCCGACCCCACTCCACCTC 60
Qy 109 GCGGTCCCCGACCATGGAGTGGTGGCTTACTCCAGCGCCCGAGCCAGGCTCCCTCGG 168
Db 61 GCGGTCCCCGACCATGGAGTGGTGGCTTACTCCAGCGCCCGAGCCAGGCTCCCTCGG 120
Qy 169 CTTCCGCTTGGCTCTGGAGAGCGCGCGCTGTGGCGGACGGGCTCATCAAGTCGCTTA 228
Db 121 CTTCCGCTTGGCTCTGGAGAGCGCGCGCTGTGGCGGACGGGCTCATCAAGTCGCTTA 180
Qy 229 AACCTCTGATGAAGAAGCAGCGGCTGAAGCGGCACCATCAACAACACACCTGGGCAAC 288
Db 181 AACCTCTGATGAAGAAGCAGCGGCTGAAGCGGCACCATCAACAACACACCTGGGCAAC 240
Qy 289 GCTACGAGTTCTCTGGAGAGCGCTGGGCAAGGGCACCTACGGAAGGTGAAGAAGCAGAG 348
Db 241 GCTACGAGTTCTCTGGAGAGCGCTGGGCAAGGGCACCTACGGAAGGTGAAGAAGCAGAG 300
Qy 349 AGAGCTCGGGCGCTCTGTGGCCATCAAGTCCATCAAGAAAGCAAAAATCAAAAGATGAGC 408
Db 301 AGAGCTCGGGCGCTCTGTGGCCATCAAGTCCATCAAGAAAGCAAAAATCAAAAGATGAGC 360
Qy 409 AGGATCTGTGCACATACGAGGGAGATTGAGATCATGTCTTCACTCAACACCCCA 468
Db 361 AGGATCTGTGCACATACGAGGGAGATTGAGATCATGTCTTCACTCAACACCCCA 420
Qy 469 TCATTGCCATCCATGAAGTGTGAGATAGCAGCAAGATTGTGATGTCATGAGATG 528
Db 421 TCATTGCCATCCATGAAGTGTGAGATAGCAGCAAGATTGTGATGTCATGAGATG 480
Qy 529 CMAGCGAGGCGATCTGTATGATTAATCAGTGAAGCGGCAACGGCTGAGTGAAGCGGAGC 588
Db 481 CMAGCGAGGCGATCTGTATGATTAATCAGTGAAGCGGCAACGGCTGAGTGAAGCGGAGC 540
Qy 589 CAGGCAATTTCTCCGACAGATCGTCTGCTCCCTGCACTACTGCCACCAAGAGCGGATCG 648
Db 541 CAGGCAATTTCTCCGACAGATCGTCTGCTCCCTGCACTACTGCCACCAAGAGCGGATCG 600
Qy 649 TTCACCGAGATCTCAAGCTGGAAAACATCTTTCTAGATGCCAATGGAAAATCAAGATTG 708
Db 601 TTCACCGAGATCTCAAGCTGGAAAACATCTTTCTAGATGCCAATGGAAAATCAAGATTG 660
Qy 709 CTGACTTTGGCTCTCAACCTGTACCAAGGCAAGTTCTCTCAGAGCTTCTGTGGGA 768
Db 661 CTGACTTTGGCTCTCAACCTGTACCAAGGCAAGTTCTCTCAGAGCTTCTGTGGGA 720
Qy 769 GCCTCTCTACGCTCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAAGAGTGG 828
Db 721 GCCTCTCTACGCTCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAAGAGTGG 780
Qy 829 ACAGTGTGCTCTGGGCGTTCTCTGTATACATCTGTGTGATGCAACCATGCTTTGACG 888
Db 781 ACAGTGTGCTCTGGGCGTTCTCTGTATACATCTGTGTGATGCAACCATGCTTTGACG 840
Qy 889 GGCAGGATCATAAACACTGGTGAAGCAATCAGTAAACGGGGCTTACCGTGAGCCGCCCA 948
Db 841 GGCAGGATCATAAACACTGGTGAAGCAATCAGTAAACGGGGCTTACCGTGAGCCGCCCA 900
Qy 949 AGCGGTCCCATGCTGTGGCCTGATCCGGTGGCTGTAAATGTGTAACCCCAACCGCTGGG 1008
Db 901 AGCGGTCCCATGCTGTGGCCTGATCCGGTGGCTGTAAATGTGTAACCCCAACCGCTGGG 960
Qy 1009 CCACACTGAGGATGTAGCCAGTCAATTGTGGGTCAACTGTGGGTTCACACCGGAGTGG 1068
Db 961 CCACACTGAGGATGTAGCCAGTCAATTGTGGGTTCACACTGGGTTCACACCGGAGTGG 1020

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QY 1069 GGGACAGAGAGCCCTGCTGAGGGTGGGACACCTAGTGTGACTTTGGCCGGGCTCTCA 1128
Db 1021 GGGACAGAGAGCCCTGCTGAGGGTGGGACACCTAGTGTGACTTTGGCCGGGCTCTCA 1080
QY 1129 TGGCGAGTCTGTTACGTGCTCTCTGGGCCCCCTCTCGGAGATGAGACCAAGGTGTGA 1188
Db 1081 TGGCGAGTCTGTTACGTGCTCTCTGGGCCCCCTCTCGGAGATGAGACCAAGGTGTGA 1140
QY 1189 GCTTCTTCAAGCAGCAGTCCGGGAGGTGGAAGCAGTGTACCTGGGCTGGAGCGGCAAC 1248
Db 1141 GCTTCTTCAAGCAGCAGTCCGGGAGGTGGAAGCAGTGTACCTGGGCTGGAGCGGCAAC 1200
QY 1249 ATTCTCTTAAGAGTCCCGAAGAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1308
Db 1201 ATTCTCTTAAGAGTCCCGAAGAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1260
QY 1309 CTGAGGATACCTCTTCTGGCCCTGGGCAAGAGAGCCTTAAAGCTTCGAAAGGCAATTCTCA 1368
Db 1261 CTGAGGATACCTCTTCTGGCCCTGGGCAAGAGAGCCTTAAAGCTTCGAAAGGCAATTCTCA 1320
QY 1369 AGAAAGATCTCTTACCTCTCAGGGAGGTACAGGAGGACCTCAGGAACCTCAGACCGG 1428
Db 1321 AGAAAGATCTCTTACCTCTCAGGGAGGTACAGGAGGACCTCAGGAACCTCAGACCGG 1380
QY 1429 TGCTTGATCTCAGGAGCAGCTGTCTCTGCTGTATCTCTGCTCCCAAGGAAAGGCAATCC 1488
Db 1381 TGCTTGATCTCAGGAGCAGCTGTCTCTGCTGTATCTCTGCTCCCAAGGAAAGGCAATCC 1440
QY 1489 TTAAGAGTCTCGACAGCGTGAATCTGGTTACTCTCTCTCAGAGCCCGAGGTCTG 1548
Db 1441 TTAAGAGTCTCGACAGCGTGAATCTGGTTACTCTCTCTCAGAGCCCGAGGTCTG 1500
QY 1549 GGGAACTCTTAGAGCGCAGTGTGTGTGAGTGGGACCCCGTGGAGCAGAGTCTC 1608
Db 1501 GGGAACTCTTAGAGCGCAGTGTGTGTGAGTGGGACCCCGTGGAGCAGAGTCTC 1560
QY 1609 CACAGGCTTCAGGGCTCTCTCTCCACCGCAAGGGCAATTCATAAATCAATGGCAAGTTCT 1668
Db 1561 CACAGGCTTCAGGGCTCTCTCTCCACCGCAAGGGCAATTCATAAATCAATGGCAAGTTCT 1620
QY 1669 CCGGCAAGCTTTAGAGGCACTACCCCTAGACCTTTGGCTCTCTGGAACAACTGGCCT 1728
Db 1621 CCGGCAAGCTTTAGAGGCACTACCCCTAGACCTTTGGCTCTCTGGAACAACTGGCCT 1680
QY 1729 CTTCCCATCTCAGCGCCGCGCAGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1788
Db 1681 CTTCCCATCTCAGCGCCGCGCAGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1740
QY 1789 TGTCTCCGAGTCTTTTGACCAATTGGACTTGGCTGAACTGTCTTCCGAAACCCCACTGA 1848
Db 1741 TGTCTCCGAGTCTTTTGACCAATTGGACTTGGCTGAACTGTCTTCCGAAACCCCACTGA 1800
QY 1849 GGGGCTGTGTGTGTGTGGAACCTGAGGGGGTTGAGAGCCTCTCAGAAAGGTCTGA 1908
Db 1801 GGGGCTGTGTGTGTGTGGAACCTGAGGGGGTTGAGAGCCTCTCAGAAAGGTCTGA 1860
QY 1909 AGCGATGGTGGCAGGAATCTTGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGG 1968
Db 1861 AGCGATGGTGGCAGGAATCTTGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGG 1920
QY 1969 TGAATGAGCTCAGACAAAGCCCTAGGAATCTGCTCAAAAGCTCAGCTGAGGAAGGAGA 2028
Db 1921 TGAATGAGCTCAGACAAAGCCCTAGGAATCTGCTCAAAAGCTCAGCTGAGGAAGGAGA 1980
QY 2029 TGGTGCCCTAGTAGGGGTAGGCTCTGAGAGGTTTGCAGAGAAAC 2075
Db 1981 TGGTGCCCTAGTAGGGGTAGGCTCTGAGAGGTTTGCAGAGAAAC 2027
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RESULT 5

US-10-322-281-21

; Sequence 21, Application US/10322281

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; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 37278
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(37278)
; OTHER INFORMATION: n = A,T,C or G
; US-10-322-281-21
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Query Match 66.8%; Score 1938.8; DB 17; Length 37278;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1940; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 955 CCATGCCCTGTGGCCTGATCCGCTGGCTGTAAATGGTGAACCCACCCGTCGGGCCACAC 1014
Db 25129 CAGATGCCCTGTGGCCTGATCCGCTGGCTGTAAATGGTGAACCCACCCGTCGGGCCACAC 25188
QY 1015 TGAGAGATGTAGCAGTCAATTGGTGGTCACTGGGGTTACACACCGGAGTGGGGAAC 1074
Db 25189 TGGAGATGTAGCAGTCAATTGGTGGTCACTGGGGTTACACACCGGAGTGGGGAAC 25248
QY 1075 AGGAACCTCTGCTGAGGGTGGGACCCCTAGTGGTGAATTTGGCCGGGCTCCATGGCGG 1134
Db 25249 AGGAACCTCTGCTGAGGGTGGGACCCCTAGTGGTGAATTTGGCCGGGCTCCATGGCGG 25308
QY 1135 ACTGTTAGTCTGCTCTCTCGCCCTCTCTGGAGAAATGGAGCAAGGTGTGACGTTCT 1194
Db 25309 ACTGTTAGTCTGCTCTCTCGCCCTCTCTGGAGAAATGGAGCAAGGTGTGACGTTCT 25368
QY 1195 TCAAGCAGACCTGTCGGGAGGTGGAGCACTGTACTTGGGCTGGAGCGGCAATTTCTC 1254
Db 25369 TCAAGCAGACCTGTCGGGAGGTGGAGCACTGTACTTGGGCTGGAGCGGCAATTTCTC 25428
QY 1255 TTAAGAAGTCCCGAAAGGAGATGACATGCTCAAAATCTGCAAGGTGACCCGGCTGAGG 1314
Db 25429 TTAAGAAGTCCCGAAAGGAGATGACATGCTCAAAATCTGCAAGGTGACCCGGCTGAGG 25488
QY 1315 ATACCTCTTCTCGCCCTGGCAAGAGCAGCTTAAAGCTTCCGAAAGGCAATTTCTCAAGAAA 1374
Db 25489 ATACCTCTTCTCGCCCTGGCAAGAGCAGCTTAAAGCTTCCGAAAGGCAATTTCTCAAGAAA 25548
QY 1375 AGTCTCTTACCTGTCAGGGAGGTACAGGAGACCTCAGGAACCTCAGACCGGTGCTG 1434
Db 25549 AGTCTCTTACCTGTCAGGGAGGTACAGGAGACCTCAGGAACCTCAGACCGGTGCTG 25608
QY 1435 ATACTCCAGGGACCTGTCCTGCTGTATCCCTGCTCCCAAGAAAGGCAATCCTTAAGA 1494
Db 25609 ATACTCCAGGGACCTGTCCTGCTGTATCCCTGCTCCCAAGAAAGGCAATCCTTAAGA 25668
QY 1495 AGTCTCGACAGCGTGAATCTGGTTACTTCTCTCCAGAGCCAGCAGTCTGGGGAAC 1554
Db 25669 AGTCTCGACAGCGTGAATCTGGTTACTTCTCTCCAGAGCCAGCAGTCTGGGGAAC 25728
QY 1555 TCTTAGACCGCAGTGTGTGTGTGAGTGGGAGCCCGCTGGAGCAGAAAGTCTTCCACAGG 1614
Db 25729 TCTTAGACCGCAGTGTGTGTGTGAGTGGGAGCCCGCTGGAGCAGAAAGTCTTCCACAGG 25788
QY 1615 CTTTACGGGCTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGAAGTCTTCCCGCA 1674
Db 25789 CTTTACGGGCTCTCTCCACCGCAAGGCAATCTCAAACTCAATGGAAGTCTTCCCGCA 25848
QY 1675 CAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTCTCTCC 1734
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Db 25849 CAGCTTAGAGGACCTACCCCTAGACCTTTGGCTCCCTGGACCACTGGCCCTCCCTCCC 25908
Qy 1735 ATCTGACGCGCCGACGCGCCCTCAGGGGCTGTGAGTGAGCAGCATCCTGTCTCT 1794
Db 25909 ATCTGACGCGCCGACGCGCCCTCAGGGGCTGTGAGTGAGCAGCATCCTGTCTCT 25968
Qy 1795 CCGAGTCTTTGACCAATTTGGACTTTGGCTGACGCTTCCGGAACCCGACTGAGGGGCT 1854
Db 25969 CCGAGTCTTTGACCAATTTGGACTTTGGCTGACGCTTCCGGAACCCGACTGAGGGGCT 26028
Qy 1855 GTGTGTCTGTGGACAACTGAGGGGGCTTGAGCAGCTCCCTCAGAAGGCTCTGAAGCGAT 1914
Db 26029 GTGTGTCTGTGGACAACTGAGGGGGCTTGAGCAGCTCCCTCAGAAGGCTCTGAAGCGAT 26088
Qy 1915 GTTGGCAGGAATCTTTGGGGATAGTCTCTTTCTTGACAGACTGCCAAGAGTGACTG 1974
Db 26089 GTTGGCAGGAATCTTTGGGGATAGTCTCTTTCTTGACAGACTGCCAAGAGTGACTG 26148
Qy 1975 CAGCTACAGACAGCCCTAGGAATCTGCTCAAGCTCAGCTGAGGAGGAGATGTGTC 2034
Db 26149 CAGCTACAGACAGCCCTAGGAATCTGCTCAAGCTCAGCTGAGGAGGAGATGTGTC 26208
Qy 2035 CTTAGTAGGAGGCTCTGAGAGGCTTTCAGAGGAACTCTGGGTGCGATTCTCTCCAG 2094
Db 26209 CTTAGTAGGAGGCTCTGAGAGGCTTTCAGAGGAACTCTGGGTGCGATTCTCTCCAG 26268
Qy 2095 TGAATAGAGTACATCAAGGGCTCTACGTCTGACGCTGACTGAACCTGAAAGATGAGAGA 2154
Db 26269 TGAATAGAGTACATCAAGGGCTCTACGTCTGACGCTGACTGAACCTGAAAGATGAGAGA 26328
Qy 2155 AATCGCATTCATGTGGAAGGAACTGGGAACCTTGTCTGCCGAGTGTTATAGTGGGGTG 2214
Db 26329 AATCGCATTCATGTGGAAGGAACTGGGAACCTTGTCTGCCGAGTGTTATAGTGGGGTG 26388
Qy 2215 CTTGAAGGCTCCTACCTCTTTGTGCCATGAGTGACCCATGACATTTCCCAACCTTGTT 2274
Db 26389 CTTGAAGGCTCCTACCTCTTTGTGCCATGAGTGACCCATGACATTTCCCAACCTTGTT 26448
Qy 2275 CTCTGGCTGACCTTACATAAGTTCTTGTTTCATCAACACACGAGGTTAGAACCTTGA 2334
Db 26449 CTCTGGCTGACCTTACATAAGTTCTTGTTTCATCAACACACGAGGTTAGAACCTTGA 26508
Qy 2335 CTTCTGGGAGGTAATGTGTAGTGACCTGCAATTTATAGAGAGGAACACGCTCTGTTT 2394
Db 26509 CTTCTGGGAGGTAATGTGTAGTGACCTGCAATTTATAGAGAGGAACACGCTCTGTTT 26568
Qy 2395 CCATCTCTGTGTGCTATCTCAAGACTGGAAGACTCGGACCGCTGTTTGACTTCA 2454
Db 26569 CCATCTCTGTGTGCTATCTCAAGACTGGAAGACTCGGACCGCTGTTTGACTTCA 26628
Qy 2455 TCTCAAGGGGACAGATGCGCCCTGGACCCCATCTTAGATCTCAGAGACTTGAACCTTGA 2514
Db 26629 TCTCAAGGGGACAGATGCGCCCTGGACCCCATCTTAGATCTCAGAGACTTGAACCTTGA 26688
Qy 2515 GCTGTCTCTAGTACCCAGATGTGGATGCTGCTGTTTCTCAGGCCAACGCGACCTAGA 2574
Db 26689 GCTGTCTCTAGTACCCAGATGTGGATGCTGCTGTTTCTCAGGCCAACGCGACCTAGA 26748
Qy 2575 ATGTGCTGACTTATTTATTTTGTGATTTCTCACTTCTGTTTTTGTGTTTTTGTGTT 2634
Db 26749 ATGTGCTGACTTATTTATTTTGTGATTTCTCACTTCTGTTTTTGTGTTTTTGTGTT 26808
Qy 2635 TGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG 2694
Db 26809 TGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTGTTTTTGTG 26868
Qy 2695 GGGAACTCCAAGTGGCACTGAAGTTTATGACAGAGAGTATTTGGCAATGATGTCCT 2754
Db 26869 GGGAACTCCAAGTGGCACTGAAGTTTATGACAGAGAGTATTTGGCAATGATGTCCT 26928
Qy 2755 CTATTCAAGGGGGTGGGGGGTTTTTCAATGTATGTCTTGAGCACTGTCTGGATTGAG 2814

Db 26929 CTATTCAAGGGGGTGGGGGGTTTTTCAATGTATGTCTTGAGCACTGTCTGGATTGAG 25988
Qy 2815 TCTCCAGTCCCTTTACACCCCAAGGCTGGCCACCCCTCCCTCATCTTCTGTCGCAAAA 2874
Db 26989 TCTCCAGTCCCTTTACACCCCAAGGCTGGCCACCCCTCCCTCATCTTCTGTCGCAAAA 27048
Qy 2875 AAAAAAAAAAAAAAAAAAAAAA 2896
Db 27049 AAAAAAAAAAAAAAAAAAAAAA 27070

RESULT 6
US-10-343-514-27
; Sequence 27, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:
; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl F.
; APPLICANT: LEPEVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 2026
; TYPE: DNA
; ORGANISM: RAT
US-10-343-514-27

Query Match 61.0%; Score 1771.4; DB 17; Length 2026;

Best Local Similarity 93.1%; Pred. No. 0;

Matches 1888; Conservative 0; Mismatches 136; Indels 5; Gaps 3;

Qy 49 GTGACCTCTGAGCCGCGGCTCAGCGCGGCTGCTACTGCTGCCGACCCACTCCACCTC 108
Db 1 GTGACCTCTGAGCCTCGGCTCTCCGCGGCTGCTGCTGCCGACCCCTCCGCTC 60
Qy 109 GCGGTCCCGCACCATGAGTCTGCTGCTTACTCCAGCGCCGCGAGCCAGGCTCCCTCGG 168
Db 61 GCGGTCCCGCACCATGAGTCTGCTGCTTACTCCAGCGCCGCGGACCTGGCTCCCTCGG 120
Qy 169 CTTCCGCTCTGCTGCTGAGAGCGCCGCGCTGCGGAGCGGCTCATCAAGTCCGCTA 228
Db 121 CTTCCGCTCTGCTGCTGAGAGCGCCGCGCTGCGGAGCGGCTCATCAAGTCCGCTA 180
Qy 229 AACCTCTGATGAAGACGAGGCGGTGAAGCGGACCATCACAACACCACTGCGGCACC 288
Db 181 AACCTCTGATGAAGACGAGGCGGTGAAGCGGACCATCACAACACCACTGAGGACCC 240
Qy 289 GCTACGAGTCTCTGAGAGCTGGGCAAGGCGACCTTACGCGGAGGCTGAAGAGGACGAG 348
Db 241 GCTACGAGTCTCTGAGAGCTGGGCAAGGCGACCTTACGCGGAGGCTGAAGAGGACGAG 300
Qy 349 AGAGTCTCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 408
Db 301 AGAGTCTCGGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 409 AGGATCTGCTGACATACGAGGAGGAGTGAAGTATCATGTCTTCACTCAACACCCCAACA 468
Db 361 AGGATCTGCTGACATACGAGGAGGAGTGAAGTATCATGTCTTCACTCAACACCCCAACA 420
Qy 469 TCATTGCCATCCATGAAGTGTGAGATGAGCAGCAAGTGTGATGTCTGAGGATGAG 528

Db 421 TCATTGCCATCCATGAAGTGTGTTGAGAAACAGCAGCAAGATTGTGATTGTATCATGAGTACG 480
Qy 529 CCAGCCGAGGCGATCTCTGTATGATTTACATCATGAGCGGCCACAGGCTCAGTGAGCGGACG 588
Db 481 CCAGCCGAGGCGATCTGTACGATTACATCATGAGCGGCCACAGGCTGAATGAGCGGACG 540
Qy 589 CCAGGCAATTTCTCCGACAGATCGTGTCTGCTCCCTGCACTACTGCGCACAGAAACGGGATCG 648
Db 541 CCAGGCAATTTCTCCGACAGATCGTGTCCGCTCCCTGCACTACTGCGCACAGAAACGGGATG 600
Qy 649 TTCAACCCAGATCTCAAGCTGGAAACATCTCTCTAGATGCCAATGGAATCATCAAGATTG 708
Db 601 TTCAACCCAGATCTCAAGCTGGAAACATCTCTCTAGATGCCAATGGAATCATCAAGATTG 660
Qy 709 CTGATTTTGGCTCTCCAACTGTACCAAGCAAGTTCCTCCAGACGTTCTGTGGGA 768
Db 661 CTGATTTTGGCTCTCCAACTGTATCAAAAGCAAGTTCCTCCAGACGTTCTGTGGGA 720
Qy 769 GCCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAAGGTGG 828
Db 721 GCCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAAGGTGG 780
Qy 829 ACAGCTGCTCTGGGCGTTCTCTGTACATCTCTGTGATGCGACCATGCCCTTTGACG 888
Db 781 ACAGCTGCTCTGGGCGTTCTCTGTACATCTCTGTGATGCGACCATGCCCTTTGACG 840
Qy 889 GGCAGGATCATAAACACTGTGTGAAGCAAACTCAGTAAACGGGCTTTACCGTGAGCGGCCCA 948
Db 841 GGCAGGATCATAAACCTGTGTGAAGCAAACTCAGTAAACGGGCTTTACCGTGAGCGGCCCA 900
Qy 949 AGCGCTCCGATGCTGTGGCTGTATCGGTGCTTTAAATGGTGAACCCCAACCGCTCGGG 1008
Db 901 AACCGTCTGATGCTGTGGCTGTATCGGTGCTTTAAATGGTGAATCCCATCCGTCGGG 960
Qy 1009 CCACACTGGAGATGTAGCAGTCAATTTGGTGGGTCACTGGGTTACACCCGAGTCG 1068
Db 961 CCACACTGGAGATGTAGCAGTCAATTTGGTGGGTCACTGGGTTACACCCGAGTCG 1020
Qy 1069 GGGAAACAGGAAGCCCTCGGTGAGGCTGGGCAACCTAGTGTGACTTTGGCGGGCCCTCCA 1128
Db 1021 GGGAAACAGGAAGCTCTGGGAGAGGCTGGGCAACCTAGTGTGACTTTGGCGGGCCCTCTA 1080
Qy 1129 TGGCGGACTGGTACGTGCTCTCGGCCCTCTCTGGAGAAATGGAGCAAGGTGTGCA 1188
Db 1081 TGGCGGACTGGTACGTGCTCTCGGCCCTCTCTGGAGAAATGGAGCAAGGTGTGTA 1140
Qy 1189 GCTTCTTCAAGCAGCAGTGTGGGAGGTGGAGCAGTGTACCTGGGCTGGAGCGGCAAC 1248
Db 1141 GCTTCTTCAAGCAGCAGTGTGGGAGGTGGAGCAGTGTACCTGGGCTGGAGCGGCAAC 1200
Qy 1249 ATTCTCTTAAGAGTCCCGAAAGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCCGG 1308
Db 1201 ATTCTCTTAAGAGTCCCGAAAGAGAAATGACATGGCTCAAGTCTGACAAATGACCCAG 1260
Qy 1309 CTGAGGATACCTTTCTCGCCCTGGCAAGCAGCCTTAAGCTTCGAAAGGCAATTCCTCA 1368
Db 1261 TTGAAGATACCTTTCTCGCCCTGGCAAGCAGCCTTAAGCTTCGAAAGGTAATCTCTCA 1320
Qy 1369 AGAAAGTCTCTACTCTCTCAGGAGAGGTACAGGAGGACCTCAGGAACTCAGACGG 1428
Db 1321 AGAAAGTCTCTACTCTCTCAGGAGAGGTACAGGAGGACCTCAGGAACTCAGACCCAG 1380
Qy 1429 TGCTGTATCTCAGGAGCAGCTGTCTCTGCTGTATCTCTCTGCTCCCAAGAAAGGCATCC 1488
Db 1381 TGCTGTATCTCAGGAGCAGCTGTCTCTGCTGTATCTCTCTGCTCCCAAGAAAGGCATTC 1440
Qy 1489 TTAAGAACTCTGCAAGCAGTGAATCTGTGTTACTACTCTCTCAGAGGCCCAAGGAGTCTG 1548
Db 1441 TTAAGAACTCTGCAAGCAGTGAATCTGTGTTACTACTCTCTCAGAGGCCCAAGGAGTCTG 1500
Qy 1549 GGGAACTCTTAGAGCCAGTGTATGTTGTAGTGGGACCCCGTGGAGCAGAACTCTC 1608
Db 1501 GGGAACTCTTAGAGCCAGTGTATGTTGTAGTGGGACCCCGTGGAGCAGAACTCTC 1560

Qy 1609 CACAGGCTTCAGGCTCTCTCTCACCGCAAGGCATTTCTCAAACTCAATGCGCAAGTTCT 1668
Db 1561 CACAAGCTTCAGG---CGCTTCATCGCAAGGCATCTCTCAAACTCAATGCGCAAGTTT 1617
Qy 1669 CCGGCAAGCTTTAGAGGCACTACCCCTAGACACCTTTTGGCTCCCTGGACCAACTGGCCT 1728
Db 1618 CCGGCAAGCTTTAGAGGCACTGCCCCCTAGACACCTTTTGGCTCCCTAGACCAACTGGCCT 1677
Qy 1729 CTTCCATCTCTGAGCGCCGCCAGCGCCCTCAGGGCTGTGAGTGAGGAGCAGCATCC 1788
Db 1678 CCGCTCATCTCTACAGCCCGGCCAGCGCTCCCTCGGAGCTGTGAGTGAGGAGCAGCATCC 1737
Qy 1789 TGTCTCTCCGAGTCTTTTGACCAATTTGCACTTTGCTCTGAACGCTTTCCCGAAACCCCACTGA 1848
Db 1738 TGTCTCTCCGAGTCTTTTGACCAATTTGCACTTTGCTCTGAACGCTTTCCCGAAACCCCACTGA 1797
Qy 1849 GGGGCTGTGTCTGTGTGCAACCTGAGGGGCTTGTGAGAGCTCTCCCTCAGAAAGGTCTGA 1908
Db 1798 GAGCTGTGTGTGTGTGCAACCTGAGGAGGCTTGTGAGAGCTCTCCCTCAGAAAGGCTAA 1857
Qy 1909 AGCGATGTGTGAGGAGGATCTTGGGGGATAGTGTCTTTCTGTGACAGACTGCCAAGG 1968
Db 1858 AACGATGTGTGAGGAGGATCTTGGGGGATAGTGTCTTTCTGTGACAGACTGCCAAGG 1917
Qy 1969 TGACTGAGCTTACAGACAAAGCCCTAGGAATCTGTCTCAAGCTCAGCTGAGGAGGAGGA 2028
Db 1918 TGACAGAGCTTACAGACAAAGCCCTAGGAATCTGTCTGAACTCAGCTGAGGAGGAGG 1977
Qy 2029 TGTGCTCCCTAGT-ATGGGTAGGCTCTGAGA-GGGTTTGCAGAGGAAC 2075
Db 1978 CAGTGGCCAGTGTATGGGTAGACTCTTAGAGGGGTTTGAGAGGAAC 2026

RESULT 7

US-09-963-159-1
; Sequence 1, Application US/09963159
; Patent No. US20020077312A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700. A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-50U1
; CURRENT APPLICATION NUMBER: US/09/963,159
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3268)
; NAME/KEY: unsure
; LOCATION: (3270)
; NAME/KEY: unsure
; LOCATION: (3272)
US-09-963-159-1

Query Match 47.5%; Score 1379; DB 9; Length 3353;
Best Local Similarity 81.8%; Pred. No. 0;
Matches 1654; Conservative 0; Mismatches 335; Indels 34; Gaps 4;
Qy 92 CTACTGCTGCCCCGACCCACTCCACCTCGGGGTCCCGCACCATGAGTGGTGGCTTAC 141
Db 116 CTACTGATTTCCCTGCGGCCCTTGTCTACCTCTGCTCGCATGAGTGTGTTTCG 175
Qy 142 TCAGGCGCGGAGCGAGGCTCCCTCGGCTTCGCGCTCGGAGAGGCGCGCGCGC 201
Db 176 CGCGGCGCTCCGCGCCCACTCCCTCGGCGCGCAGAGCTA-----GCCCGCGCGC 223

QY	202	TGGCGGACGGGCTCATCAAGTCGCCCTAAACCTCTGATGAAGACGACGGCGGTGAAGCGGC	261
Db	224	TGGCGGAAGGGCTGATCAAGTTCGCCCAAGCCCTTAATGAAGAAGCAGCGGTGAAGCGGC	283
QY	262	ACCATCACAAACACAACCTGGGGCACCGCTACGAGTTCTTGAGACGCTGGGCAAGGCA	321
Db	284	ACCACCACAACCAACCTGGGCACCGCTACGAGTTCTTGAGACCTTGGGCAAGGCA	343
QY	322	CCTACGGGAAGGTGAAGAAGGCA CGAGAGAGCTCGGGCGCTTGGTGGCCATCAAGTCCA	381
Db	344	CCTACGGGAAGGTGAAGAAGGCGCGGGAGAGCTCGGGCGCTTGGTGGCCATCAAGTCAA	403
QY	382	TCAGGAAGACAAATCAAGATGAGCAGGATCTCTGCACATACGGAGGGAGATTGAGA	441
Db	404	TCCGGAAGGACAAATCAAGATGAGCAAGATCTGATGCAATACGGAGGGAGATTGAGA	463
QY	442	TCATGTTCTTCACTCAACACACCCACATCATTTGCCATCCATGAAGTGTTCGAGAAATAGCA	501
Db	464	TCATGTCATCACTCAACACACCTCACATCATTTGCCATCCATGAAGTGTTCGAGAACAGCA	523
QY	502	GCAAGATTGTGATTGTCTATGAGTATGCCACGAGGCGATCTCTGTATGATTACATCATGTG	561
Db	524	GCAAGATCGTATCGTCTATGAGTATGCCAGCGGGCGACCTTTATGACTACATCATGCG	583
QY	562	AGCGGCCACGGCTGAGTGTAGCGGGACGCCAGGCATTTCTTCGGACAGATCTGTCTGCGCC	621
Db	584	AGCGGACAGCTCAGTGTAGCGGGAAGCTAGGCAATTTCTTCGGCAGATCTGTCTGCGCG	643
QY	622	TGCACTACTGCCACACAGAACCGGGATCGTTTCAACGAGATCTCAAGCTGGAACAACTCTTC	681
Db	644	TGCACTATTGCCATCAGAACAGAGTTGTTCACCGAGATCTCAAGCTGGAGAACATCTCT	703
QY	682	TAGATGCCAATGGAACCATCAAGATTGTCTGACTTTGGCTCTCCAACTGTATCCACAAG	741
Db	704	TGGATGCCAATGGAATATCAAGATTGTGTGACTTCGGCTCTCCAACTCTTACCATCAAG	763
QY	742	GCAAGTTCTCTCAGACGTTCTGTGGAGCCCTCTAGCCCTCGCTGAGATAGTCAACG	801
Db	764	GCAAGTTCTCTCAGACATTCTGTGGAGCCCTCTATGCTCTGCCAGAGATTGTCAATG	823
QY	802	GGAAGCCCTATGTGTGGCCCCAGAGTGGACAGCTGGTCTCTGGGCGTTCTCTCTGTACATCC	861
Db	824	GGAAGCCCTACACAGGCCACAGGTGGACAGCTGGTCCCTGGGTGTTCTCTCTTACATCC	883
QY	862	TGGTGCATGGCACCATGCCCTTTTGAACGGGAGGATCATAAACACTGGTGAAGCAATCA	921
Db	884	TGGTGCATGGCACCATGCCCTTTTATGGGCAATGACCATAGATCTTAGTGAACACAGATCA	943
QY	922	GTAACGGGGCTTACCGTGTAGCGGCCCAAGCCGTCCGATGCCGTGGCTCTGATCCGGTGGC	981
Db	944	GCAACGGGGCTACCGGAGGCCACTAAACCTCTGATGCTGTGGCTGTATCCGGTGGC	1003
QY	982	TGTTAATGGTGAACCCACCCGTCGGGCCACACTGGAGGATGTAGCCAGTCAITTTGGTGGG	1041
Db	1004	TGTTGATGGTGAACCCACCCGCGGCCACCTCTGGAGGATGTGGCCAGTCACTGGTGGG	1063
QY	1042	TCAACTGGGTTTACACACCGGAGTCGGGNAACAGGAAGCCCTCGTGTAGGCTGGGCACC	1101
Db	1064	TCAACTGGGGCTACGCCACCCGAGTGGGAGACGAGAGGCTCCGCATGAGGGTGGGCACC	1123
QY	1102	CTAGTGTGTACTTTGGCGGGSCCTCCATGGCGGACTGTTACGTCGCTCTCGGCGCCCC	1161
Db	1124	CTGGCAGTGACTGTGCCCGGCCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCC	1183
QY	1162	TCCTGGAGAAATGGAGCCAAAGTGTGACGTTCTTTCAAGCAGCAGCTGCCGGGAGGTGGAA	1221
Db	1184	TCCTGGAGAAATGGGGCCAAAGTGTGACGTTCTTTCAAGCAGCATGCACTGTGGGGAA	1243
QY	1222	GCACTGTACTCTGGCTGGAGGGGCNAATTTCTTTAAGAGTCCGGAAGAGAGATGACA	1281
Db	1244	GCACCACTCTGGCTGGAGCGCCAGATTTGCTTCAAGAGTCCGCAAGAGAGATGACA	1303

Qy	1282	TGGCTCAAATCTGCAAGGTGACCCGGCTAGAGATACCTTCTTCGCTTGGCAAGCA	1341
Db	1304	TGGCCCAAGTCTCTCCACAGTGCACGGCTGATGACACTGCCCCATCGCCCTGGCAAGCA	1363
Qy	1342	GCCTTAAGCTTCGAAAGGCATTCTCAAGAAAAGTCTCTACCTCGTCAGGGAGGTAC	1401
Db	1364	ACCTCAAGCTGCCAAGGGGATTCTCAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTAC	1423
Qy	1402	AGGAGGACCTCTAGGAACTCAGACCGGTGCTGATACTCCAGGCGACCTGTCCCTGCTG	1461
Db	1424	AGGAGGACCTCTCGGAGCTCAGCCCAATCCTCGAGCCCGAGGCGAGCTGCC-----	1477
Qy	1462	TATCCCTGCTCCCAAGAAAGGCATCCTTAAGAAAGTCTCGACAGCGTGAATCTGGTTACT	1521
Db	1478	---CCCTGCTCCCAAGAAGGGCATTTCTCAAGAAGCCCGACAGCGGAGTCTGGGTACT	1534
Qy	1522	ACTCCTCTCCAGAGCCAGCAGTCTGGGGAACTCTTAGACGCCAGTGAATGTTGTGA	1581
Db	1535	ACTCCTCTCCGAGCCAGTGAACTGGGGAGCTCTTGNACGACAGGACGTGTTGTGA	1594
Qy	1582	GTGGGACCCGTGTGAGAGAGAAGTCTCCACAGGCTTCAAGGCTCTCTCCACCGCAAG	1641
Db	1595	GTGGGATCCAAAGGACAGAGCCTCCGCAAGCTTCAGGGCTCCTCTCCATCGCAAG	1654
Qy	1642	GCATTCTAAACTCAATGGCAAGTTCCTCCGACACGCCTTAGAAGCACTACCCCTAGCA	1701
Db	1655	GCATTCTAAACTCAATGGCAAGTTCCTCCAGACAGCCTTAGAGTCTGGGGCCCCCACC	1714
Qy	1702	CCTTTGGCTCCCTGGACCAACTGGCTCCTCTCCCATCTGTGACGCCGGCCAGCGGCCCT	1761
Db	1715	CCTTGGCTCCCTGGATGAATCGCCCCACCTCGCCCCCTGGCCCGGCGACCGACCT	1774
Qy	1762	CAGGGCTGTGATGAGGACAGCATCTGTCTCCGAGTCTCTTTGACCAATTGGACTTGC	1821
Db	1775	CAGGGCTGTGACGAGGACAGCATCTGTCTCTGAGTCTCTTTGACAGCTTGGACTTGC	1834
Qy	1822	CTGAACTCTTCCGAAAAACCACTCAGGGGCTGTGTGCTGTGGACAACCTGAGGGGC	1881
Db	1835	CTGAAACGGCTCCAGAGCCCCACTCGGGGCTGTGTGTGTGTGACAACCTCACGGGG	1894
Qy	1882	TTGAGCAGCTCCCTCAGAAG-----GTCTGAAGCGATGGTGGCAGGAATCTCT	1929
Db	1895	TTGAGGAGCCCCCTCAGAGGGCCCTGGAAAGCTGCTGAGGGCGCTGGCGGAGGATCTT	1954
Qy	1930	TGGGGATAGCTGCTTTTCTCTGACAGATGCCAAGAGGTGACTGCAGGCTACAGACAAG	1989
Db	1955	TGGGGACAGCTGCTTTTCCCTGACAGATGCCAAGAGGTGACAGGACCTTACCGACAG	2014
Qy	1990	CCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGAGATGGTGCCTAGTAGTGGGGTAG	2049
Db	2015	CACGTAGGGTCTGCTCAAAGCTCACTGATGGAGTAGGCATTGCCCCAG-CCCGGTAG	2073
Qy	2050	GCTCTGAGAGGGTTTGCAGAGAAACCTGGGTGGGATTCCTCC	2092
Db	2074	GCTCTCAGATGACGTGGTTGTACCCCGAGGGGAGATGCTTC	2116

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RESULT 8
US-10-423-543-43
; Sequence 43, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williamson, Mark J.

```

APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 39555 OR 593 MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MP103-0230MIN
CURRENT APPLICATION NUMBER: US/10/423,543
CURRENT FILING DATE: 2003-04-25
PRIOR FILING DATE: 2002-10-22
PRIOR FILING DATE: 2002-10-22
PRIOR FILING DATE: 2002-10-22
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/205,447
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 10/012,055
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/248,325
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 10/003,690
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/248,893
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/797,039
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 10/217,168
PRIOR FILING DATE: 2002-08-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 119
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 3353
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(3353)
OTHER INFORMATION: n = A,T,C or G
US-10-423-543-43

Query Match 47.5%; Score 1379; DB 16; Length 3353;

Best Local Similarity 81.8%; Pred. No. 0;

Matches 1654; Conservative 0; Mismatches 335; Indels 34; Gaps 4;

Qy	82	CTACTGTCGCGGACCCACCTCCACTCGCGTCCCGGCCCGCCCTCGGAGAGCGCCCGCGGC	141
Db	116	CTACTGATTCCTCCGCGCCCTTCTCCTCCTCGCTCGCCATGGATCGCTGCTGTTTCG	175
Qy	142	TCCAGCGCCCGAGCGAGGCTCCCTCGGCTCCCGCCCTCGGCTCGGAGAGCGCCCGCGGC	201
Db	176	CGCGGCGCTCCGCGCCCACTCCCTCGCGCGCAGAGCTA-----GCCCGCGGC	223
Qy	202	TGGCGGAGCGGCTCATCAAGTCGCTTAACTCTGTGTAAGAACGACGCGGTGAAGCGGC	261
Db	224	TGGCGGAAGGCTGATCAAGTCGCGCCCAAGCCCTTAATGAAGAACGACGCGGTGAAGCGGC	283
Qy	262	ACCATCAACAACTCGGCGACGCTACGAGTTCCTGAGTTCCTGAGACGCTGGGCAAGGCA	321
Db	284	ACCACCAAGCAAACTCGGCGACGCTACGAGTTCCTGAGACGCTGGGCAAGGCA	343
Qy	322	CCTACGGAAGGTGAAGAACGACGAGAGCTCGGCGCTCTGGTGCCATCAAGTCCA	381
Db	344	CCTACGGAAGGTGAAGAACGCGGGAGAGCTCGGCGCTCTGGTGCCATCAAGTCAA	403
Qy	382	TCAGAAAGCAAAATCAAGATGAGCAGGATCTGCTGCAATACGAGGAGATTGAGA	441
Db	404	TCGGAAGGCAAAATCAAGATGAGCAGGATCTGCTGCAATACGAGGAGATTGAGA	463
Qy	442	TCATGCTTCACTCAACCAACCCCATCTGCGATTCGATGAGTCTTTGAGATAGCA	501
Db	464	TCATGTCATCACTCAACCAACCCCATCTGCGATTCGATGAGTCTTTGAGAACAGCA	523

Qy	502	GCAAGATTGTGATTGTATGAGTATGCCAGCCGAGCGGATCTCTATGATTACATCAGTG	561
Db	524	GCAAGATCGTGATCGTATGAGTATGCCAGCCGAGCGGACCTTTATGATACATCAGCG	583
Qy	562	AGCGGCCACGCGTGTGAGTGTGAGCGGAGCGCCAGGCAATTTCTTCCGACAGATCGTGTGCC	621
Db	584	AGCGGCAGCAGCTCAGTGAGCGGAGCTAGGCAATTTCTTCCGCGAGATCGTCTCTGCCG	643
Qy	622	TGCACTACTGCCACCAAGCGGATCGTTCACCGAGATCTCAAGCTGGAAGCAATCTCTTC	681
Db	644	TGCACTATTGCCATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAAGCAATCTCTTC	703
Qy	682	TAGATGCCAATGGAACATCAAGATTCTGACTTTGGCCCTCTCCAACTGTACCACAAAG	741
Db	704	TGATGCCAATGGAATATCAAGATTCTGACTTTGGCCCTCTCCAACTGTACCACAAAG	763
Qy	742	GCAAGTTCTCCAGACGCTTCTGTGGAGCCCTCTCTACGCTCGCCTCGAGATAGTCAACG	801
Db	764	GCAAGTTCTCCAGACATTTCTGTGGAGCCCTCTATGCTCGCCAGAGATTGTCAATG	823
Qy	802	GGAAGCCCTATGTGGGCCAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG	861
Db	824	GGAAGCCCTATACAGGCCAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG	883
Qy	862	TGATGATGTCACCATGCTTGTGAGCGGAGGATCATAAACACTGCTGTGAAGCAATCA	921
Db	884	TGATGATGTCACCATGCTTGTGAGCGGAGGATCATAAACACTGCTGTGAAGCAATCA	943
Qy	922	GTAACGCGGCTTACCGTGTGAGCGCCCAAGCGTCCGATGCTGTGGCTGATCGGTGGC	981
Db	944	GCAACGCGGCTTACCGGAGGCCACCTAAACCTCTGATGCTGTGGCTGATCGGTGGC	1003
Qy	982	TGTTAATGTTGAACCCCGCTCGGCGCACACTGGAGGATGTAGCCAGTCTATGTTGGG	1041
Db	1004	TGTTAATGTTGAACCCCGCTCGGCGCACACTGGAGGATGTAGCCAGTCTATGTTGGG	1063
Qy	1042	TCAACTGGGCTTACACACCGGAGTTCGGGGAACAGGAAGCCCTGCGTGAGGTTGGGCACC	1101
Db	1064	TCAACTGGGCTTACACACCGGAGTTCGGGGAACAGGAAGCCCTGCGTGAGGTTGGGCACC	1123
Qy	1102	CTAGTGTGATCTTTGGCGCGGCTTCCATGCGGAGTGTGTTTACGTCGCTCTCTCGCGCCCC	1161
Db	1124	CTGCGAGTGTCTGCGCGCGCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1183
Qy	1162	TCCTGGAGATGAGCCAGTGTGAGCTTCTTCAAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT	1221
Db	1184	TCCTGGAGATGAGCCAGTGTGAGCTTCTTCAAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCT	1243
Qy	1222	GCACTGTACCTGGCTGGAGCGGCAACATTTCTTAAAGAGTCCCGAAAGAGAGATGACA	1281
Db	1244	GCACTGTACCTGGCTGGAGCGGCAACATTTCTTAAAGAGTCCCGAAAGAGAGATGACA	1303
Qy	1282	TGGCTCAAAATCTGCAAGGTGACCGCGCTGAGGATCTCTTCTGCGCTTGGGCAAGAGCA	1341
Db	1304	TGGCTCAAAATCTGCAAGGTGACCGCGCTGAGGATCTCTTCTGCGCTTGGGCAAGAGCA	1363
Qy	1342	GCCTTAAGCTTCCGAAGGCAATTTCTCAAGAAAGTCTCTACTCTCTGAGGAGGATGAC	1401
Db	1364	GCCTTAAGCTTCCGAAGGCAATTTCTCAAGAAAGTCTCTACTCTCTGAGGAGGATGAC	1423
Qy	1402	AGGAGGACCTTCAGGAACTCAGACCCGCTGCTGATCTCCAGGCGAGCTGTCTCTCTGCTG	1461
Db	1424	AGGAGGACCTTCAGGAACTCAGACCCGCTGCTGATCTCCAGGCGAGCTGTCTCTCTGCTG	1477
Qy	1462	TATCTCTGCTCCCAAGAAAGGATCTCTTAAAGAGTCTCGACAGCGTGAATCTGTTTACT	1521
Db	1478	---CCCTGCTCCCAAGAAAGGATCTCTTAAAGAGTCTCGACAGCGGAGTCTGGTACT	1534
Qy	1522	ACTCTCTCCAGAGCCGAGTCTGGGAACTCTTAGAGCCAGTGTGTTTGTGA	1581
Db	1535	ACTCTCTCCAGAGCCGAGTGTGAGTCTGGGAGTCTTGGAGCGAGCGGAGTGTGTTGTGA	1594


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Qy 1582 GTGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCCTCTCCACCGCAAGG 1641
Db 1595 GTGGGGATCCCAAGAGCAGAAGCCTCGCAAGCTTCAGGGCTCCTCTCCATCGAAG 1654
Qy 1642 GCATTCTCAAACTCAATGGCAAGTCTCCCGCAAGCTTTAGAAAGCACTACCCCTAGCA 1701
Db 1655 GCATCCTCAAACTCAATGGCAAGTCTCCCGCAAGCTTTAGAAAGCACTACCCCTAGCA 1714
Qy 1702 CCTTTGCTCCTCGACCAACTGCGCTCCTCCCATCTCGAGCCGCGCCAGCGCCCT 1761
Db 1715 CCTTCGGCTCCTCGATGAATCGCCCACTCGCCCTCGCGCCGCGCCAGCCCT 1774
Qy 1762 CAGGGCTGTGAGTGAGGACAGCATCTCTGCTCCGAGTCTTTGACAAATGGACTTGC 1821
Db 1775 CAGGGCTGTGAGCGAGGACAGCATCTCTGCTCTGAGTCTTTGACAGCTGACTTGC 1834
Qy 1822 CTGAACGCTTCCCGAAACCCCACTGAGGGCTGTGTGCTGTGGACAACTGAGGGGGC 1881
Db 1835 CTGAACGGCTCCAGAGCCCACTGCGGGCTGTGTGCTGTGGACAACTGAGGGGGC 1894
Qy 1882 TTGAGCAGCTCCTCCTCAGAAG-----GTCTGAGCGATGTGGCAGGAATCCT 1929
Db 1895 TTGAGGAGCCCCCTCAGAGGGCCCTGGAAGCTCGCTGAGCGCTGGCGGAGGATCCTT 1954
Qy 1930 TGGGGATAGTGTCTTTCTCTGACAGACTGCCAAGAGTGACTGACGCTTACAGCAAG 1989
Db 1955 TGGGGACAGCTGCTTTCTCTGACAGACTGCCAAGAGTGACTGACGCTTACAGCAGG 2014
Qy 1990 CCCTAGGAATCTGCTCAAACTGCTGAGGAGGAGATGGTCCCTAGTATGGGGTAG 2049
Db 2015 CACTGAGGGTGTGCTCAAACTGCTGAGTGGAGTAGGCAATGCGCCAG-CCCGGTGAG 2073
Qy 2050 GCTCTGAGAGGTTTGCAGAGGAACCTGGTGGATTCCTCC 2092
Db 2074 GCTCTGAGTGCAGCTGGTTGCACCCCGAGGGAGATGCTTTC 2116

RESULT 9
US-10-322-281-25
; Sequence 25, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-25

Query Match 47.4%; Score 1375.8; DB 17; Length 3404;
Best Local Similarity 81.7%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 337; Indels 34; Gaps 4;

Qy 82 CTACTGTGCCGACCCACCTCCACCTCGCGGTCCCGCACCACTGGAGTCGGTGGCCTTAC 141
Db 87 CTACTGATTCCTCGCGCTTGTCTCAGCTCTGCTCGCCATGGAGTCGCTGTTTTCG 146
Qy 142 TCAGGCGCCGAGCAGGCTCCCTCGGCTCCGCTCGGCTCGGAGAGCGCCCGCGC 201
Db 147 CGGGGCGCTCGGCGCCCACTCCCTCGGCGCAGAGTCA-----GCCGCGCGC 194
Qy 202 TGGCGGACGGGCTCATCAAGTCGCTAAACTCTGTATGAAGAAGCAGCGGTGAAGCGC 261
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Db 1866 TTGAGAGCCTTCTCTCAAGGGCCCTCGAAGCTCTCTGAGGCGCTGGCGGAGATCCTT 1925
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Qy 1990 CCCTAGGAATCTGCTCAAAAGCTCAGCTCAGGAAGGAGATGGTGCCTTAGTATGGGTAG 2049
Db 1986 CACTGAGGGTCTGCTCAAAAGCTCACTGAGTGGAGTAGGCATTCGCCAG-CCCGGTAG 2044
Qy 2050 GCTCTGAGAGGGTTTGACAGAGAACCTCTGGGTGCGATTCCTCC 2092
Db 2045 GCTCTCAGATGAGTGTGTTGACCCCGGAGGAGATGCTTTC 2087

RESULT 10

US-10-370-715B-639
; Sequence 639, Application US/10370715B
; Publication No. US20040258678A1

GENERAL INFORMATION:

; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 639
; LENGTH: 3443

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-639

Query Match 47.4%; Score 1374.2; DB 18; Length 3443;

Best Local Similarity 81.8%; Pred. No. 0;
Matches 1651; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

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Db 2045 GCTCTCAGATGCAGCTGGTTGCACCCCGAGGGGAGATGCTCTTC 2087
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US-10-618-941-11
; Sequence 11, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 3463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-11
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Query Match 47.4%; Score 1374.2; DB 18; Length 3463;
Best Local Similarity 81.6%; Pred.No. 0;
Matches 1651; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

Qy 82 CTACTGCTGCCGACCCACTCCACCTCGCGGTCCCGCACCATGAGTGTGGCTTAC 141
Db 148 CTATGATTCCTCGCGCTTGTCTCACCTCTGCTCGCCATGAGTGTGCTGTTTCG 207
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Qy 2050 GCTCTGAGAGGGTTTGACAGAGAACCTCTGGGTGGATTCCTCC 2092
Db 2106 GCTCTCAGATGCACTGGTTGACCCCGAGGGAGATGCCCTTC 2148

RESULT 12
US-10-302-172-215
; Sequence 215, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids an
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 1CNP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 215
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)..(1989)
US-10-302-172-215

Query Match 47.3%; Score 1372.2; DB 16; Length 2501;
Best Local Similarity 81.6%; Pred. No. 0;
Matches 1649; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

Qy 82 CTACTGCTGCCGACCCACCTCCACCTCGCGGTCCCGCACCATTGGAGTCGGTGGCCTTAC 141
Db 65 CTATTGATTCCCTGCGGCCCTTGTCTCACCCTCTGCTCGCCATTGGAGTCGCTGGTTTCG 124
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Db 353 TCCGGAAGCAAAATCAAAAGATGAGCAGGATCTGATGCAATACGAGGGAGATTGAGA 412
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Qy 442 TCATGTTCTTCACTCAACACCCACACATCATTTGCCATCCATGAAGTGTGTTGAGATAGCA 501
Db 413 TCATGTCATCATCAACACCCCTCACATCATTTGCCATCCATGAAGTGTGTTGAGAACAGCA 472
Qy 502 GCAAGATGTTGATTTGTCATGAGTATGCGAGCGGAGGATCTGTATGATTAATACATCAAGT 561
Db 473 GCAAGATCGTATGTCATGAGTATGCCAGCGGGGAGCTTTATGACTATCATCAGCG 532
Qy 562 AGCGGCCACGGCTGAGTGAAGCGGAGCGCAGGCAATTTCTCCGACAGATCGTGTCTGCC 621
Db 533 AGCGGCAGCAGCTCAGTGAAGCGGAGCGGAGGATTTCTCCGCGAGATCGTCTCTCGCG 592
Qy 622 TGCACTACTGCCACAGAACGGGATCGTTCAACGAGATCTCAAGCTGGAACATCTTC 681
Db 593 TGCATATTTGCCATCAGAACAGATTTGTCACCGAGATCTCAAGCTGGAACATCTTC 652
Qy 682 TAGATGCCAATGGAACATCAAGATTTGCTGACTTTGGCTCTCCAACTGTACCAAAAG 741
Db 653 TGGATGCCAATGGAATATCAAGATTTGCTGACTTCGGTCTCTCCAACTGTACCATCAG 712
Qy 742 GCAAGTTCCTCCAGAGCTTTGTTGGAGCGCTCTCTACGCTCGCTGAGATAGTCAAG 801
Db 713 GCAAGTTCCTCGACAGCATTTCTGTGGAGCGCCCTCTATGCTCGCTCGCCAGAGATTCTCAATG 772
Qy 802 GGAAGCCCTATGTGGGCCCGCAGAGTGGACAGCTGTCTCTGGGGGTTCTCTGTACATCC 861
Db 773 GGAAGCCCTACAGAGCGCCAGAGTGGACAGCTGTCTCTGGGGTTCCTCTCTACATCC 832
Qy 862 TGGTGCATGGCACCACCTTTTGAAGCGGAGGATCATAAACATCGTGAAGCAAAATCA 921
Db 833 TGGTGCATGGCACCACCTTTGATGGCATGACCATTAAGATCTAGTGAACAGATCA 892
Qy 922 GTAACGGGGCTTACGTTGAGCGGCCCAAGCGTCCGATGCGCTGAGCTGATCCGGTGGC 981
Db 893 GCAACGGGGCTTACCGGGAGCGCACCTAAACCTCTGATGCTGTGGCTGTATCCGGTGGC 952
Qy 982 TGTTAATGTTGAACCCACCGCTCGGGCCACACTGGAGGATGTAGCCAGTCAATTTGGTGG 1041
Db 953 TGTTGATGTTGAACCCACCGCTCGGGCCACCTCTGGAGGATGTAGCCAGTCAATTTGGTGG 1012
Qy 1042 TCAACTGGGTTACACACCGAGTTCGGGGACAGGAGCCCTCGTGAAGGTTGGGAC 1101
Db 1013 TCAACTGGGTTACCGCCACCGAGTGGGAGAGCAGGAGCTCCGATGAGGTTGGGAC 1072
Qy 1102 CTAGTGTGATTTGGCGGGCTCCATGGCGGAGTGGTACGTCTCTCGCGGCCCTCC 1161
Db 1073 CTGGCAGTGTCTGCGCGGCTCCATGGCTGACTGGCTCGCGGCTTCTCTCCCGGCCCT 1132
Qy 1162 TCCTGGAGATGGAGCCAAAGTGTGAGTCTTTCAAGCAGCAGTGTCCGGAGGTGGAA 1221
Db 1133 TCCTGGAGATGGGCGCAAGTGTGAGTCTTTCAAGCAGCAGTGTCCGGAGGTGGAA 1192
Qy 1222 GCATGTACTGGCTGGAGCGGCAACATTTCTTAAAGATCCCGAAAGAGAGATGACA 1281
Db 1193 GCACCACTGGCTGGAGCGCAGCATTCGCTCAAGAGTCCCGCAAGAGAGATGACA 1252
Qy 1282 TGGCTCAAAATCTCAAGTGAACCGGCTGAGGATACCTCTTCTCGCGCTGGGAGAGCA 1341
Db 1253 TGGCCCCAGTCTCTCCACAGTGAACCGGCTGATGACACTGGCCATCGCCCTGGCAAGAGCA 1312
Qy 1342 GCCTTAAGTCTCCGAAAGGATTTCTCAAGAAAAAGTCTCTTACCTCTGTCGGGAGGTAC 1401
Db 1313 ACCTCAAGTCTCCGAAAGGATTTCTCAAGAAAGGTGTGAGCTCTGCAAGAGGGTAC 1372
Qy 1402 AGGAGGACCTTCAGGAATCTAGACCGGTGCTGATCTCCAGGCGAGCCTGTCCCTGCTG 1461
Db 1373 AGGAGGACCTTCGAGCTCAGCCCAATCCCTGCGAGCCAGGCGAGGCTGCC- 1426
Qy 1462 TATCCCTGCTCCCAAGGAAGGATCTTAAAGTCTCGACAGCGTGAATCTGGTTACT 1521
Db 1427 ---CCCTGCTCCCAAGAGGGGATTTCTCAAGAAAGCCCGACGCGGAGTCTGGCTACT 1483

Qy 1522 ACTCCTCTCCAGAGCCAGCGAGTCTGGGGAACTCTTAGAGCCAGTGTGTTGTGA 1581
Db 1484 ACTCCTCTCCCGAGCCAGTGAATCTGGGAGCTCTTTGGAGCGGAGCGTGTGTTGTGA 1543
Qy 1582 GTGGGAGCCCGTGGAGCAGAGTCTCCACAGGCTTCAGGGCTCCTCCTCCACCGCAAG 1641
Db 1544 GTGGGATCCCAAGGAGCAGAGCTCCCGAAGCTTCAGGGCTGCTCTCCATCGCAAG 1603
Qy 1642 GCATCTCAAACTCAATGGCAAGTTCCTCCGCAAGCTTCAGGGCTAGAGGACTACCCCTAGCA 1701
Db 1604 GCATCTCAAACTCAATGGCAAGTTCCTCCAGAGCAGCTTCGAGCTCGCGGCCCAACCA 1663
Qy 1702 CTTTGGCTCCCTGGACCAACTGSCCTCTCCCATCTCGCAGCCCGGCCCGAGCCCT 1761
Db 1664 CTTTGGCTCCCTGGATGAATCTGCCCCACTGCCCCCTGGGCCCGGGCCAGCGACCT 1723
Qy 1762 CAGGGCTGTGAGTGAAGCAGCATCCTGTCTCCGAGTCTTTTGACAAATGGACTTGC 1821
Db 1724 CAGGGCTGTGAGGAGCAGCATCCTGTCTCTGAGTCTTTGACCACTGAGCTTGC 1783
Qy 1822 CTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTCTGTGGAACAACCTGAGGGG 1881
Db 1784 CTGAACGGCTCCAGAGCCCACTGCGGGCTGTGTCTGTGGAACAACCTCAGCGGGC 1843
Qy 1882 TTGAGCAGCTCTCCTCAGAAAG-----GTCTGAAGCGATGTGGCAGGAATCCT 1929
Db 1844 TTGAGGAGCCCTCTCAGAGGGCTTGAAGCTGCTTGAAGCTGTGGCGAGATCCTT 1903
Qy 1930 TGGGGATAGTCTCTTTCTTCTGACAGACTGCCAAGAGTGTGACTGCGAGCTTACAGCAAG 1989
Db 1904 TGGGGAGCAGCTCTTTCTTCTGACAGACTGCCAAGAGTGTGACTGCGAGCTTACAGCAAG 1963
Qy 1990 CCTAGGATCTCTCAAGCTCAGCTGAGGAGGAGATGTTGCTCTAGTATGGGGTAG 2049
Db 1964 CACTGAGGGTCTCTCAAGCTCAGCTGAGTGAAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 2022
Qy 2050 GCTCTGAGAGGGTTTGAGAGGAACCTGCGGTGCGATTCT 2090
Db 2023 GCTCTGAGTGAAGTGTGCTGAGGAGGAGTGTGCTGAGGAGGAGTGTGCT 2063

RESULT 13

US-10-311-034-38
; Sequence 38, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROMSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyring Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajesopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.

APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Yalda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GREYER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 38
LENGTH: 3360
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CB1
US-10-311-034-38

Query Match 47.2%; Score 1370.6; DB 16; Length 3360;
Best Local Similarity 81.5%; Pred. No. 0;
Matches 1649; Conservative 0; Mismatches 339; Indels 35; Gaps 4;

82 CTACTGCTGCGCGACCACTCCACCTCGCGTCCCGCACCACCATGGAGTCGGTCCCTTAC 141
98 CTACTGATCCCTGCGCGCTTCTCACTCTGCTCGCATGAGTCTGCTGTTTCG 98
142 TCACGCGCGCGAGCAGGCTCCCTGCGCTCCCGCTCGGAGAGCGCGCGCGC 201
99 CGCGCGCTCGCGCGCGCTCCCTCGCGC-----CAGAGTAGCGCGCGC 145
202 TGGCGAGCGGCTCATCAAGTCGCTAAACCTCTGATGAGAGCAGCGCGTGAAGCGC 261
146 TGGCGAGAGGCTGATCAAGTCGCGCGCGCGCTTAAAGAGAGCAGCGCGTGAAGCGC 205
262 ACCATCAAAACAAACCTCGCGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAGGCA 321
206 ACCACCAACAGCAACCTCGCGCACCGCTACGAGTTCCTGGAGACCTTGGGCAAGGCA 265
322 CCTACGGGAAGGTGAAGAGGCAAGAGAGCTCGGCGCGCTTGGTGGCCATCAAGTCCA 381
266 CCTACGGGAAGGTGAAGAGGCGCGGAGAGCTCGGCGCGCTTGGTGGCCATCAAGTCAA 325
382 TCAGGAAGACAAATCAAGATGAGCAGGATCTGCTGCAATACGAGGAGATTGAGA 441
326 TCAGGAAGACAAATCAAGATGAGCAGGATCTGATGCAATACGAGGAGATTGAGA 385
442 TCATGCTCTCACTCAACCAACCCACATCTGCTGCAATGAGTCTTGGAGATGAGA 501
386 TCATGCTCTCACTCAACCAACCCACATCTGCTGCAATGAGTCTTGGAGATGAGA 445
502 GCAAGATTGATGTTGATGAGTATGCCAGCGGAGCGGATCTGATGATGATGATGATG 561
446 GCAAGATCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 505
562 AGCGGCCACCGCTGAGTGAAGGAGCGCGAGGATCTGCTGCAATACGAGGAGATTGAGA 621
506 AGCGGAGAGCTGAGTGAAGGAGCGCGAGGATCTGCTGCAATACGAGGAGATTGAGA 565
622 TGCACTACTGCAACAGAGAGGATCTGCTCAACGAGATCTCAAGCTGAGAAACATCTTC 681
566 TGCACTACTGCAACAGAGAGGATCTGCTCAACGAGATCTCAAGCTGAGAAACATCTTC 625
682 TAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACTGTACCACAAAG 741

626 TGGGTGCCAATGGGAATATCAAGATTGCTGACTTGGSCCTCTCCAACTCTACCATCAAG 685
742 GCAAGTTCTCCAGAGGTTCTGTGGGAGCCCTCTACGCGCTCGCCTGAGATAGTCAACG 801
686 GCAAGTTCTCCAGAGATCTGTGGGAGCCCTCTATGCTCGCCAGAGATTGCAATG 745
802 GGAAGCCCTATGTGGGCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCTGTACATCC 861
746 GGAAGCCCTACACAGGCCAGAGGTGGACAGCTGGTCTCTGTGGGTTCTCTCTACATCC 805
862 TGGTGCATGACACATGCTCTTTGACGGGAGGATCTATAAACAACCTGGTGAAGCAATCA 921
806 TGGTGCATGACACATGCTCTTTGATGGGATGACCATTAAGATCTCTAGTGAACAGATCA 865
922 GTAACGGGGCTTACCGTGAGCGCCCAAGCCCTCCGATGCTGTGGCTGATCCGGTGGC 981
866 GCAACGGGGCTTACCGGAGCCACCTTAACCTCTGATGCTGTGGCTGATCCGGTGGC 925
982 TGTAAATGGTGAACCCCGCTCGGGCCACACTGGAGGATGTAGCCAGTCAATTTGGTGG 1041
926 TGTGATGTTGAACCCCGCTCGGGCCACCTTGGAGGATGTGGCCAGTCACTTGGTGG 985
1042 TCAACTGGGGTTACACACCGGAGTGGGGAAACAGGAGCCCTGCTGTGAGGGTGGGACC 1101
986 TCAACTGGGGCTACGCCACCGGAGTGGGAGCAGGAGGCTCCGCTATGAGGGTGGGACC 1045
1102 CTAGTGGTGAATTTGGCGCGCTCCATGCGGAGCTGGTTACGCTGCTCTCGCGCCCC 1161
1046 CTGGCAGTGAATCTGCGCGCGCTTCCATGGCTGACTGGCTTCCGCGCTCTCTCGCGCCCC 1105
1162 TCCTGGAGATGGAGCAAGGTGTGAGCTTTTCAAGCAGCAGCTGCGCGGAGGTGGAA 1221
1106 TCCTGGAGATGGGCAAGGTGTGAGCTTTTCAAGCAGCAGCTGCGCTTGGTGGGGA 1165
1222 GCACTGTACTGGGCTGGAGCGCAACATTTCTTTAAGAGTCCCGAAGAGAGATGACA 1281
1166 GCACCACTTGGCTGGAGCGCAGCATTCGCTCAAGAGTCCCGCAGGAGAGATGACA 1225
1282 TGCTCAAAATCTGCAAGGTGACCGCTGAGGATACCTTCTCGCGCTGCGGAGAGCA 1341
1226 TGCGCCAGTCTCTCAAGTGAACGCTGATGACATGCGCCATCGCGCTTGGCAGAGCA 1285
1342 GCCTTAAGCTTCCGAAAGCATTTCTCAAGAAAGTCTCTACCTCTGCTCAGGGGAGTAC 1401
1286 ACCTCAAGCTGCCAAGGGCATTTCTCAAGAAAGTGTGAGCTCTGCGAAGAGGGTAC 1345
1402 AGAGGACCTCTAGGAACTCAGACCGGTGCTGATCTCAGGGGAGCTGCTCTGCTG 1461
1346 AGAGGACCTCTCGGAGCTCAGCCCAATCTCTGAGCGCCAGGGAGCTGCGCC----- 1399
1462 TATCCCTGCTCCCAAGGAGGATCTCTTAAGAGTCTCGACAGCGTGAATCTGGTTACT 1521
1400 ----CCCTGCTCCCAAGAGGGCATTTCTCAAGAAAGCCCGCAGCGGAGTCTGGTACT 1456
1522 ACTCTCTCCAGAGCCAGCGAGTCTGGGAACTTTAGACGCGCAGTGTGTTCTGA 1581
1457 ACTCTCTCCAGAGCCAGTGAATCTGGGAGCTCTTGGAGCGCAGGAGCGTGTGTTGA 1516
1582 GTGGGACCCCGTGGAGAGAGAGTCTCCACAGGCTTCAAGGGCTCTCTCTCCACGCAAG 1641
1517 GTGGGATCCCAAGAGGAGAGGCTCCGCAAGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1576
1642 GCATTTCTCAAACTCAATGGCAAGTCTCCGCGCAGCTTTAGAGGAGTACCCCTAGCA 1701
1577 GCATTTCTCAAACTCAATGGCAAGTCTCCGCGCAGCTTTAGAGGAGTACCCCTAGCA 1636
1702 CTTTGGCTCCCTGGAGCAACTGCGCTCTCTCCATCTGCGAGCCCGCGCCAGCGCCCT 1761
1637 CTTTGGCTCCCTGGAGCAACTGCGCTCTCTCCATCTGCGCCCGCGCCAGCGCCCT 1696
1762 CAGGGCTGTGAGTGGAGCAGCATCTCTGCTCCGAGTCTTTGACCAATGAGCTTGC 1821

Db 1697 CAGGGCTGTGAGCGAGGACAGCATCTCTGCTCTGAGTCTCTTGAACAGCTGACTTGC 1756
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Db 1757 CTGAACGGCTCCAGAGCCCACTGCGGGCTGTGTGTGTGAGCAACCTCAGGGGC 1816
Qy 1882 TTGAGCAGCTTCCCTCAGAAG-----GTCTGAAGCGATGGTGGCAGGAATCCT 1929
Db 1817 TTGAGGAGCCCTCTCAGAGGGCCCTGGAAGCTGCTGAGCGCTGCGGAGAGATCCTT 1876
Qy 1930 TGGGGGATAGTGTCTTTCTGTGACAGACTGCCAAGAGGTGACTGACGCTTACAGACAAG 1989
Db 1877 TGGGGGACAGTGTCTTTCTGTGACAGACTGCCAAGAGGTGACTGACGCTTACCGACAGG 1936
Qy 1990 CCTAGGAATCTGCTCAAGCTCAGCTGAGGAGGAGATGGTCCCTAGTATGGGTAG 2049
Db 1937 CACTGAGGCTGTCTCAAGCTCACTGAGTGGAGTAGGCAATGCCCGAG-CCCGGTGAG 1995
Qy 2050 GCTCTGAGAGGTTTTCAGAGAGAACCTCTGGTGGGATTCCTCC 2092
Db 1996 GCTCTCAGATGACGTGTTGACCCCGAGGGGAGATGCCTTC 2038

RESULT 14

US-09-963-159-3
; Sequence 3, Application US/09963159
; Patent No. US2002007312A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-50U1
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/234,922
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-159-3

Query Match 46.9%; Score 1360.2; DB 9; Length 1884;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;

Qy 169 CCTCCGCTGGCTCGGAGAGCGCCCGCGCTGCGGACGGGCTCATCAAGTCGCCCTA 228
Db 35 CCACTCCCTCGGCGCAGAGCTAGCCCGCGCTGCGGAGGGCTGATCAAGTCGCCCA 94
Qy 229 AACTCTGATGAAAGCAGCGGTGAAGCGGACCATCAAAACAACTCGGGCACC 288
Db 95 AGCCCTTAATGAAGACAGCGGTGAAGCGGACCATCAAAACAACTCGGGCACC 154
Qy 289 GCTACAGATTCCTGGAGACGCTGGGCAAGGCGACCTACGGGAAGGTGAAGAAGCGACG 348
Db 155 GCTACAGATTCCTGGAGACCTTGGGCAAGGCGACCTACGGGAAGGTGAAGAAGCGCGG 214
Qy 349 AGAGCTCGGGCGCTGTGGTGGCCATCAAGTCCATCAGGAAGAGCAAAATCAAGATGAGC 408
Db 215 AGAGCTCGGGCGCTGTGGTGGCCATCAAGTCCATCAGGAAGAGCAAAATCAAGATGAGC 274
Qy 409 AGAGCTCGGCGATCAGACGAGGAGATGAGATCATGTCTTCACTCAACCAACCCCAACA 468
Db 275 AAGATCTGATGCAATACGAGGAGATGAGATCATGTCTTCACTCAACCAACCCCAACA 334
Qy 469 TCATTGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATGTGATGTCTATGGAGTATG 528
Db 335 TCATTGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATGTGATGTCTATGGAGTATG 394
Qy 529 CCAGCGAGGCGATCTGTATGATTATCATAGTGAAGCGGCCACCGCTGAGTGAAGCGGACG 588

Db 395 CCAGCGGGCGGACCTTTATGACTACATCAGCAGCGGAGCAGCTCAGTGAAGCGCGAG 454
Qy 589 CAGGCAATTTCTTCGACAGATCGTGTCTGCCCTGCACTACTGCCACAGACGGGATCG 648
Db 455 CTAGGCAATTTCTTCGCGCAGATCGTCTCTGCCGTGCACTATTGCCATCAGAACAGATTG 514
Qy 649 TTCAACGAGATCTCAAGCTGGAAACATCTTCTAGATGCCAATGGAAACATCAAGATTG 708
Db 515 TCACCGAGATCTCAAGCTGGAAACATCTTCTTGGATGCCAATGGAAATATCAAGATTG 574
Qy 709 CTGACTTTGGCCCTCTCAACCTGTACCAAGGCAAGTTCTCTCCAGACGCTTCTGTGGGA 768
Db 575 CTGACTTGGCCCTCTCAACCTCTACCATCAAGGCAAGTTCTCTCGACACATTTCTGTGGGA 634
Qy 769 GCCTCTCTACAGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCGAGAGTGG 828
Db 635 GCCTCTCTATGCTGCGCAGAGATTTCTCAATGGGAAGCCCTACACAGGCCCGAGAGTGG 694
Qy 829 ACAGCTGTCTCTGGGGTCTCTCTGTACATCTCTGTGTGATGCGACCATGCGCTTTGACG 888
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Qy 889 GGCAGGATCAATAAACACATGCTGTAAGCAATCAGTAACGGGGCTTACCGTGAAGCGGCCA 948
Db 755 GGCATGACCATAGATCTTAGTGAACAGATCAGCAACGGGGCTTACCGGAGGCCACTTA 814
Qy 949 AGCGTCCGATGCTGTGGCTGATCCGGTGGCTGTGTAATGTGTGAACCCACCGTGGGG 1008
Db 815 AACCTCTGATGCTGTGGCTGATCCGGTGGCTGTGTAATGTGTGAACCCACCGTGGGG 874
Qy 1009 CCACACTGGAGGATGTAGCAGCTCATTGTGGGTCAACTGGGGTTCACACACCGAGTGG 1068
Db 875 CCACCTGGAGGATGTGGCGAGTCACTGTGGGTCAACTGGGGTTCACACACCGAGTGG 934
Qy 1069 GGGAAACAGGAAGCCCTCGCTGAGGGTGGGCAACCTAGTGTGTGACTTTGGCGGGCTCCA 1128
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Qy 1129 TGGCGACTGTGTTACGTGCTCTCTCGCGCCCTCTCTGGAGAAATGGAGCAAGGTGCA 1188
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Qy 1189 GCTTCTTCAAGCAGCAGCTGCCGGAGGTGGAAGCACTGTACTCTGGCTGGAGCGGCAAC 1248
Db 1055 GCTTCTTCAAGCAGCAGTCACTGTGTGGGGAGGACCAACCTCTGGCTGGAGCGGCAAC 1114
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Qy 1429 TGCTGATGATCTCAGGGCAGCTGTCCCTGTGTATCTCTCTTCCCAAGAAAGGATTC 1488
Db 1295 TCCCTCGAGGCCCGAGGAGGCTGCC-----CCCTGCTCCCAAGAGGAGATTC 1345
Qy 1489 TTAAGAGTCTGACAGCGTGAATCTGTTTACTCTCTCTCAGAGCCAGGAGTCTG 1548
Db 1346 TCAAGAGGCCCGAGCAGCGAGTCTGGCTTACTCTCTCTCCGAGCCAGGATCTG 1405
Qy 1549 GGGAACTCTTAGACCGCAGTGTGTTTGTAGTGGGACCCCGCTGGAGCAGAGTCTC 1608
Db 1406 GGGAGCTCTTGGACCGCAGGCGAGCTGTTTGTAGTGGGATCCCAAGGAGCAGAGCCCTC 1465
Qy 1609 CACAGGCTTCAGGGCTCTCTCCACCGCAAGGGCAATTCCTCAAACTCAATGGCAAGTTCT 1668

Db 1466 CGAAGCTTCAGGCTCTCTCCATCGCAAGGATCTCTCAAACTCAATGGCAAGTTCT 1525
Qy 1669 CCCGACAGCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGACCAACTGGCCT 1728
Db 1526 CCAGACAGCTTAGAGCTGGGGCCCCACCACTTCGGCTCCCTGGATGAATCGCCC 1585
Qy 1729 CTTCCCATCTGACGCGCGCCAGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC 1788
Db 1586 CACCTCGCCCTCGCGCGCCAGCGGACCTCAGGGGCTGTGAGCGAGGACAGCATCC 1645
Qy 1789 TGTCTCCGAGTCTTTGACCAATGCACTGCTGCACTCTCCGGAACCCCACTGA 1848
Db 1646 TGTCTCTGAGTCTTTGACAGCTGAGCTGACCTGACGCTCCAGAGCCGCCCACTGC 1705
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Db 1706 GGGGCTGTGTCTGTGCAAACTGAGGGGCTTGTAGGAGCCCCCTCAGAGGGCCCTG 1765
Qy 1903 -----GTCTGAAGCGATGTGGGAGGAATCTTTGGGGGATAGCTGCTTTCTGTGACAG 1956
Db 1766 GAAGCTGCTGAGCGCTGGCGGAGGATCTTTGGGGGACAGCTGCTTTCTGTGACAG 1825
Qy 1957 ACTGCCAAGAGTGTGAGCTGAGCCCTACAGACAGCCCTAGGAATCTGCTCAAGCTCAGC 2015
Db 1826 ACTGCCAAGAGTGTGAGCGACCTTACCACAGGCACTGAGGGTCTGCTCAAGCTCACC 1884

RESULT 15
US-10-423-543-45
; Sequence 45, Application US/10423543
; Publication No. US20040058355A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Teal, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williamson, Mark J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MPI03-0230MINIM
; CURRENT APPLICATION NUMBER: US/10/423,543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-423-543-45

Query Match 46.9%; Score 1360.2; DB 16; Length 1884;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;

Qy 169 CTTCCGCTTGGCTTCGAGAGCGCCCGCTGGCGGACCGGCTCATCAAGTCGCTA 228
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GenCore version 5.1.6
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Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

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Listing first 45 summaries

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- 7: gb.ph.*
- 8: gb.pl.*
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- 13: gb.un.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2820.4	97.2	2938	10	BC046833 Sequence
3	2763.8	95.2	2917	10	BC033302 Mus muscu
4	2066.8	71.2	2929	6	AX380960 Sequence
5	2022.2	69.7	2027	6	AX381046 Sequence
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11	1375.8	47.4	3395	9	AK074830 Homo sapi
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	22	1071.4	36.9	1186	6	AX380972	AX380972 Sequence
	23	943.4	32.5	1186	6	AX381029	AX381029 Sequence
	24	849.2	29.3	2616	6	AX430369	AX430369 Sequence
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ALIGNMENTS

RESULT 1	AR279568	Sequence 4 from patent US 6514719.	2902 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR279568	Sequence 4 from patent US 6514719.	2902 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	AR279568	Sequence 4 from patent US 6514719.	2902 bp	DNA	linear	PAT 10-APR-2003
ACCESSION	AR279568	Sequence 4 from patent US 6514719.	2902 bp	DNA	linear	PAT 10-APR-2003
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SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 2902)					
AUTHORS	Bird,T.A., Virca,G.D., Martin,U. and Anderson,D.M.					
TITLE	Methods for identifying compounds that alter kinase activity					
JOURNAL	Patent: US 6514719-A 4 04-FEB-2003;					
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ACCESSION BC046833
VERSION BC046833.1 GI:29145027
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2938)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S.,
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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalios,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
PUBMED 12477932
2 (bases 1 to 2938)
Strausberg,R.
Direct Submission
TITLE Submitted (13-FEB-2003) National Institutes of Health, Mammalian
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REMARK
COMMENT
GeneCollection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgaps-k@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Schetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
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This clone was selected for full length sequencing because it
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Qy	1039	GGCTCACTGGGGTTACACACCGGATCGGGNAAGGAAAGCCCTGCGTGGGGTGGC	1098

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Db	1081	ACCTAGTGTGACTTTGGCCGGGCTCCATGCGGACTGTTTACGTGCTCTCTCGGCC	1140
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Qy	1219	GAAGCACTGTACCTGGGCTGAGCGCAACATTTCTTTAAGAGTCCCGAAGAGAGATG	1278
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Qy	1399	TACAGAGGACCCCTCAGGAACTCAGACCGGTGCTGATCTCCAGGSCAGCTGTCCCTG	1458
Db	1381	TACAGAGGACCCCTCAGGAACTCAGACCGGTGCTGATCTCCAGGSCAGCTGTCCCTG	1440
Qy	1459	CTGTATCCCTGCTCCAAAGAAAGGATCTTTAAGAAAGTCTCGACAGCGTGAATCTGGTT	1518
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Db	1561	TGAGTGGGACCCCGTGGAGCAGAACTCTCCAGAGCTTCAGGGCTCTCTCCACCGCA	1620
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RESULT 3

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BC033302
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DEFINITION Mus musculus RIKEN cDNA 1200013B22 gene, mRNA (cDNA clone MGC:30598
IMAGE:3663595), complete cds.
ACCESSION BC033302
VERSION BC033302.1 GI:23271085
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2917)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, T.E., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.M., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullihy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Helton, E., Kettaman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blackesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2917)

Strausberg, R.

Direct Submission

Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 40 Row: d Column: 21

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.

FEATURES

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misc_feature

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catalytic domain. Phosphotransferases of the serine or
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activity of these protein kinases is controlled by
phosphorylation of specific residues in the activation
segment of the catalytic domain, sometimes combined with
reversible conformational changes in the C-terminal
autoregulatory tail"

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ORIGIN

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RESULT 4

AX380960

LOCUS

DEFINITION

Sequence 1 from Patent WO0212456. 2929 bp DNA linear PAT 18-MAR-2002

ACCESSION

AX380960.1 GI:19575800

VERSION

Rattus sp.

KEYWORDS

Rattus sp.

SOURCE

Rattus.

ORGANISM

Rattus.

REFERENCE

1

Drucker, D.J., Rosen, C.F. and Lefebvre, D.L.

Ampk-related serine/threonine kinase, designated snrk

Patent: WO 0212456-A 1 14-FEB-2002;

1149336 ONTARIO INC. (CA)

FEATURES

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity

Matches 2488; Conservative

71.2%; Score 2066.8; DB 6; Length 2929;

86.4%; Pred. No 0;

Mismatches 277; Indels 115; Gaps 14;

QY 49 GTGACCTCTGAGCCCGCGCTCAGCGCGCTGCTACTGCTGCCGACCCCACTCCACTC 108

Db 9 GTGACCTCTGAGCTCGCGCTCTCCGCGCTGCTGCTGCCGCGGAACTTGGCTCCGCTC 68

QY 109 GCGGTCCCGCACCATGGAGTGGTGGCTTACTCCAGCGCCCGAGCAGGCTCCCTCGG 168

Db 69 GCGGTCCCGCACCATGGAGTGGTGGCTTACTCCAGCGCGCGGAACTTGGCTCCCTCGG 128

QY 169 CTTCCGCCCTGGCTCGGAGAGCGCGCGCTGCGGACGGCTCATCAAGTCGGCTA 228

Db 129 CTTCCGCCCTGGCCACGAGAGCGCGCGCTGCGGACGGCTCATCAAGTCGGCTA 188

QY 229 AACCTCTGATGAAGAAGCAGCGGCTGAAGCGGACCATCAAAACAACAACTCGGCGACC 288

Db 189 AACCTCTGATGAAGAAGCAGCGGCTGAAGCGGACCATCAAAACAACAACTCGGCGACC 248

QY 289 GCTACAGATTCCTGGAGAGCGTGGGCAAGGGACCTACGGGAAGGTGAAGAAGCAGCAG 348

Db 249 GCTACAGATTCCTGGAGAGCGTGGGCAAGGGACCTACGGGAAGGTGAAGAAGCAGCAG 308

QY 349 AGAGCTCGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAAAGATGAGC 408

Db 309 AGAGCTCGGAGCGCTCTGGTGGCCATCAAGTCCATCAGGAAGACAAATCAAAAGATGAGC 368

QY 409 AGGATCTGTGCACATACGAGGAGGAGTGAAGATCATGTCTTCACTCAACCAACCCACCA 468

Db 369 AGGATCTGTGCACATACGAGGAGGAGTGAAGATCATGTCTTCACTCAACCAACCCACCA 428

QY 469 TCATTGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATGTGTCATGGAGTATG 528

Db 429 TCATTGCCATCCATGAAGTGTGAGAAATAGCAGCAAGATTGTGATGTGTCATGGAGTATG 488

QY 529 CCAGCCGAGCGATCTGTATGATTATCAGTCAAGCGCGCCAGCGCTGAGTGAGCGGACG 588

Db 489 CCAGCCGAGCGATCTGTATGATTATCAGTCAAGCGCGCCAGCGCTGAGTGAGCGGACG 548

QY 589 CCAGGCAATTTCTTCGACAGATCGTGTCTGCCCTGCACTACTGCCACCCAGACGGGATCG 648

Db 549 CCAGGCAATTTCTTCGACAGATCGTGTCTGCCCTGCACTACTGCCACCCAGACGGGATCG 608

QY 649 TTCACCGAGATCTCAAGCTGGAAAAATCTCTTCTAGATGCGCAATGGAACATCAAGATTG 708

Db 609 TTCACCGAGATCTCAAGCTGGAAAAATCTCTTCTAGATGCGCAATGGAACATCAAGATTG 668

QY 709 CTGACTTTGGCTCTCCAACTGTATCAAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA 768

Db 669 CTGACTTTGGCTCTCCAACTGTATCAAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA 728

QY 769 GCCTCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCAGAGGTGG 828

[illegible]

Db	1806	GGAGCTGTGTGTTCTGTGTGGACAACCTCTGAGGAGGCTTGCAGCAGCCTCCCTCAGAAAGGCCTAA	1861
Qy	1909	AGCGATGTTGCGCAGGAATCCTTCGGGGATAGCTGCTTTTCTCTGACAGACTGCGCAAGAGG	1968
Db	1866	AACGATGTTGCGCAGGAATCCTTCGGGGATAGCGCTTTCTCTGACAGACTGCGCAAGAGG	1925
Qy	1969	TGACTGCAAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAAGCTCAGCTGAGGAAGGGAGA	2028
Db	1926	TGACAGCAGCCTACAGACAAGCCCTAGGAATCTGCTCGAAGCTCAGCTGAGGAGGAGAGG	1985
Qy	2029	TGTTGCCCTTAGT-ATGGGGTAGGCTCTGAGAGGGTTTGCAGAGAAACCCCTGGGTCCGATT	2087
Db	1986	CAGTGCCTCAGTGTGATGCGGTAGAGCTCTTACAGGGGTTTGCAGAGGAACCTGGGT-AGATT	2044
Qy	2088	CCTCCAGTGAATAGAGTACATCAAG---GGCTCTAGCTCTGCAGCCTGACTGAACTGA	2143
Db	2045	CCCAGGGTTGTAGAGTACATCAAGAACTCTCTCTCTGCTTTCAGGCTGATTGAACTGG	2104
Qy	2144	AAGATGAGAAATTCGATTGATGTGGAAGGAATGGAAACCCCTGTCGCCGAGTGTTA	2203
Db	2105	AGGCTGAGAGNAATAGCAGAGATATGGAAGGACTGACCTACAGAGCTGCACTGCAAGATG	2164
Qy	2204	TAGTGGGT--GGCCTGAAGGTGCCCTACTCTCTTTGTGCCATGAGTGTCAACCATGACA	2260
Db	2165	TGACGGCACAGAGACTGAAAGTGCCCTACCTCCTTTATGC--TGAGTGTCTACCATGGCA	2222
Qy	2261	TTTCCCACCTGTTCTCTGCTGCCTGCAC------TTCATATGATTTCTGTTTCCATCA	2312
Db	2223	TCCTCC-CCCTGCTCTCTGCACTGTGAGGGTGACCCACATAGTTCCTGTTTCGATCG	2281
Qy	2313	ACCACAGGGTTAGAACCCCTGACTTCTCTGGAGGTAAATGTAGTGACTGCCATTAATTTA	2372
Db	2282	ACCACAGGGTTAGAACCCCTGACATCCCTGGAAGTAAATGTGAGCAACCTCGCTTAATTTA	2341
Qy	2373	GAGAGGAAACAGCCTCTGGTTTCCATCTCTGCTGTGTGATCTCAAAGACCTCGGAAGA	2432
Db	2342	AAGAGGAAACAGCCTCTGGTTTCCATCTCTGCTGTGTCATCTCAAAGACCTAGAAAGA	2401
Qy	2433	CTCGGACCGCTGTTGACTTCATCTCAAGGGACAGATGCCCTCGACCCCATCTTAGA	2492
Db	2402	CTC-AACTGCTGTTTCACTTCATCTCAAGGGAC-----	2434
Qy	2493	TCTCAGAGACTTGAACTTTGAAGCTGTCTTAGTACCAGATGTGGATGGAT-GCTCTGT	2551
Db	2435	-CTCAGAGACTGAGCCTTGAAGCTGTTCTGTATACAGACTATGATGCGATATGCTGT	2493
Qy	2552	TTCTCAGGCCAACGGGACCTTAGAATGTGTGACTTAATTTTTTTTGTGATTTCTCACAT	2611
Db	2494	TTCTCAGGCCAGCAGGACCCAGAAATGTGTGACTTAATTTA--TTTTTGTGATTTCTCACAT	2551
Qy	2612	CTGTTTTTTGGTT-----	2624
Db	2552	CTGGTCTGTTTCGTTTTTTTTTTGTTGTTGTTGTTGTTGTTGTTTCTGTGTTTT	2611
Qy	2625	-----TTTGTGTTGTTGTTGTTTTTTTAAGTGAATTTTGTGCTGCTTTTCAATAATG	2678
Db	2612	TGTTTTGTTGTTGTTGTTGTTTTTTTAAGTGAATTTTGTGCTGCTTTTCGGTAATG	2671
Qy	2679	TGAATGCTGTGTTCTCGGGAACTCCACTGTGCCACTGAAAGTTTATGTACAGAGAAATTT	2738
Db	2672	TGAATGCTGTGTTCTCGGGAAAGCCACTGTGTCAATTGAAGTGTGTGTACAGAGAAATTT	2731
Qy	2739	TGGCAATGATGCTCCTTAATCAAGGGGGGTGGGGCGTTTTTCAAATGATGCTTGAG	2798
Db	2732	TGGCAGTGAATCCTCTAAT-----GGGGGGGTGGCCCTTTTTCAGATGATGTCTTGAG	2783
Qy	2799	CAGTGTCTGGATTGAGTCTCCAGTCCCTTACACCCAGGCTGGCCACCCCTCCCTCATCT	2858
Db	2784	CATGTCTGGATTGGGTCTCTGTCCCTTACACACAGAGGCTGTCCACCCCTCCCTCATCT	2843

RESULT 5
AX381046

LOCUS	AX381046	2027 bp	DNA	linear	PAT 18-MAR-2002
DEFINITION	Sequence 87 from Patent WO0212456.				
ACCESSION	AX381046				
VERSION	AX381046.1	GI:19575868			
KEYWORDS					
SOURCE	Mus sp.				
ORGANISM	Mus sp.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Drucker D.J., Rosen,C.F. and Lefebvre,D.L.				
TITLE	Amph-related serine/threonine kinase, designated snark				
JOURNAL	Patent: WO 0212456-A 87 14-FEB-2002;				
FEATURES	1149336 ONTARIO INC. (CA)				
source	Location/Qualifiers				
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	/organism="Mus sp."				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:10095"				
ORIGIN					
Query Match	69.7%; Score 2022.2; DB 6; Length 2027;				
Best Local Similarity	99.9%; Pred. No. 0;				
Matches 2024; Conservative	0; Mismatches 3; Indels 0; Gaps 0;				
Qy	49	GTGACCTCTGAGCCCGCGGTCTAGCGCGCGTCTACTGTGCTGCGGACCCCACTCCACCTC	108		
Db	1	GTGACCTCTGAGCCCGCGGTCTAGCGCGCGTCTACTGTGCTGCGGACCCCACTCCACCTC	60		
Qy	109	GCAGTCCCGGACCATGGAGTGGTGGCTTATCTCCAGCGCGGAGCAGGCTCCCTCGG	168		
Db	61	GCAGTCCCGGACCATGGAGTGGTGGCTTATCTCCAGCGCGGAGCAGGCTCCCTCGG	120		
Qy	169	CTTCGCGCCCTGGCTCGGAGCGCGCGCGTGGCGGAGCGGCTCATCAAGTCGCGCTA	228		
Db	121	CTTCGCGCCCTGGCTCGGAGCGCGCGCGTGGCGGAGCGGCTCATCAAGTCGCGCTA	180		
Qy	229	AACCTCTGATGAAGACGCGGTGAAGCGGACCATCAACACAACTCGCGGACCC	288		
Db	181	AACCTCTGATGAAGACGCGGTGAAGCGGACCATCAACACAACTCGCGGACCC	240		
Qy	289	GCTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACGCGAAGGTGAAGACGAG	348		
Db	241	GCTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACGCGAAGGTGAAGACGAG	300		
Qy	349	AGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAGATGAGC	408		
Db	301	AGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAATCAAGATGAGC	360		
Qy	409	AGGATCTGCTGCACATACGAGGAGAGATTGAGATCATGTCTTCACTCAACACCCCCACA	468		
Db	361	AGGATCTGTTGCACATGAAGGAGGAGATCGAGATCATGTCTTCACTCAACACCCCCACA	420		
Qy	469	TCATTGCCATCCATGAAGTGTGTTGAGAAATAGCAGCAAGATTGTGATGATGATG	528		
Db	421	TCATTGCCATCCATGAAGTGTGTTGAGAAATAGCAGCAAGATTGTGATGATGATG	480		
Qy	529	CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCGCACCGCTCAGTGAGGAGCG	588		
Db	481	CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCGCACCGCTCAGTGAGGAGCG	540		
Qy	589	CCAGGCAATTTCTTCGACAGATCGTGTCTGCGCTGCACTACTGCGCACAGAAAGGGATCG	648		
Db	541	CCAGGCAATTTCTTCGACAGATCGTGTCTGCGCTGCACTACTGCGCACAGAAAGGGATCG	600		
Qy	649	TTCAACGAGATCTCAAGCTGGAAACATCTCTTCTAGATGCCAATGGAAACATCAAGATTG	708		
Db	601	TTCAACGAGATCTCAAGCTGGAAACATCTCTTCTAGATGCCAATGGAAACATCAAGATTG	660		
Qy	709	CTGACTTTGGCCCTCTCAACCTGTATACCAAGGCAAGTTCTCTCCAGACGCTTCTGTGGGA	768		
Db	661	CTGACTTTGGCCCTCTCAACCTGTATACCAAGGCAAGTTCTCTCCAGACGCTTCTGTGGGA	720		
Qy	769	GCCTCTCTACGCTCGCTGAGATAGTCAACGGAAGCCCTATGTGGGCCAGAGGTGG	828		
Db	721	GCCTCTCTACGCTCGCTGAGATAGTCAACGGAAGCCCTATGTGGGCCAGAGGTGG	780		
Qy	829	ACAGCTGGTCTCTGGGCGTTCTCTCTGTATACCTCTGTGTGATGGACACCATGCTTTGACG	888		
Db	781	ACAGCTGGTCTCTGGGCGTTCTCTCTGTATACCTCTGTGTGATGGACACCATGCTTTGACG	840		
Qy	889	GGCAGGATCATATAAACACTGCTGAAGCAATCAGTAACGGGGCTTACCGTGAGCGGCCCA	948		
Db	841	GGCAGGATCATATAAACACTGCTGAAGCAATCAGTAACGGGGCTTACCGTGAGCGGCCCA	900		
Qy	949	AGCGCTCCGATGCTGTGGCTGATCCGCTGGCTGTTAAATGGTGAACCCCAACCGTGGGG	1008		
Db	901	AGCGCTCCGATGCTGTGGCTGATCCGCTGGCTGTTAAATGGTGAACCCCAACCGTGGGG	960		
Qy	1009	CCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAACTGGGGTTACACACCGGAGTGG	1068		
Db	961	CCACACTGGAGGATGTAGCCAGTCAATGGTGGGTCAACTGGGGTTACACACCGGAGTGG	1020		
Qy	1069	GGGAAACAGGAAGCCCTGCGTGGGTGGGCACTAGTGTGACTTTTGGCGGGCCCTCCA	1128		
Db	1021	GGGAAACAGGAAGCCCTGCGTGGGTGGGCACTAGTGTGACTTTTGGCGGGCCCTCCA	1080		
Qy	1129	TGGCGGACTGGTTACGCTCGCTCGCGCCCTCTCTGGAGAAATGGAGCCCAAGGTGTGCA	1188		
Db	1081	TGGCGGACTGGTTACGCTCGCTCGCGCCCTCTCTGGAGAAATGGAGCCCAAGGTGTGCA	1140		
Qy	1189	GCTTCTTCAAGACGAGTCCCGGAGGTGGAGACACTGTACTGGGCTGGAGCGGCAAC	1248		
Db	1141	GCTTCTTCAAGACGAGTCCCGGAGGTGGAGACACTGTACTGGGCTGGAGCGGCAAC	1200		
Qy	1249	ATTCTCTTAAGAAAGTCCCGAAAGAGAAATGACATGGCTCAAAATCTCAAGAGGTGACCCGG	1308		
Db	1201	ATTCTCTTAAGAAAGTCCCGAAAGAGAAATGACATGGCTCAAAATCTCAAGAGGTGACCCGG	1260		
Qy	1309	CTGAGGATACCTTCTCGCCCTGGCAAGACGACCTTAAAGCTTCCGAAAGGCAATTTCTCA	1368		
Db	1261	CTGAGGATACCTTCTCGCCCTGGCAAGACGACCTTAAAGCTTCCGAAAGGCAATTTCTCA	1320		
Qy	1369	AGAAAGTCTCTACTCTGTAGGGGAGGTACAGGAGACCTCTCAGGAATCTAGACCGG	1428		
Db	1321	AGAAAGTCTCTACTCTGTAGGGGAGGTACAGGAGACCTCTCAGGAATCTAGACCGG	1380		
Qy	1429	TGCTGTATCTCCAGGCGACCTGCTCTGCTGATCCCTGCTCTCCCAAGGAAAGGCAATCC	1488		
Db	1381	TGCTGTATCTCCAGGCGACCTGCTCTGCTGATCCCTGCTCTCCCAAGGAAAGGCAATCC	1440		
Qy	1489	TTAAGAGTCTCGACAGCGTGAATCTGGTTACTCTCTCTCCAGAGCCCGAGGATCTG	1548		
Db	1441	TTAAGAGTCTCGACAGCGTGAATCTGGTTACTCTCTCTCCAGAGCCCGAGGATCTG	1500		
Qy	1549	GGGAACTCTTAGACGCGCAGTGTGTGTGTAGTGGGACCCCGTGGAGAGAGTCTC	1608		
Db	1501	GGGAACTCTTAGACGCGCAGTGTGTGTGTAGTGGGACCCCGTGGAGAGAGTCTC	1560		
Qy	1609	CACAGCTCTCAGGCTCTCTCCACCGCAAGGCGCATTTCTCAAACTCAATGGCAAGTTCT	1668		
Db	1561	CACAGCTCTCAGGCTCTCTCTCCACCGCAAGGCGCATTTCTCAAACTCAATGGCAAGTTCT	1620		
Qy	1669	CCGCGACAGCTTTAGAAGGCACTACCCCTAGACACCTTTGGCTCCCTGGAGCAACTGGCCT	1728		
Db	1621	CCGCGACAGCTTTAGAAGGCACTACCCCTAGACACCTTTGGCTCCCTGGAGCAACTGGCCT	1680		
Qy	1729	CTTCCCATCTTGACGCGCGCCCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC	1788		
Db	1681	CTTCCCATCTTGACGCGCGCCCGCCCTCAGGGGCTGTGAGTGAGGACAGCATCC	1740		
Qy	1789	TGTCTCTCCGAGTCTTTTGAACCAATTTGACTTGTGCTTCCCGAAACCCCACTGA	1848		
Db	1741	TGTCTCTCCGAGTCTTTTGAACCAATTTGACTTGTGCTTCCCGAAACCCCACTGA	1800		
Qy	1849	GGGGCTGTGTGTGTGTGGACAACTGAGGGGGCTTGAGAGCGCTCCCTCAGAAAGTCTGA	1908		

Db 1801 GGGCTGTGTCTGTGTGACAACTGAGGGGCTTGAGCAGCTCCCTCAGAGGTCTGA 1860
Qy 1909 AGCATGGTGGCAGGAATCCTTGGGGATAGCTGCTTTCTCTGACAGACTGCGCAAGG 1968
Db 1861 AGCATGGTGGCAGGAATCCTTGGGGATAGCTGCTTTCTCTGACAGACTGCGCAAGG 1920
Qy 1969 TGACTGAGCCTCAGACAAAGCCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAGGAGA 2028
Db 1921 TGACTGAGCCTCAGACAAAGCCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAGGAGA 1980
Qy 2029 TGGTGCCCTAGTATGGGTAGGCTCTGAGAGGGTTTGAGAGGAACC 2075
Db 1981 TGGTGCCCTAGTATGGGTAGGCTCTGAGAGGGTTTGAGAGGAACC 2027

RESULT 6
AX380986
LOCUS AX380986 2026 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 27 from Patent WO0212456.
ACCESSION AX380986
VERSION AX380986.1 GI:19575826
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1
REFERENCE
AUTHORS Drucker, D.J., Rosen, C.F. and Lefebvre, D.L.
TITLE Ampk-related serine/threonine kinase, designated snark
JOURNAL Patent: WO 0212456-A 27 14-FEB-2002;
1149336 ONTARIO INC. (CA)
FEATURES
source Location/Qualifiers
1..2026
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"

ORIGIN
Query Match 61.0%; Score 1771.4; DB 6; Length 2026;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 1888; Conservative 0; Mismatches 136; Indels 5; Gaps 3;
Qy 49 GTGACCTCTGAGCCGCGGCTCAGCGCGCTGCTACTGCTGCCCGACCCACTCCACTC 108
Db 1 GTGACCTCTGAGCTGCGGCTCTCCGCGGCTGCTGCTGCCCGACCCCTCCGCTC 60
Qy 109 GCGGTCCCGCAGCATGAGTGGTGGCTTACTTCCAGCGCCCGAGCCAGGCTCCCTCG 168
Db 61 GCGGTCCCGCAGCATGAGTGGTGGCTTACTTCCAGCGCCCGAGCCAGGCTCCCTCG 120
Qy 169 CCTCGGCTGGCTCGAGAGCGCCGCGCTGCTGCGGAGCGGCTCATCAAGTCGGCTA 228
Db 121 CCTCGGCTGGCTCGAGAGCGCCGCGCTGCTGCTGCCCGACCCCTCCGCTC 180
Qy 229 AACCTCTGATGAAGAACGAGCGGTGAAGCGGACCATCAAAACACAACTCGGCAAC 288
Db 181 AACCTCTGATGAAGAACGAGCGGTGAAGCGGACCATCAAAACACAACTCGGCAAC 240
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Qy 349 AGAGCTCGGGGCTGCTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC 408
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Qy 409 AGGATCTGTGCATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACACA 468
Db 361 AGGATCTGTGCATACGAGGAGGAGATTGAGATCATGTCTTCACTCAACACCCACACA 420
Qy 469 TCATTGCCATCCATGAAGTGTGTTGAGAAATAGCAAGATGTTGTTGTCATGGATG 528

Db 421 TCATTGCCATCCATGAAGTGTGTTGAGAACAGCAGCAAGATTGATTGTCTATGGAGTACG 480
Qy 529 CCAGCCGAGCGATCTGTATGATTATCATCAGTACAGCGGCCACCGCTGAGTACGCGGACG 588
Db 481 CCAGCCGAGCGATCTGTATGATTATCATCAGTACAGCGGCCACCGCTGAGTACGCGGACG 540
Qy 589 CCAGCCATTTCTTCCGACAGATCGTGTGCGCTGCACTACTGCGCAGCAAGCGGATTCG 648
Db 541 CCAGCCATTTCTTCCGACAGATCGTGTGCGCTGCACTACTGCGCAGCAAGCGGATTCG 600
Qy 649 TTCACCGAGATCTCAAGCTGGAAAAATCTCTTAGATGCCAATGAAACATCAAGATTG 708
Db 601 TTCACCGAGATCTCAAGCTGGAAAAATCTCTTAGATGCCAATGAAACATCAAGATTG 660
Qy 709 CTGACCTTGGCTCTCCAACTGTATCCAAAGGCAAGTTCTTCCAGACGTTCTGTGGGA 768
Db 661 CTGATTTGGCTCTCCAACTGTATCCAAAGGCAAGTTCTTCCAGACGTTCTGTGGGA 720
Qy 769 GCGCTCTACGCTCGCTGAGATAGTCAACGGGAAGCCCTATCTGGGCCAGAGGTG 828
Db 721 GCGCTCTATGCTCACCTGAGATCGTCAACGGGAAGCCCTATCTGGGCCAGAGGTG 780
Qy 829 ACAGCTGCTCTGCGGCTTCTCTGTATCATCTCTGTGATGCCACATGCCCTTTGACG 888
Db 781 ACAGCTGCTCTGCGGCTTCTCTGTATCATCTCTGTGATGCCACATGCCCTTTGACG 840
Qy 889 GGAGGATCATAAACACACTGGTGAAGCAAAATCAGTAAACGGGGTTTACCTGAGCCGCCA 948
Db 841 GGAGGATCATAAACACCTGGTGAAGCAAAATCAGTAAACGGGGTTTACCTGAGCCGTGCA 900
Qy 949 AGCCGTCCTGCTGCTGCGCTGATCCGCTGCTGTTTATGTTGAACCCACCCCTCGGG 1008
Db 901 AACCTGCTGATGCTCTGCGCTGATCCGCTGCTGTTTATGTTGAATCCCATCCCTCGGG 960
Qy 1009 CCACACTGGAGATGTAGCCAGTCACTTGTGGTCAACTGGGGTTTACACACCGAGTTCG 1068
Db 961 CCACACTGGAGATGTAGCCAGTCACTTGTGGTCAACTGGGGTTTACACACCGAGTTCG 1020
Qy 1069 GGGACAGGAAGCCCTGCTGAGGGTGGGACCCCTAGTGGTGAATTTGGCGGGCTTCCA 1128
Db 1021 GGGACAGGAAGCTCTGCGAGAGGGTGGGACCCCTAGCGGTGACTTGGCGGGCTCTA 1080
Qy 1129 TGGCGACTGTTTACGCTGCTCTGCGGCCCTCTCTGAGAGATGAGCAAGGTGTGCA 1188
Db 1081 TGGCGACTGTTTACGCTGCTCTCTCCGCCCTCTCTGAGAAATGGAGCAAGGTGTGTA 1140
Qy 1189 GCTTCTTCAAGCAGCACGTCGCCGGAGGTGGAAGCACTGTACTTGGGCTGGAGCGCAAC 1248
Db 1141 GCTTCTTCAAGCAGCATGTGCCGGAGGTGGAAGCACCGGGCTGGAGCGCAAC 1200
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Db 1201 ATTCTTTAAGAAATCCGCAAGGAGATGACATGGCTCAAAATCTGCAAGATGACCCAG 1260
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Qy 1429 TGCCTGATCTCCAGGAGGCTGCTCCCTGCTGATCTCCCTGCTCCCAAGAAAGGATCC 1488
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Qy 1489 TTAAGAAAGTCTCGACAGCGTGAATCTGTTACTTCTCTCAGAGCCAGCGAGTCTG 1548
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Qy 1549 GGGAACTCTTAGACGCGAGTGAATGTTTGTGAGTGGGAGCCCTGTTGAGCAAGATCTTC 1608

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Db      1501 GGGAACTCTTAGACGCGAGGTGATGTGTTGTAGTGGGAGCCCCGTGGAGCAGAGTCTC 1560
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Db      1561 CACAAGCTTCAGG--CGCTTCATGCGAGGCGATCTCTCAAACTCAATGGCAAGTTT 1617
Qy      1669 CCAGCAGCTTTAGAGGCACTACCTCTAGCACTTTGGCTTCCCTGGACCAACTGGCCT 1728
Db      1618 CCGCAGCAGCTTAGAGGCACTCCCTCTAGCACTTTGGCTTCCCTAGCACTAGCACTGGCCT 1677
Qy      1729 CTTCCCTCTCGAGCGCGCCGCGAGCGCCCTCAGGGGCTGTAGTGGAGCAGCATCC 1788
Db      1678 CCGCTCATCTTACAGCGCGCGCGAGCGCTCCCTCGGAGCTGTAGTGGAGCAGCATCC 1737
Qy      1789 TGTCTCTCGAGCTCTTTGACCAATTTGCACTTGGCTGAACTGCTTCCCGAAACCCCACTGA 1848
Db      1738 TGTCTCTCGAGCTCTTTGACCAATTTGCACTTGGCTGAACTGCTTCCCGAAACCCCACTGA 1797
Qy      1849 GGGCTGTGTCTGTGTGGACAACTGAGGGGCTTTGAGAGCTTCTCTCAGAGAGGTCTGA 1908
Db      1798 GGAGCTGTGTCTGTGTGGACAACTGAGGGGCTTTGAGAGCTTCTCTCAGAGAGGTCTGA 1857
Qy      1909 AGCATGCTGCGAGGATCTTTGGGGGATAGCTGCTTTCTCTCAGAGCTGCGCAAGG 1968
Db      1858 AACGATGCTGCGAGGATCTTTGGGGGATAGCTGCTTTCTCTCAGAGCTGCGCAAGG 1917
Qy      1969 TGACTGCGCTACAGCAAGCCCTAGGAATCTCTCAAGCTCAGCTGAGGAGGAGGA 2028
Db      1918 TGACAGAGCTACAGCAAGCCCTAGGAATCTCTCGAGCTCAGCTGAGGAGGAGG 1977
Qy      2029 TGGTGCCTTAGT-ATGGGGTAGGCTCTGAGA-GGGTTTGACAGGAAACC 2075
Db      1978 CAGTGCCCGAGTGATGGGTAGACTCTTAGAGGGGTTTGACAGGAAACC 2026

RESULT 7
AC125887
LOCUS      291762 bp      DNA      linear      HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS
***, 13 unordered pieces.
AC125887
AC125887.3 GI:25008671
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 291762)
Muzny,D,Marie., Metzker,M, Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsebrook,S., Amin,A., Auguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Blawalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A.,
Chacko,J., Chavez,C., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Dengson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dungan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Evans,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
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Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 291762)
Worley,K.C.

Direct Submission
Submitted (02-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 291762)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23269681.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GWLD
Center clone name: CH230-274J3
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 226053 bases at least Q40
Consensus quality: 230853 bases at least Q30
Consensus quality: 233437 bases at least Q20
Estimated insert size: 233445; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is

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RESULT 10
LOCUS BD127309 3395 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD127309
VERSION BD127309.1 GI:23222254
KEYWORDS JP 2002017375-A/2740.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3395)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
Koga, H.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017375-A/2740
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
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PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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FT CDS (118)..(2001).
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ORIGIN

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VERSION	AK074830.1	GI:22760531	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Isogai, T., Ota, T., Nishikawa, T., Hayaishi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masuh, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Ninomiya, K.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3395)		
AUTHORS	Isogai, T. and Otsuki, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).		
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induction"

118..2004

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ORIGIN

Query Match 47.4%; Score 1375.8; DB 9; Length 3395;

Best Local Similarity 81.7%; Pred. No. 0;

Matches 1652; Conservative 0; Mismatches 337; Indels 34; Gaps 4;

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DB	785	GGAGCCCTATACACAGGCCCGAGAGTGGACAGCTGGTCTCCTGGGTCTCTCCTTACATCC	844
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AUTHORS Haerlach, T.; Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,
Dugas, M., Ellis, R., Brors, B. and Mergenthaler, S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 2508 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haerlach, Torsten,
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 SOURCE

ORGANISM

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REFERENCE

1 (bases 1 to 3443)
 Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 Direct Submission

AUTHORS

TITLE
 JOURNAL
 COMMENT
 Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152
 Martinried, GERMANY
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Charite,
 Berlin/Germany) within the cDNA sequencing consortium of the German
 Genome Project.

This clone (DKFPZp434J037) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
 information about the clone and the sequencing project is available
 at http://mips.gsf.de/proj/cDNA/.

FEATURES

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Qy 1882 TTGAGCAGCTCCTCTCAGAAG-----GTCTGAAGCGATGGTGGCAGGATCCT 1929
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1866 TTGAGGAGCCCCCTCAGAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGAGATCCTT 1925
Qy 1930 TGGGGGATAGTGTCTTTCTGTGACAGACTGCCAAGAGGTGACTGACGCTTACAGACAAG 1989
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1926 TGGGGGACAGTGTCTTTCTGTACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGG 1985
Qy 1990 CCCTAGGAATCTGCTCAAGCTAGCTGAGGAAGGGAGATGGTCCCTAGTATGGGGTAG 2049
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1986 CACTGAGGGTCTGCTCAAAAGCTCACTGAGTGGAGTAGGCAATTGCCCCAG-CCCGGTGAG 2044
Qy 2050 GCTCTGAGAGGGTTTGACAGAGGAACCTGGTCTGATTCCTCC 2092
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2045 GCTCTCAGATGCAGCTGGTTGACCCCGGAGGGAGATGCTCTTC 2087
```

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 05:56:58 ; Search time 1342.36 Seconds
(without alignments)
11348.500 Million cell updates/sec

Title: US-09-980-464-4
Perfect score: 2902
Sequence: 1 cactagtgcacaaagaat.....aaaaaaaaaaaaaaaaaaaaa 2302

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2902	100.0	2902	4 AAC90433	Aac90433 Murine Ly
2	2066.8	71.2	2929	6 AAD31710	Aad31710 Rat SNF1
3	1379	47.5	3353	6 ABK14000	Abk14000 cDNA enco
4	1379	47.5	3353	12 ADL14160	Adl14160 Novel hum
5	1375.8	47.4	3395	4 AAK94280	Aak94280 Human ful
6	1375.8	47.4	3395	12 ADL130885	Adl130885 Full leng
7	1374.2	47.4	3443	5 ABX71420	Abx71420 Human cel
8	1374.2	47.4	3443	10 ADF76964	Adf76964 Novel hum
9	1374.2	47.4	3443	10 ADF81952	Adf81952 Leukaemia
10	1374.2	47.4	3443	12 ADO20171	Ado20171 Human PRO
11	1374.2	47.4	3463	12 ADJ96554	Adj96554 Human cal
12	1372.2	47.3	2501	12 ADM43851	Adm43851 Novel hum
13	1371.8	47.3	2043	6 ABZ11333	Abz11333 Human pol
14	1370.6	47.2	3360	6 AAD26459	Aad26459 Human kin
15	1360.2	46.9	1884	12 ADL14162	Adl14162 Novel hum
16	1349.2	46.5	2291	4 AAF44659	Aaf44659 Novel pro
17	1349.2	46.5	2291	12 ADI29357	Adi29357 Human MAR
18	1323.2	45.6	3200	4 AAF75338	Aaf75338 Human TGF
19	1230	42.4	1833	10 ABZ77163	Abz77163 Human pro
20	849.2	29.3	2616	6 ABQ72599	Abq72599 Human MDD
21	849.2	29.3	2619	6 ABQ72698	Abq72698 Human MDD

22	507.6	17.5	6828	4 AAD14327	Aad14327 Human pro
23	507.6	17.5	6828	10 ADE38420	Ade38420 Human pro
24	507.6	17.5	6828	11 ADN95767	Adn95767 Human BEC
25	507.6	17.5	6828	12 ADJ74808	Adj74808 Marker ge
26	507.6	17.5	6828	12 ADL25352	Adl25352 Human ARK
27	507.6	17.5	6828	12 ADQ19733	Adq19733 Human sof
28	507.6	17.5	6828	12 ADP43253	Adp43253 Human sof
29	507.6	17.5	6854	12 ADQ23883	Adq23883 Human sof
30	506.4	17.5	2884	4 AAD14328	Aad14328 Human pro
31	360.2	12.4	587	4 AAK93296	Aak93296 Human CDN
32	360.2	12.4	587	4 AAK91887	Aak91887 Human CDN
33	360.2	12.4	587	12 ADL29723	Adl29723 5' end of
34	360.2	12.4	587	12 ADL28314	Adl28314 5' end of
35	356.8	12.3	3594	5 AAD03994	Aad03994 Human pro
36	296.8	10.2	1454	4 ABL21269	AbL21269 Drosophil
37	268.2	9.2	1723	4 AAH13802	Aah13802 Human CDN
38	236.6	8.2	1594	4 AAF44655	Aaf44655 Novel pro
39	236.6	8.2	1594	8 AAL60326	Aal60326 Human 207
40	236.6	8.2	1594	12 ADI29353	Adi29353 Mouse MAR
41	236.6	8.2	3170	6 ABA05737	Abao5737 Murine ne
42	236.6	8.2	3250	6 ABA05738	Abao5738 Murine ne
43	233.6	8.0	1549	6 ABS64386	Abse64386 Human ser
44	233.6	8.0	2085	8 AAD51409	Aad51409 Human mic
45	233.6	8.0	2085	10 ADG91747	Adg91747 Human mic

ALIGNMENTS

RESULT 1
AAC90433
ID AAC90433 standard; cDNA; 2902 BP.

AC AAC90433;

XX 19-MAR-2001 (first entry)

DE Murine Lymph node Stromal cell kinase 1 coding sequence.

KW Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder;
KW wound healing; periodontal disease; inflammatory disease; tumour;
KW infection; allergy; ss.

OS Mus musculus.

XX WO2000073468-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014696.

XX 28-MAY-1999; 99US-0136781P.

XX (IMMV) IMMUNEX CORP.

XX Bird TA, Virca GD, Martin U, Anderson DM;

XX WPI; 2001-061546/07.

XX P-PSDB; AAB50056.

XX Novel murine and human kinase nucleic acids useful for treating
XX inflammations, infections, tumors, allergies, autoimmune diseases, and
XX for stimulating or suppressing immune responses.

XX Claim 1; Page 86-87; 106pp; English.

XX The present sequence is the coding sequence for Murine Lymph node Stromal
XX cell kinase 1 (MLSK-1). The protein encoded by the present sequence is
XX useful for treating a variety of disorders listed in the disclosure of
XX the specification, including autoimmune disorders, allergic reactions,
XX myeloid or lymphoid cell deficiencies, wound healing and tissue repair,
XX and replacement, burns, incisions and ulcers, periodontal disease,
XX inflammatory diseases, tumours and bacterial, viral or fungal infection

XX	Sequence	2902 BP; 654 A; 794 C; 796 G; 658 T; 0 U; 0 Other;
SQ	Query Match	100.0%; Score 2902; DB 4; Length 2902;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2902; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CAC TAGTGGATCCAAAGATTGCGCAGGAGCGCTGCTCGGTGCGGTGTGACCTCTGAG 60
DB	1	CAC TAGTGGATCCAAAGATTGCGCAGGAGCGGTGCTCGGTGCGGTGTGACCTCTGAG 60
QY	61	CCC CGGCTCAGCGCGCTCTACTGCTGCCGACCCACCTCCACCTCGCGGTCCCGGCA 120
DB	61	CCC CGGCTCAGCGCGCTCTACTGCTGCCGACCCACCTCCACCTCGCGGTCCCGGCA 120
QY	121	CCATGGAGTGGTGGCTTACTCAGGCGCCGAGCGAGCTCCCTCGGCTCGCGCTCGG 180
DB	121	CCATGGAGTGGTGGCTTACTCAGGCGCCGAGCGAGCTCCCTCGGCTCGCGCTCGG 180
QY	181	CCTCGAGAGCGCCGCGCTGCGGACGGCTCATCAAGTCCCTAAACCTCTGATGA 240
DB	181	CCTCGAGAGCGCCGCGCTGCGGACGGCTCATCAAGTCCCTAAACCTCTGATGA 240
QY	241	AGAACGAGCGGTGAAGCGGCAACATCAAAACAACCTCGCGCACCGCTACGAGTTC 300
DB	241	AGAACGAGCGGTGAAGCGGCAACATCAAAACAACCTCGCGCACCGCTACGAGTTC 300
QY	301	TGGAGACGCTGGCAAGGCGACCTACCGGAGGTGAAGAGGACGAGAGCTCGGGGC 360
DB	301	TGGAGACGCTGGCAAGGCGACCTACCGGAGGTGAAGAGGACGAGAGCTCGGGGC 360
QY	361	GTCTGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCAGGATCTGTGC 420
DB	361	GTCTGTGGCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGCAGGATCTGTGC 420
QY	421	ACATACGAGGAGATTGAGATCATGCTTCACTCAACCCACCATCATTTGCCATCC 480
DB	421	ACATACGAGGAGATTGAGATCATGCTTCACTCAACCCACCATCATTTGCCATCC 480
QY	481	ATGAAGTGTGAGATGAGCAGGAGATTGATGTGATGTCATGAGTATGCCAGCGGCG 540
DB	481	ATGAAGTGTGAGATGAGCAGGAGATTGATGTGATGTCATGAGTATGCCAGCGGCG 540
QY	541	ATCTGTATGATTAATCAGTGGCGGCGACGGCTGAGTGGAGCGGACGCCAGGCAATTCT 600
DB	541	ATCTGTATGATTAATCAGTGGCGGCGACGGCTGAGTGGAGCGGACGCCAGGCAATTCT 600
QY	601	TCCGACAGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB	601	TCCGACAGATCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY	661	TCAAGCTGGAAGAACATCCTTCTAGATGCCAATGMAACATCAAGTGTGCTGCTGCTG 720
DB	661	TCAAGCTGGAAGAACATCCTTCTAGATGCCAATGMAACATCAAGTGTGCTGCTGCTG 720
QY	721	TCTCCACCTGTATACCAAGGCAAGTTCCTCCAGAGCTTCTGAGGAGCCCTCTCTACG 780
DB	721	TCTCCACCTGTATACCAAGGCAAGTTCCTCCAGAGCTTCTGAGGAGCCCTCTCTACG 780
QY	781	CCTCGCTGAGATGATCAAGGAGCCCTATGTTGGGCCAGAGGTGGAACAGTGTGCTC 840
DB	781	CCTCGCTGAGATGATCAAGGAGCCCTATGTTGGGCCAGAGGTGGAACAGTGTGCTC 840
QY	841	TGGCGCTTCTCTGTATACCTCTGTGATGCCACCATGCTTGTGAGGCGAGGATCAT 900
DB	841	TGGCGCTTCTCTGTATACCTCTGTGATGCCACCATGCTTGTGAGGCGAGGATCAT 900
QY	901	AAACACTGTGTAAGCAAAATCAGTAACGGGCTTACCGTGGAGCGGCCCAAGCCGTCG 960
DB	901	AAACACTGTGTAAGCAAAATCAGTAACGGGCTTACCGTGGAGCGGCCCAAGCCGTCG 960
QY	961	CTGTGGCTGATCCGGTGTCTTAATGTGTAAACCCCGCTCGGGCCACACTGAGG 1020
DB		CTGTGGCTGATCCGGTGTCTTAATGTGTAAACCCCGCTCGGGCCACACTGAGG 1020

DB	961	CTGTGGCTGATCCGGTGTCTTAATGTGTAAACCCCGCTCGGGCCACACTGAGG 1020
QY	1021	ATGTAGCAGTCAATGGTGGTCAACTGGGTTTACACACCGAGTGGGAAACAGGAAG 1080
DB	1021	ATGTAGCAGTCAATGGTGGTCAACTGGGTTTACACACCGAGTGGGAAACAGGAAG 1080
QY	1081	CCCTGGTGGGTTGGGCAACCTAGTGGTACATTTGGCGGGGCTCCATGGCGGACTG 1140
DB	1081	CCCTGGTGGGTTGGGCAACCTAGTGGTACATTTGGCGGGGCTCCATGGCGGACTG 1140
QY	1141	TACGTGCTCTCTCGCGCCCTCTCTGAGAAATGAGACCAAGGTGTGAGCTTCTTCAAGC 1200
DB	1141	TACGTGCTCTCTCGCGCCCTCTCTGAGAAATGAGACCAAGGTGTGAGCTTCTTCAAGC 1200
QY	1201	AGCAGTGGCGGAGGTGAGACCTGTGTACCTGGCTGGAGCGGCAACATTTCTTAAAG 1260
DB	1201	AGCAGTGGCGGAGGTGAGACCTGTGTACCTGGCTGGAGCGGCAACATTTCTTAAAG 1260
QY	1261	AGTCCCGAAGGAGATGATGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCT 1320
DB	1261	AGTCCCGAAGGAGATGATGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCT 1320
QY	1321	CTTCTCGCTCGCAAGAGCAGCTTTAAGCTTCCGAAAGGCATTTCTCAAGAAAAGTCT 1380
DB	1321	CTTCTCGCTCGCAAGAGCAGCTTTAAGCTTCCGAAAGGCATTTCTCAAGAAAAGTCT 1380
QY	1381	CTACCTGTGAGGAGGTACAGGAGACCTCAGAACTCAGACCGGTGCTGATCTC 1440
DB	1381	CTACCTGTGAGGAGGTACAGGAGACCTCAGAACTCAGACCGGTGCTGATCTC 1440
QY	1441	CAGGCGAGCTGTCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB	1441	CAGGCGAGCTGTCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY	1501	GACAGCTGAATCTGTTTACTCTCTCTCAGAGCCGAGCGAGTCTGGGAACTCTTAG 1560
DB	1501	GACAGCTGAATCTGTTTACTCTCTCTCAGAGCCGAGCGAGTCTGGGAACTCTTAG 1560
QY	1561	ACGCCAGTGTGTTTGTGAGTGGGAGCCCGTGGAGCAGAGTCTCCACAGGCTTCAG 1620
DB	1561	ACGCCAGTGTGTTTGTGAGTGGGAGCCCGTGGAGCAGAGTCTCCACAGGCTTCAG 1620
QY	1621	GGCTCTCTCTCCACCCCAAGGCAATTTCTCAAACTCAATGGCAAGTTCCTCCGACAGCCT 1680
DB	1621	GGCTCTCTCTCCACCCCAAGGCAATTTCTCAAACTCAATGGCAAGTTCCTCCGACAGCCT 1680
QY	1681	TAGAAGCACTACCTCTAGACCTTTGGCTCTCTGACCAACTGGCTCTCTCCATCTCTG 1740
DB	1681	TAGAAGCACTACCTCTAGACCTTTGGCTCTCTGACCAACTGGCTCTCTCCATCTCTG 1740
QY	1741	CAGCCCGGCGGCGCCCTCAGGGCTGTGAGTGGAGCAGCATCTCTCTCTCTCTCTCT 1800
DB	1741	CAGCCCGGCGGCGCCCTCAGGGCTGTGAGTGGAGCAGCATCTCTCTCTCTCTCTCT 1800
QY	1801	CTTTTGACCAATTTGAGCTTGTCTGAACTCTTCCGAAACCCCACTGAGGGGCTGTGTGT 1860
DB	1801	CTTTTGACCAATTTGAGCTTGTCTGAACTCTTCCGAAACCCCACTGAGGGGCTGTGTGT 1860
QY	1861	CTGTGAGCAACCTGAGGGGCTTGGAGCGCTCTCTCAGAACTGTGAAGCGATGTGTGC 1920
DB	1861	CTGTGAGCAACCTGAGGGGCTTGGAGCGCTCTCTCAGAACTGTGAAGCGATGTGTGC 1920
QY	1921	AGGAATCTTTGGGAGTGTCTCTGACAGCTGCAAGAGGTGACTTCTCTCTCTCTCTCT 1980
DB	1921	AGGAATCTTTGGGAGTGTCTCTGACAGCTGCAAGAGGTGACTTCTCTCTCTCTCTCT 1980
QY	1981	ACAGCAAGCCCTTAGGAATCTCTCAAACTCAGCTGAGGAAAGGAGATGTGTCTCTCT 2040
DB	1981	ACAGCAAGCCCTTAGGAATCTCTCAAACTCAGCTGAGGAAAGGAGATGTGTCTCTCT 2040
QY	2041	ATGGGGTGTGCTGTGAGGAGTTCAGAGGAACTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
DB	2041	ATGGGGTGTGCTGTGAGGAGTTCAGAGGAACTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100

```
QY 2101 GAGTACATCAAGGGCTCTAGCTCTGCGAGCTGACTGAACCTGAAAGATGAGAAATCGC 2160
DB 2101 GAGTACATCAAGGGCTCTAGCTCTGCGAGCTGACTGAACCTGAAAGATGAGAAATCGC 2160
QY 2161 ATTGATGTGAAAGGAATGGAAACCCCTGTGTCGCCGAGTGTATAGTGGGGTGGCCTGAA 2220
DB 2161 ATTGATGTGAAAGGAATGGAAACCCCTGTGTCGCCGAGTGTATAGTGGGGTGGCCTGAA 2220
QY 2221 GGTGCTTACCTCTCTTGTGCGCATGAGTGTACCCATGACATTTCCACCCCTGTCTCTGG 2280
DB 2221 GGTGCTTACCTCTCTTGTGCGCATGAGTGTACCCATGACATTTCCACCCCTGTCTCTGG 2280
QY 2281 CTGCACCTTCACATAAGTCTTCTGTTTCCATCAACACCCAGGGTTAGAACCTCGACTTCCT 2340
DB 2281 CTGCACCTTCACATAAGTCTTCTGTTTCCATCAACACCCAGGGTTAGAACCTCGACTTCCT 2340
QY 2341 GGGAGGTAAATGTGTAGTACTGCCATTAATTTAGAGAGAAACAGCCTCTGGTTTCCATCT 2400
DB 2341 GGGAGGTAAATGTGTAGTACTGCCATTAATTTAGAGAGAAACAGCCTCTGGTTTCCATCT 2400
QY 2401 CTGCTGTGTGCATCTCAAGAGACTGGGAAGACTCGGACCGCTGTTTGTGACTTCTATCTCA 2460
DB 2401 CTGCTGTGTGCATCTCAAGAGACTGGGAAGACTCGGACCGCTGTTTGTGACTTCTATCTCA 2460
QY 2461 GGGGACAGATGCCCTCGACCCCATCTTAGATCTCAGAGACTTGAACCTTGAAGCTGTT 2520
DB 2461 GGGGACAGATGCCCTCGACCCCATCTTAGATCTCAGAGACTTGAACCTTGAAGCTGTT 2520
QY 2521 CCTAGTACCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAAATGTC 2580
DB 2521 CCTAGTACCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAAATGTC 2580
QY 2581 TGACTTATTTATTTTGTGTGATCTCAGTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 2640
DB 2581 TGACTTATTTATTTTGTGTGATCTCAGTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 2640
QY 2641 TTTTGTGTTTAAAGTGAATTTTGTGCTTTCAATAATGTAATGCTGTGTTTCTGGGGAAC 2700
DB 2641 TTTTGTGTTTAAAGTGAATTTTGTGCTTTCAATAATGTAATGCTGTGTTTCTGGGGAAC 2700
QY 2701 TCCACTGTGCTGCTGAAAGTTATGTACAGAGATATTTGGCAATGATGTCCTCTATTC 2760
DB 2701 TCCACTGTGCTGCTGAAAGTTATGTACAGAGATATTTGGCAATGATGTCCTCTATTC 2760
QY 2761 AAGGGGGTGGGGCGTTTTCAAATGTATGCTTGGAGCTGCTGGATTGATCTCCA 2820
DB 2761 AAGGGGGTGGGGCGTTTTCAAATGTATGCTTGGAGCTGCTGGATTGATCTCCA 2820
QY 2821 GTCCCTTTCACACCCAGGCTGGCCACCCTCCCTCATCTTTCATCTGTGGCCAAAAA 2880
DB 2821 GTCCCTTTCACACCCAGGCTGGCCACCCTCCCTCATCTTTCATCTGTGGCCAAAAA 2880
QY 2881 AAAAAAAAAAAAAAAAAAAAAA 2902
DB 2881 AAAAAAAAAAAAAAAAAAAAAA 2902

RESULT 2
AAD31710
ID AAD31710 standard; cdna; 2929 BP.
XX
AC AAD31710;
XX
XX
DT 18-JUN-2002 (first entry)
XX
DE DE
XX
KW Rat; SNF1/AMPK-Related Kinase (SNARK) cdna.
XX
KW Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes;
XX
KW glucose deprivation; lipid metabolism; therapy; lipoprotein disorder;
XX
KW hyperglycaemic; drug screening; hypoglycaemia; ss.
XX
OS Rattus sp.
```

```
XX Key Location/Qualifiers
PH CDS 83..1975
FT /tag= a
FT /product= "Rat SNARK protein"
XX
XX MO200212456-A2.
XX
XX 14-FEB-2002.
XX
XX 02-AUG-2001; 2001WO-CA001109.
XX
XX 03-AUG-2000; 2000US-0222650P.
XX
XX 12-MAR-2001; 2001US-0274613P.
XX
XX 28-MAR-2001; 2001CA-02340783.
XX
XX (ONEO-) 1149336 ONTARIO INC.
XX
XX Drucker DJ, Rosen CF, Lefebvre DL;
XX
XX WPI; 2002-241747/29.
XX
XX P-PSDB; AAE19885.
XX
XX AMPK (AMP-activated protein kinase)-related kinase, designated SNARK
XX
XX polypeptides and polynucleotides, useful for treating or preventing
XX
XX diabetes, or other disorders of lipoprotein production leading to
XX
XX increased levels of cholesterol.
XX
XX Example; Fig 2; 94pp; English.
XX
XX The invention relates to an AMPK (AMP-activated protein kinase)-related
XX
XX kinase, designated SNARK polypeptides and polynucleotides. SNARK
XX
XX (SNIF/AMP-activated protein kinase) is involved in stress response to
XX
XX glucose deprivation. The polynucleotides are useful for expressing SNARK
XX
XX protein in isolated form or as a protein conjugate. Activation of SNARK
XX
XX stimulates liver CPT-1 thus enhances lipid metabolism in liver cells and
XX
XX in other cell types such as heart and skeletal muscles, as well as
XX
XX increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted
XX
XX to have insulin-like effects that would enhance the disposal of glucose
XX
XX into muscle and reduce plasma glucose for the treatment of diabetes and
XX
XX some type of disorders of lipoprotein production leading to increased
XX
XX levels of cholesterol or triglycerides. SNARK or its variants may be
XX
XX administered to a subject to treat or prevent a disease associated with
XX
XX decreased expression of SNARK, such as diabetes. SNARK antibodies are
XX
XX used to modulate SNARK activity either in vivo for therapeutic purposes,
XX
XX or in vitro, for drug screening and related investigational purposes.
XX
XX SNARK antagonists may be administered to increase fuel production,
XX
XX decrease glucose uptake and increase levels of blood glucose in a patient
XX
XX suffering from hypoglycaemia. The present sequence is rat SNARK cdna
XX
XX
XX Sequence 2929 BP; 650 A; 788 C; 791 G; 700 T; 0 U; 0 Other;
XX
XX
XX Query Match 71.2%; Score 2066.8; DB 6; Length 2929;
XX
XX Best Local Similarity 86.4%; Pred. No. 0;
XX
XX Matches 2488; Conservative 0; Mismatches 277; Indels 115; Gaps 14;
XX
XX
XX QY 49 GTGACCTCTGAGCCCGGCTCAGCGCTGCTACTGCTGCCGCCACCTCCACCTC 108
XX
XX DB 9 GTGACCTCTGAGCTCGGCTCTCCGCGCTGCTGCTGCCGCCACCTCCCGCTC 68
XX
XX
XX QY 109 GCGGTCCCGCACCATGGAGTGGTGGCTTACTCCAGCGCCCGAGGCTCCCTCGG 168
XX
XX DB 69 GCGGTCCCGCACCATGGAGTGGTGGCTTACTCCAGCGCGGGAACCTGGCTCCCTCGG 128
XX
XX
XX QY 169 CTTCCGCTTGGCTCGGAGAGCGCGCGCTGCGGAGCGGCTCATCAAGTCGCTA 228
XX
XX DB 129 CTTCCGCTTGGCTCGGAGAGCGCGCGCTGCGGAGCGGCTCATCAAGTCGCTA 188
XX
XX
XX QY 229 AACCTCTGATGAAGAAGAGCGGCTGAAGCGGACCATCAACAACCACTCGGGCACC 288
XX
XX DB 189 AACCTCTGATGAAGAAGAGCGGCTGAAGCGGACCATCAACAACCACTGAGGACC 248
XX
XX
XX QY 289 GCTACGAGTTCTTGGAGACGCTGGGCAAGGSCACTACGGGAAGGTGAAGAAGCAGAG 348
```


Db 704 TGGATGCCAATGGGAATATCAAGATTGCTGACTTCGGCTCTCCAACTCTACCATCAAG 763
Qy 742 GCAAGTTCTCCAGACGTTCTGTGGAGCCCTCTACAGCCCTCGCTGAGATAGTCAAG 801
Db 764 GCAAGTTCTCCAGACATTTCTGTGGAGCCCTCTATGCTTCGCCAGAGATTGCAATG 823
Qy 802 GGAAGCCCTATGTGGGCCCCAGAGGTGGACAGTCTGTCTGTGGGGTCTCTCTGTACATCC 861
Db 824 GGAAGCCCTACAGGCCCCAGAGGTGGACAGTCTGTCTGTGGGGTCTCTCTGTACATCC 883
Qy 862 TGGTGCATGGCACCATGCCCTTTGACGGGACAGGATCATAAACACTGGTGAAGCAAAATCA 921
Db 884 TGGTGCATGGCACCATGCCCTTTGATGGGATGACCATAGATCTAGTGAACAGATCA 943
Qy 922 GTAACGGGGTTACCGTACGGCCCAAGCGTCCGATGCTGTGGCTGATCCGCTGTC 981
Db 944 GCAACGGGGCTTACCGGGAGCCACTAAACCCCTGTGATGCTGTGGCTGATCCGGTGGC 1003
Qy 982 TGTTAATGGTGAACCCCAACCGCTGGGCCCACTGAGGATGTAGCCAGTCAATTTGGTGG 1041
Db 1004 TGTGTATGGTGAACCCCAACCGCGGGCCACCTTGGAGGATGTGGCCAGTCACTGGTGGG 1063
Qy 1042 TCAACTGGGTTACACACCGGAGTCCGGGAAACAGGAAGCCCTGCGTGAGGGTGGGCACC 1101
Db 1064 TCAACTGGGCTACGCCACCGAGTGGGAGACGAGGAGCTCCGATGAGGGTGGGCACC 1123
Qy 1102 CTAGTGTGATTTGGCGGGCCCTCATGGGAGTCTGGTACGTCGCTCTCGGGCCCCC 1161
Db 1124 CTGGCAGTGTCTGCGCGGGCCCTCCATGGCTGAGTGGCTCCGGCGTTCCTCCGGCCCC 1183
Qy 1162 TCCTGGAGATGGAGCAAGTGTGACGTTCTTCAAGCAGCAGCTGCCGGGAGTGGAA 1221
Db 1184 TCCTGGAGATGGGCCCAAGTGTGACGTTCTTCAAGCAGCAGTGCACCTGTGGGGGAA 1243
Qy 1222 GCACTGTACTGGGCTGGAGCGGCAACATTTCTTTAAGAAAGTCCCGAAGGAGAATGACA 1281
Db 1244 GCACCACTGGGCTGGAGCGCCAGCATTCGCTCAAGAAAGTCCCGAAGGAGAATGACA 1303
Qy 1282 TGGCTCAAAATCTGCAAGGTGACCGGCTGAGGATCTCTTTCGCGCTTGGCAGAGCA 1341
Db 1304 TGGCCCCAGTCTCTCCAGTGAACGCGCTGATGACACTGCGCCATGCGCTGGCAAGAGCA 1363
Qy 1342 GCCTTAAGTCTCCGAAGGATTTCAAGAAAGTCTCTACTCTGTGAGGGAGGTAC 1401
Db 1364 ACTCAAGCTGCCAAGGGATTTCAAGAAAGTGTGAGCTCTGCAAGAGGGTAC 1423
Qy 1402 AGGAGGACCTTCAGGAATCAGACCGGTGCTGATCTCCAGGCGACGCTGTCCCTGCTG 1461
Db 1424 AGGAGGACCTTCGGAGCTCAGCCCAATCCCTGCGAGCCAGGCGAGCTGCC----- 1477
Qy 1462 TATCCCTGCTCCCAAGGAAGGATCTTAAAGTCTCAGACGCTGAATCTGGTTACT 1521
Db 1478 ---CCCTGCTCCCAAGGAAGGATTTCAAGAAAGTCTCAGAGGCGCCGACAGCGGCTACT 1534
Qy 1522 ACTCTCTCCAGAGCCAGCGAGTCTGGGAACTCTTAGACGCGAGTGTGTTGTGA 1581
Db 1535 ACTCTCTCCAGAGCCAGTGAATCTGGGAGCTCTTGGAGCGAGGCGAGTGTGTTGTGA 1594
Qy 1582 GTGGGAGCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCTCTCCACCGCAAGG 1641
Db 1595 GTGGGATCCCAAGGAGCAGAGCTCCGCAAGCTTCAGGGCTCTCTCCATCGCAAG 1654
Qy 1642 GCATTTCAACTCAATGGCAAGTCTCCGCGCAGAGCTTAGAGGCACTACCCCTAGCA 1701
Db 1655 GCATCTCAAACTCAATGGCAAGTCTCCAGACAGCCTTAGAGCTCGCGGCCCCACCA 1714
Qy 1702 CCTTTGGCTCCCTGGACCAACTGGCTCTCCATCTGAGCCCGCCAGCGCCCT 1761
Db 1715 CCTTCGGCTCCCTGGATGAATCGCCCCACTGCCCCCTGGCCCGGGCCAGCGACCT 1774
Qy 1762 CAGGGCTGTGATGAGGACAGCATCTGTCTCCGAGTCTTTGACCAATTTGACTTGC 1821

Db 1775 CAGGGCTGTGAGCGAGGACAGCATCTGTCTCTGAGTCTCTTGACCAGCTGACTGC 1834
Qy 1822 CTGAACGTTCTCCGAAACCCCACTGAGGGCTGTGTCTGTGTGGAACAACCTGAGGGGC 1881
Db 1835 CTGAACGTTCTCCGAGACCCCACTGCGGGCTGTGTCTGTGTGGAACAACCTCAGGGGC 1894
Qy 1882 TTGAGCAGCTCTCTCAGAAAG-----GTCTGAAGCGATGTTGSCAGGAATCCT 1929
Db 1895 TTGAGAGCCCTCTCAGAGGGCCCTGGAAGCTGCTGAGGCGCTGGCGCAGATCCTT 1954
Qy 1930 TGGGGATAGTCTCTTTCTCTGACAGACTGCCAAGAGTGACTGACGCTACAGACAAG 1989
Db 1955 TGGGGACAGCTGCTTTTCTCTGACAGACTGCCAAGAGTGAACGACCTACCGACAG 2014
Qy 1990 CCTGAGATCTCTCAAGCTCAGCTGAGGAAGGAGATGTTGCCCTAGTATGGGGTAG 2049
Db 2015 CACTGAGGGTCTCTCAAGCTCAGCTGAGTGGAGTAGGCAATGCCCCAG-CCCGGTGAG 2073
Qy 2050 GCTCTCAGAGGGTTCGACAGGAACTTGGTTCGAGTTCCTCC 2092
Db 2074 GCTCTCAGATGAGCTGGTTGACCCCGAGGAGATGCTTC 2116

RESULT 4
ADL14160
ID ADL14160 standard; cDNA; 3353 BP.
XX ADL14160;
XX DT 17-JUN-2004 (first entry)
XX Novel human gene 3700 cDNA.
DE
XX
KW cyostatic; cardiac; hypotensive; antiangiogenic; osteopathic;
KW antiarthritic; antirheumatic; neuroprotective; antiinflammatory;
KW antipsoriatic; antiasthmatic; cardiovascular; virucide; analgesic; CNS;
KW angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective;
KW nephrotropic; antithyroid; dermatological; immunomodulator;
KW cell proliferation disorder; cell differentiation disorder;
KW brain disorder; platelet disorder; breast disorder; colon disorder;
KW kidney disorder; renal disorder; lung disorder; ovarian disorder;
KW prostate disorder; cervical disorder; spleen disorder; thymus disorder;
KW thyroid disorder; testes disorder; haematopoietic disorder;
KW pancreatic disorder; skeletal muscle disorder; skin disorder;
KW dermal disorder; bone metabolism disorder; immune disorder;
KW inflammatory disorder; cardiovascular disorder;
KW endothelial cell disorder; liver disorder; erythroid disorder;
KW metabolic disorder; neurological disorder;
KW central nervous system disorder; erythroid disorder;
KW blood vessel disorder; angiogenic disorder; cancer; heart failure;
KW hypertension; angina; osteoarthritis; rheumatoid arthritis;
KW multiple sclerosis; Crohn's disease; psoriasis; asthma;
KW cell proliferation; cell differentiation; cell growth; cell division;
KW human; gene; ss.
XX
OS Homo sapiens.
XX
XX US2004058355-A1.
XX
XX 25-MAR-2004.
XX
XX 25-APR-2003; 2003US-00423543.
XX
XX 30-SEP-1998; 98US-00163821.
PR 27-JAN-1999; 99US-0117580P.
PR 25-MAR-1999; 99US-00276400.
PR 30-JUL-1999; 99US-00365162.
PR 09-SEP-1999; 99US-00392189.
PR 05-OCT-1999; 99US-00412210.
PR 23-NOV-1999; 99US-00448076.
PR 29-FEB-2000; 2000US-0186061P.
PR 28-APR-2000; 2000US-0200688P.
PR 19-MAY-2000; 2000US-0205447P.

Db 1064 TCAACTGGGGCTACGCCACCCGAGTGGGAGAGCAGGAGCTCCGATGAGGGTGGGCACC 1123
Qy 1102 CTAGTGTGATTTGGCGGGCTCCATGGCGGAGTGGTTAGCTCGCTCTCGCGCCCCC 1161
Db 1124 CTGCGAGTGAATGCGCGGCGCTCCATGGCTGAGTGGCTCCGCGGTTCCTCCGCGCCCC 1183
Qy 1162 TCCTGGAGATGGAGCAGGAGTGGAGTCTTCAAGCAGCAGCTGCGCGGAGTGGAA 1221
Db 1184 TCCTGGAGATGGGCGCAGGAGTGGAGTCTTCAAGCAGCAGCTGCGCGGAGTGGAA 1243
Qy 1222 GCATGTACCTGGGCTGGAGCGGCAACATCTTTAAGAACTCCCGAAGAGAGATGACA 1281
Db 1244 GCACACCCCTGGGCTGGAGCGGCGAGCATTCGCTCAAGAGTCCCGAAGGAGATGACA 1303
Qy 1282 TGGCTCAAAATCTGCAAGTGAACCGGCTGAGGATACCTCTTCTCGGCTGGCGAAGAGCA 1341
Db 1304 TGGCCCAATCTCTCCAGTGAACCGGCTGATGACACTGCGCCATCGCGCTGGCAAGAGCA 1363
Qy 1342 GCCTTAAGCTTCCGAAAGGCAATCTCAAGAAAGTCTCTTACCTCTGTCAGGGGAGGTAC 1401
Db 1364 ACCTCAAGCTGCCAAGGGCAATCTCAAGAAAGTGTGAGCTCTGCGAAGGGGTAC 1423
Qy 1402 AGGAGACCTTCAGAACTCAGACCGGTGCTGATCTCCAGGCGAGCTGTCCCTGCTG 1461
Db 1424 AGGAGACCTTCAGGAGTCAAGCCAAATCCCTGGAGCCCGAGGCGAGGCTGCC- 1477
Qy 1462 TATCCCTGCTCCCAAGGAGGCAATCTTAAGAGTCTGACAGCGTGAATCTGGTTACT 1521
Db 1478 ---CCCTGCTCCCAAGGAGGCAATCTCAAGAAAGCCCGCAGCAGCGAGTCTGGCTACT 1534
Qy 1522 ACTCTCTCCAGAGCCAGCGAGTCTGGGGAATCTTTAGAGCGCCAGTGAATGTTCTGA 1581
Db 1535 ACTCTCTCCAGAGCCAGTGAATCTGGGAGTCTTTGAGCGAGGCGAGTGTGTTGA 1594
Qy 1582 GTGGGACCCGCTGGAGCAGAAAGTCTCCAGGCTTCAGGCTCTCTCCACCGCAAG 1641
Db 1595 GTGGGATCCCAAGGAGCAGAAAGCTCCGAAAGTTCAGGCTCTCTCCATCGCAAG 1654
Qy 1642 GCATTCCTCAACTCAAGTGAAGTCTCCGCGAGCTTAGAAGGCACTACCTTAGCA 1701
Db 1655 GCATTCCTCAACTCAAGTGAAGTCTCCGCGAGCTTAGAGCTCGCGGCGCCCA 1714
Qy 1702 CCTTTGGCTCCCTGGACCAACTGGGCTCTCCATCTCGAGCGCGGCGCGCCCT 1761
Db 1715 CCTCGGCTCCCTGGATGAATCGCCCACTCGCCCTCGCGCGGCGAGCGACCT 1774
Qy 1762 CAGGGCTGTAGTGAGCAGCAATCTGCTCCGAGTCTTTGACCAATGAGCTTC 1821
Db 1775 CAGGGCTGTGAGCGAGCAGCAATCTGCTCTGAGTCTCTTGAACAGCTGACTTC 1834
Qy 1822 CTGAACGCTCTTCCGAAACCCCTGAGGGGCTGTGTCTGTGACAACTGAGGGGC 1881
Db 1835 CTGAACGGCTCCAGAGCCCTCTGCGGGCTGTGTCTGTGACAACTCAGCGGC 1894
Qy 1882 TTGAGCAGCTCTCTCAGAAAG-----GTCTGAAGCAGATGTGTGCGAGATTCCT 1929
Db 1895 TTGAGGAGCCCTCTCAGAGGGCCCTTGAAGCTGCTTGAAGCGCTGCGCGAGATTCCT 1954
Qy 1930 TGGGGATAGCTGCTTTTCTGACAGACTGCCAAGAGGTGACTGACGCTTACAGACAAG 1989
Db 1955 TGGGGGACAGCTGCTTTTCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGCAGG 2014
Qy 1990 CCTTAGGAATCTGCTCAAGCTCAGCTGAGGAGGAGATGTTGCCCTAGTATGGGGTAG 2049
Db 2015 CACTGAGGGTCTGCTCAAGACTTACCTGAGTGAAGTAGGCAATGGCCCCAG-CCCGGTGAG 2073
Qy 2050 GCTCTGAGAGGGTTTGAGAGGAACTCTGGGTGCGATTCCTCC 2092
Db 2074 GCTCTCAGATGCAGCTGTTGTCACCCCGAGGGGAGATGCTCTC 2116

RESULT 5
AAK94280

ID AAK94280 standard; cDNA; 3395 BP.
XX
AC AAK94280;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human full-length cDNA, SEQ ID NO: 2918.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
XX Homo sapiens.
XX OS
XX EP1130094-A2.
XX
XX PD 05-SEP-2001.
XX
XX PF 07-JUL-2000; 2000EP-00114089.
XX
XX PR 08-JUL-1999; 99JP-00194486.
XX
XX PR 11-JAN-2000; 2000JP-00118774.
XX
XX PR 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX PI Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX DR WPI; 2001-524255/58.
XX DR P-PSDB; AAM93360.
XX
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX
XX PS Claim 8; SEQ ID NO 2918; 1380pp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesising full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesising the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a full length human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in CD-ROM format directly
XX from EPO
SQ Sequence 3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;

Query Match 47.4%; Score 1375.8; DB 4; Length 3395;
Best Local Similarity 81.7%; Pred. NO. 4.2e-294;
Matches 1652; Conservative 0; Mismatches 337; Indels 34; Gaps 4;
Qy 82 CTACTCTGCTCCGAGCCCACTCCACCTCGGGTCCCGCACCACCTGGAGTGGTGGCTTAC 141
Db 77 CTACTGATTCCTGCGGCTTGTCTACCTCTGCTCGCCATGGAGTGGTGGTTCG 136
Qy 142 TCAGCGCCGAGCCAGGTTCCTCGGCTTCGCGCTTCGCGCTCGGAGAGCGCCCGCGC 201
Db 137 CGCGGCTTCGCGCCCACTCCCTCGCGCGCAGAGCTA-----GCCCGCGCGC 184
Qy 202 TGGCGGACGGGTTCATAGTCCCTTAACCTCTGATGAAGAGCAGCGGTGAGCGGC 261
Db 185 TGGCGGAAGGGTGTATCAAGTCCGCCAAGCCCTTATGAAGAAGCAGCGGTGAAGCGC 244
Qy 262 ACCATCACAACACCAACCTGCGGCACCGCTAGAGTTCCTGGAGAGCTGGGCAAGGGCA 321
Db 245 ACCACCAAGCAGCAACCTGCGGCACCGCTACAGATTCTCGAGACCTTGGGCAAGGCA 304
Qy 322 CCTACGGGAAGGTGAAGAAGGCAACGAGAGCTCGGGGCTCTGTGGCCATCAAGTCCA 381
Db 305 CCTACGGGAAGGTGAAGAAGGCGCGGAGAGCTCGGGGCGCTGTGTGGCCATCAAGTCAA 364


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QY 382 TCAGGAAGACAAATCAAGATGAGCAGGATCTGTGCATACATACGAGGAGATTGAGA 441
DB 365 TCCGGAAGGACAAATCAAGATGAGCAGGATCTGTGCATACATACGAGGAGATTGAGA 424
QY 442 TCATGTCTTCACTCAACACCCCAATCAATATGTCATCCATGAGTGTGTTGAGATAGCA 501
DB 425 TCATGTCTTCACTCAACACCCCAATCAATATGTCATCCATGAGTGTGTTGAGATAGCA 484
QY 502 GCAAGATTGTGATTGTCATGAGTATGCCAGCGGAGCGGATCTGTATGATTACATCAGTG 561
DB 485 GCAAGATTCGTGATGTCATGAGTATGCCAGCGGAGCGGATCTGTATGATTACATCAGTG 544
QY 562 AGCGGCCACCGCTGAGTGAGCGGAGCGGAGCGGATCTGTATGATTACATCAGTG 621
DB 545 AGCGGCCACCGCTGAGTGAGCGGAGCGGAGCGGATCTGTATGATTACATCAGTG 604
QY 622 TGCACTACTGCGACCAAGGAGTGTTCACCGAGATCTCAAGCTGGAAGAAATCCTTTC 681
DB 605 TGCACTACTGCGACCAAGGAGTGTTCACCGAGATCTCAAGCTGGAAGAAATCCTTTC 664
QY 682 TAGATGCCAATGGAACATCAAGATTGCTGACTTTGGGCTCTCCAACTGTACCAAG 741
DB 665 TGATGCCAATGGAATATCAAGATTGCTGACTTTGGGCTCTCCAACTGTACCAAG 724
QY 742 GCAAGTTCTCTCCAGACGTTCTGTGGAGCGCTCTCTACGCTCGCTGAGATAGTCAACG 801
DB 725 GCAAGTTCTCTCCAGACGTTCTGTGGAGCGCTCTCTATGCTCGCCAGAGATTGTCATG 784
QY 802 GGAAGCCCTATGTGGGCCACAGAGTGACAGTGTCTCTGGGCTGTCTCTGATATCC 861
DB 785 GGAAGCCCTATACAGGCCACAGAGTGACAGTGTCTCTGGGCTGTCTCTGATATCC 844
QY 862 TGTGTATGTCACCATGCCCTTTGACGGGAGGATCATTAACACTGGTGAAGCAATCA 921
DB 845 TGTGTATGTCACCATGCCCTTTGACGGGAGGATCATTAACACTGGTGAAGCAATCA 904
QY 922 GTAAAGGGGCTTACCGTGAAGCGCCCAAGCGCTCGATGCTGTGGCTGATCCGGTGGC 981
DB 905 GCAAGGGGCTTACCGGAGCGCCCAACCTCTGATGCTGTGGCTGATCCGGTGGC 964
QY 982 TGTATATGTTGAACCCCAACCGCTCGGGCCACATGTGAGGATGTAGCAGTCAATGTGGG 1041
DB 965 TGTATATGTTGAACCCCAACCGCTCGGGCCACATGTGAGGATGTAGCAGTCAATGTGGG 1024
QY 1042 TCAACTGGGGTTACACACCGGAGTGGGGAAAGGAGCGCTGCGTGAAGGTTGGGACC 1101
DB 1025 TCAACTGGGGTTACACACCGGAGTGGGGAAAGGAGCGGAGGCTCGGATGAGGGTGGGACC 1084
QY 1102 CTAGTGTGACTTTGGCGGGGCTTCCATGCGGAGCTGTTACGTCGCTCGCTCGCGCCCC 1161
DB 1085 CTGGCAGTACTTGGCGGGGCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
QY 1162 TCTGTGAGAAATGAGGCAAGGTTGACGTTCTTCAAGCAGCAGTGTGCGGGAGGTGAA 1221
DB 1145 TCTGTGAGAAATGAGGCAAGGTTGACGTTCTTCAAGCAGCAGTGTGCGGGAGGTGAA 1204
QY 1222 GCACTGTACTGCTGGGCGGACATCTCTTAAAGAGTCCGAAAGGAGNATGCA 1281
DB 1205 GCACTGTACTGCTGGGCGGACATCTCTTAAAGAGTCCGAAAGGAGNATGCA 1264
QY 1282 TGGCTCAAAATCTGCAAGGTGACCCGCTGAGGATCTCTTCTGCGCTTGGCAAGAGCA 1341
DB 1265 TGGCCAGTCTCTCCAGTACACAGGCTGATGACATGCTGCCATGCGCTTGGCAGAGCA 1324
QY 1342 GCCTTAAGTCTCGAAAGGATCTTCAAGAAAAGTCTTACTCTGTCAAGGGAGGTAC 1401
DB 1325 ACCTTAAGTCTCGAAAGGATCTTCAAGAAAAGTCTTACTCTGTCAAGGGAGGTAC 1384
QY 1402 AGAGGACCTCTAGGAACTCAGACCGGTGCTGATCTCTCAGGGCAGCTGTCTCTGCTG 1461
DB 1385 AGAGGACCTCTCAGGAGCTCAGCCCAATCTCTCGAGCCCGGAGGCTGCTCTCTCTCT 1438
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QY 1462 TATCCCTGTCTCCCAAGGAAAGGATCTTTAAGAGTCTCGACAGCGTGAATCTGGTTACT 1521
DB 1439 ---CCCTGTCTCCCAAGGAAAGGATCTTTAAGAGGATCTTTAAGAGGATCTGGCTACT 1495
QY 1522 ACTCTCTCTCAGAGCCCGAGGATCTTGGGAACTCTTTAGAGCGCAGTGTGTGTGTA 1581
DB 1496 ACTCTCTCTCAGAGCCCGAGGATCTTGGGAGCTCTTGGAGCGCAGGCGAGTGTGTGTA 1555
QY 1582 GTGGGAGCCCGTGGAGCAGGATCTCCACAGGCTTCCAGGCTCTCCCTCCACGCAAGG 1641
DB 1556 GTGGGATATCCCAAGGAGCAGGATCTCCGCAAGCTTCCAGGCTGTCTCTCATCGCAAG 1615
QY 1642 GCATTTCTCAAACTCAATGGCAAGTCTTCCGCAAGCTTCTAGAGGCACTTACCCCTAGCA 1701
DB 1616 GCATTTCTCAAACTCAATGGCAAGTCTTCCGCAAGCTTCTAGAGGCACTTACCCCTAGCA 1675
QY 1702 CTTTGGCTCTTGGAGCAACTGGCTCTCTCCATCTGTGAGCGCCGCGCCGCGCCCT 1761
DB 1676 CTTTGGCTCTTGGAGCAACTGGCTCTCTCCATCTGTGAGCGCCGCGCCGCGCCCT 1735
QY 1762 CAGGGCTGTGAGTGGAGCAGCATCTGTCTCCGAGTCTTGTGACCAATTTGACATTTGC 1821
DB 1736 CAGGGCTGTGAGTGGAGCAGCATCTGTCTCCGAGTCTTGTGACCAATTTGACATTTGC 1795
QY 1822 CTGAAGCTCTTCCGAAACCCCACTGAGGGGCTGTGTCTGTGGAACAACCTGAGGGGGC 1881
DB 1796 CTGAAGCTCTTCCGAAACCCCACTGAGGGGCTGTGTCTGTGGAACAACCTGAGGGGGC 1855
QY 1882 TTGAGCAGCTCTCTCAGAAAG-----GTCTGAAGCATGTGTGAGGAAATCTCT 1929
DB 1856 TTGAGCAGCTCTCTCAGAAAG-----GTCTGAAGCATGTGTGAGGAAATCTCT 1915
QY 1930 TGGGGGATAGTCTCTTCTGACAGACTGCAAGAGTGTGCTGAGCAGCTTACAGACAAG 1989
DB 1916 TGGGGGATAGTCTCTTCTGACAGACTGCAAGAGTGTGCTGAGCAGCTTACAGACAAG 1975
QY 1990 CCTAGGAATCTGCTCAAAAGCTCAGCTGAGGAAAGGAGATGTGCTGCTAGTATGGGGTAG 2049
DB 1976 CACTGAGGGTCTGCTCAAAAGCTCAGCTGAGTGGAGTGGATTTGCCCGAG-CCCGGTGAG 2034
QY 2050 GCTCTGAGAGGTTTTCAGAGGAAACCTTGGGTGCGATTCCTCC 2092
DB 2035 GCTCTGAGAGTGTGCTGAGGAAACCTTGGGTGCGATTCCTCC 2077

RESULT 6
ADL30885
ID ADL30885 standard; cDNA; 3395 BP.
XX
AC ADL30885;
XX
DT 20-MAY-2004 (first entry)
XX
DE Full length human cDNA clone SeqID 2918.
XX
KW human; medicine; signal transduction; glycoprotein; transcription;
XX oligo-capping method; ss; gene.
XX
OS Homo sapiens.
XX
PN EP1396543-A2.
XX
PD 10-MAR-2004.
XX
PF 07-JUL-2000; 2003EP-00025638.
XX
PR 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
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PI	Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;	
PI	Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;	
XX	WPI; 2004-204755/20.	
DR	P-PSDB; ADL30886.	
XX		
PT	New oligonucleotide primers (930 cDNAs) useful for synthesizing full	
PT	length human cDNAs.	
XX		
XX	Example 1; SEQ ID NO 2918; 1340pp; English.	
CC	This invention relates to a novel primers useful for synthesizing full	
CC	length cDNA molecules that encode human proteins. Specifically, it refers	
CC	to secretory or membrane proteins that are potential therapeutic agents/	
CC	target molecules in the field of medicine, and in particular genes	
CC	encoding proteins that are associated with signal transduction,	
CC	glycoproteins and transcription. The present invention describes a method	
CC	for efficiently cloning a full length human cDNA from both the 5' and 3'	
CC	ends using the oligo-capping method. This polynucleotide sequence is a	
CC	full length human cDNA clone of the invention.	
XX		
XX	Sequence 3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;	
Query Match	47.4%; Score 1375.8; DB 12; Length 3395;	
Best Local Similarity	81.7%; Pred. No. 4.2e-294;	
Matches 1652; Conservative	0; Mismatches 337; Indels 34; Gaps 4	
QY	82 CTACTGTCGCCGACCCACTCCACTCGCGGTCCCGCACCATGGAGTCGTGGCCTTAC 141	
DB		
DB	77 CTACTGATTCCTCTCGCGCCCTTGCTACCTCTGCTCGCCATGGAGTCGTGGTTTTCG 136	
QY	142 TCCAGCGCCGAGCGCAGGCTCCCTCGGCTTCGGCCCTGGCCCTCGSAGAGCGCCGCGCGC 201	
DB		
DB	137 CGCGCGCTCGGCGCCCACTCCCTCGGCGGAGACTA-----GCCCGCGCGC 184	
QY	202 TGGCGGACGGGCTCATCAAGTCGGCTAAACCTCTGATGAAGAAGCAGCGGTGAAGCGCG 261	
DB		
DB	185 TGGCGGAAGGGCTGATCAAGTCGCCCAAGCCCTTAATGAAGAAGCAGCGGTGAAGCGCG 244	
QY	262 ACCATCAACAACACAACCTGGGCACCGCTACGAGTTCTCTGGAGACGCTGGGCAAGGCA 321	
DB		
DB	245 ACCACCAAGCAACAACCTGGGCACCGCTACGAGTTCTCTGGAGACCTTGGGCAAGGCA 304	
QY	322 CCTACGGGAAGGTGAAGAAGCAGCAGAGAGCTCGGGCGCTCTGGTGGCCATCAAGTCCA 381	
DB		
DB	305 CCTACGGGAAGGTGAAGAAGCAGCGGGAGAGCTCGGGCGCTCTGGTGGCCATCAAGTCAA 364	
QY	382 TCAGGAAGACAAAATCAAGATGACGAGGATCTGCTGCACATACGAGGGAGATTGAGA 441	
DB		
DB	365 TCCGGAAGGACAAAATCAAGATGAGCAAGATCTGATGCACATACGGAGGAGATTGAGA 424	
QY	442 TCATGCTTTCACCTCAACACCCACATCATTTGCCATCCATGAAGTGTTCAGAAATAGCA 501	
DB		
DB	425 TCATGTCATCACTCAACACCCCTCACATCATTTGCCATCCATGAAGTGTTCAGAACAGCA 484	
QY	502 GCAAGATTGTGATTGTGTCATGAGGTATGCGACCGAGGCGATCTCTGTATGATTACATCAGT 561	
DB		
DB	485 GCAAGATCGTGATCGTATGAGGTATGCGACCGGGCGACCTTTATGACTACATCAGCG 544	
QY	562 AGCGGCCACGCTCAGGTAGCGGGACCGCAGGCATTTCTCCGACAGATCTGTGCTGCC 621	
DB		
DB	545 AGCGGACGAGCTCAGGTAGCGCGAAGTAGGCATTTCTTCGGGAGATCGTCTCTGCCG 604	
QY	622 TGCACTACTGCCACAGAAAGGGATCGTTTACCGAGATCTCAAGCTGGAACATCTCTTC 681	
DB		
DB	605 TGCACTATTGCCATCAGAACAGAGTTGTGCCACCGAGATCTCAAGCTGGAGAATCTCTCT 664	
QY	682 TAGATGCCAATGGAAATCATCAAGATTCTGACTTTGGCTCTCCAACTGTACCACAAG 741	
DB		
DB	665 TGAATGCCAATGGGAATATCAAGATTGCTGACTTTCGGCTCTCCAACTGTACCATCAAG 724	
QY	742 GCAAGTTCTCCAGACGTTCTGTGGGAGCCCTCTCTACGCTCTCGCTGAGATAGTCAACG 801	

QY 322 CCTACGGGAAGGTGAAGAGGACGAGAGAGCTCGGGGGTCTGGTGGCCATCAAGTCCA 381
DB 315 CCTACGGGAAGGTGAAGAGGCGGGGAGAGCTCGGGGGTCTGGTGGCCATCAAGTCAA 374
QY 382 TCAGGAAGACAAATCAAGAGTACGAGGATCTGCTGACATACGAGGAGGAGTTGAGA 441
DB 375 TCCGGAAGGACAAATCAAGATAGCAAGATCTGATGACATACGAGGAGGAGTTGAGA 434
QY 442 TCATGTCTTCACTCAACACCCACATCATTTGCGATCCATGAAGTGTGTTGAGAATAGCA 501
DB 435 TCAATGTCACTCAACACCCCTCACATCATTTGCCATCCATGAAGTGTGTTGAGAACAGCA 494
QY 502 GCAAGATTGTGATGTGATGAGTATGCGAGGATGCGAGGCGGATCTGTATGATTAATCAGTG 561
DB 495 GCAAGATCTGATGATGATGAGTATGCGAGGATGCGAGGCGGATCTGTATGATTAATCAGTG 554
QY 562 AGCGGCCACGGCTGAGTACGAGGAGGCGGAGGATTTCTCCGACAGATCGTCTGCGCC 621
DB 555 AGCGGAGCAGCTGAGTACGAGGAGGCGGAGGATTTCTCCGCGAGATCGTCTGCGCG 614
QY 622 TGCACTACTGCCACAGAGCGGATCGTTTCAACGAGATCTCAAGCTGGAAAAATCCTTTC 681
DB 615 TGCACTATTGCCATCAGAACAGAGTGTGTCACCGAGATCTCAAGCTGGAGAACATCCTCT 674
QY 682 TAGATGCCAATGGAACATCAAGATTGCTGACTGTTGGCTCTCCAACTGTACCAAAAG 741
DB 675 TGGATGCCAATGGAATATCAAGATTGCTGACTTGGGCTCTCCAACTGTACCAATCAAG 734
QY 742 GCAAGTTCCTCCAGACGTTCTGTGGAGCCCTCTCTACGCTCGCTGAGATAGTCAAG 801
DB 735 GCAAGTTCCTCGACACATCTGTGGAGCCCTCTATGCTCGCCAGAGATTGTCAATG 794
QY 802 GGAAGCCCTATGTGGGCCACAGAGTGGACAGCTGGTCTCTGGGGTCTCTCTGTATACATCC 861
DB 795 GGAAGCCCTACACAGGCCACAGAGTGGACAGCTGGTCTCTGGGGTCTCTCTGTATACATCC 854
QY 862 TGGTGCATGCGACATGCCCTTTGAACGGGAGGATCAATAAACAATGGTGAAGCAATCA 921
DB 855 TGGTGCATGCGACATGCCCTTTGAACGGGAGGATCAATAAACAATGGTGAAGCAATCA 914
QY 922 GTAAAGGGGCTTACCGTGAGCGCCCAAGCCGCTCGATGCTGTGGCTGATCCGGTGGC 981
DB 915 GCAAGCGGGCTTACCGTGAGCGCCCAAGCCGCTCGATGCTGTGGCTGATCCGGTGGC 974
QY 982 TGTAAATGTGTAACCCACCCGCTCGGGCCACATCTGAGGAGTGTAGCCAGTCAATGTGGG 1041
DB 975 TGTGATGTGTAACCCACCCGCGGGCCACCTCTGAGGATGTGGCCAGTCACTGTGGG 1034
QY 1042 TCAACTGGGGTTACACACCGAGTTCGGGAAACAGGAAGCCCTGCGTGAAGGTTGGCACC 1101
DB 1035 TCAACTGGGGTTACCGCCACCGAGTGGGAGAGCAGGAGGCTCGGCATGAGGGTGGGCACC 1094
QY 1102 CTAGTGTGACTTTGGCCGGGCTTCCATGCGGAGCTGGTTACGTGCTGCTCGGCCCCC 1161
DB 1095 CTGGAGTGTACTTGGCCGGGCTTCCATGAGTGTGACTGGCTCGCGGCTTCTCGGCCCCC 1154
QY 1162 TCTTGGAGATGGAAGCAAGGTGTGACGTTCTTCAAGCAGCAGCTGCGCGGAGGTGGAA 1221
DB 1155 TCTTGGAGATGGAAGCAAGGTGTGACGTTCTTCAAGCAGCAGCTGCGCGGAGGTGGAA 1214
QY 1222 GCACTGTACTGGGCTGGAGCGGCAACATTTCTTTAAGAGTCCCGAAAGAGAGATGACA 1281
DB 1215 GCACCAACCCCTGGCCTGGAGCGGCAGCATTCGCTCAAGAGTCCCGCAAGGAGATGACA 1274
QY 1282 TGGCTCAAAATCTGCAAGGTGACCGGCTGAGGATACCTTTCTCGCCCTGGCAAGAGCA 1341
DB 1275 TGGCCCAAGTCTCTCCACAGTGACACGGCTGATGACATGCGCCATCGCCCTGGCAAGAGCA 1334
QY 1342 GCCTTAAGCTTCCGAAGGCAATTTCTCAAGAAAAAGTCTCTACTCTGTAGGGGAGGTAC 1401
DB 1335 ACCTCAAGCTGCCAAGGGCAATTTCTCAAGAAAGAGGTGTGAGCTCTGCAAGAGGGGTAC 1394
QY 1402 AGAGGACCCCTCAGGAACCTCAGACCGGTGCTGATCTCCAGGGGAGCCTGTCCCTGCTG 1461

DB 1395 AGGAGGACCCCTCGGAGCTCAGCCCAATCCCTCGAGCCCGGAGGCTGCCC----- 1448
QY 1462 TATCCCTGCTCCCAAGAAAGGAGCATCTTTAAGAGTCTCCACAGCGTGAATCTGGTACT 1521
DB 1449 ---CGTGTCTCCCAAGAAAGGAGCATTTCTCAAGAAAGCCCGACAGCGGAGTCTGGTACT 1505
QY 1522 ACTCTCTCTCAGAGCCCGAGCTCTGGGGAATCTTTAGACGCGAGTGTGTTGTGA 1581
DB 1506 ACTCTCTCTCAGAGCCCGAGTGAATCTGGGAGCTCTTTGACGCGAGCGAGCTGTTGTGA 1565
QY 1582 GTGGGAGCCCGTGGAGAGCAAGTCTCCACAGGCTTCAGGGCTCTCTCTCACCGCAAGG 1641
DB 1566 GTGGGAGTCCCAAGAGGAGCAGAGCTCCCGAAGCTTCAGGGCTGCTCTCCATCGCAAG 1625
QY 1642 GCATTTCTCAAACTCAATGGCAAGTCTCCCGCAGCAGCTTTAGAGGCACTTACCCCTAGCA 1701
DB 1626 GCATTTCTCAAACTCAATGGCAAGTCTCCCGCAGCAGCTTTGGAGCTCGCGGCCCCACCA 1685
QY 1702 CCTTTGGCTCTCTGGAGCAACTGGCTCTCTCCATCTCGCAGCCCGGCCCGAGCCCTCT 1761
DB 1686 CCTTTGGCTCTCTGGAGCAACTGGCTCTCGCCCACTCGCCCTCGGCCCGAGCCCTCT 1745
QY 1762 CAGGGCTGTGAGTGGAGCAGCATCTGTCTCTCGAGTCTTTGACCAATTTGACTTGC 1821
DB 1746 CAGGGCTGTGAGGAGGAGCAGCATCTGTCTCTCTGAGTCTTTGACCAAGTGTGCTGC 1805
QY 1822 CTGAAGCTCTTCCGGAACCCCACTGAGGGGCTGTGTCTGTGGACAACTCAGGGGC 1881
DB 1806 CTGAAGCGGCTCCAGAGCCCGCACTCGGGGCTGTGTCTGTGGACAACTCAGGGGC 1865
QY 1882 TTGAGCAGCTCTCTCAGAAAG-----GTCTGAAGCGATGGTGGCAGGAATCCT 1929
DB 1866 TTGAGGAGCCCTCTCAGAGGCGCTTGAAGCTGCTGAGCGCTGGCGCAGGATCCTT 1925
QY 1930 TGGGAGTGTGCTCTTCTGACAGACTGTCGAAGAGTGACTGACGCTTACAGCAAG 1989
DB 1926 TGGGAGCAGCTGCTTTCTCTGACAGACTGTCGAAGAGTGAAGGAGCTTACCGCAGG 1985
QY 1990 CCTTGAAGTCTCTCAAGCTCAGCTGAGGAAGGAGATGGTGGCTTATGAGGTAG 2049
DB 1986 CACTGAGGGTCTCTCAAGCTCACCTGAGTGGAGTGGCAATTTGCCCTCAG-CCCGGTGAG 2044
QY 2050 GCTCTGAGAGGGTTTCAGAGGAACCTTGGGTCGGATTTCTCC 2092
DB 2045 GCTCTCAGATGCACTGGTTGCAACCGGAGGAGATGCTTTC 2087

RESULT 9

ADP81952

ID ADP81952 standard; DNA; 3443 BP.

XX

AC ADP81952;

XX

DT 26-FEB-2004 (first entry)

XX

XX Leukaemia-related DNA sequence #2508.

XX

XX Cytostatic; Gene therapy; leukaemia; ss.

XX

XX Unidentified.

OS

XX WO2003039443-A2.

XX

PD 15-MAY-2003.

XX

XX 04-NOV-2002; 2002WO-EP012303.

XX

PR 05-NOV-2001; 2001EP-00126244.

XX

PR 30-APR-2002; 2002EP-00009758.

XX

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA (UYLU-) UNIV LUDWIG MAXIMILIANS.

PA (HAFE/) HAERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
XX
PI Haerlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;
PI Bils R, Brors B, Mergenthaler S;
XX
XX WPI; 2003-505037/47.
XX
XX Determining the subtype of leukemia cells and whether a patient sample
PT contains leukemia cells or other cells, useful for treating leukemia,
PT comprises determining the expression profile of a group of markers in a
PT patient sample.
XX
XX Disclosure; SEQ ID NO 2508; 2938pp; English.
XX
CC The present invention relates to a method (M1) for determining the
CC subtype of leukemia cells and whether a patient sample contains
CC leukemia cells. The method comprises determining the expression profile
CC of a group of markers in a patient sample. The method is useful for
CC determining the presence of leukemia cells, its types or subtypes, and
CC for the preparation of a medicament for treating leukaemia.
XX
SQ Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;
Query Match 47.4%; Score 1374.2; DB 10; Length 3443;
Best Local Similarity 81.6%; Pred. No. 9.5e-294; Indels 34; Gaps 4;
Matches 1651; Conservative 0; Mismatches 338;
82 C T A C T G C T G C C G A C C A C C T C C A C C T C C G G T C C C C G C A C C A T G G A G T C G G T G C C T T A C 141
87 C T A C T G A T T C C C C T G C C G C C T T G C T C A C C T C C T G C T G C C A T G A G T C G G T T T C G 146
142 T C A G C C C C G A G C C A G C T C C T C G G C C T C C G C C T C C G C A C C A C C A T G G A G T C G G T G C C T T A C 201
147 C G C G G C G C T C G G C C C A C C T C C T C G C G C G A G A C T A ----- G C C C G G C G C 194
202 T G C G G A C G G C T C A T C A A G T C G C C T A A A C T C T G A T A A G A G A C G C G G T G A A G C G C 261
195 T G C G G A G G C T G A T C A G T C G C C A A G C C C T A T A T A G A A G A C G C G G T G A A G C G C 254
262 A C C A T C A A A C A A C A C C T C G G C A C C G T A C G A G T T C C T G G A G A C C T C G G C A A G G C A 321
255 A C C A C A C A A G A C A A C C T C G G C A C C G T A C G A G T T C C T G G A G A C C C T G G G A A A G G C A 314
322 C C T A C G G A A G T C A A A G A G C A G A G C T C G G G C G T C T G G T G C C A T C A A G T C C A 381
315 C C T A C G G A A G T A A A G A G C G G A G A G C T C G G G C G C C T G T G G C C A T C A A G T C A A 374
382 T C A G G A A G A C A A A T C A A A G A T G A G C A G A T C T G C T G C A C A T A C A G G A G G A T T G A G A 441
375 T C C G A A G A C A A A T C A A A G A T G A G C A G A T C T G A T G C A C A T A C G A G A G A T T G A G A 434
442 T C A T G T T C A C T C A A C C A C C C A C A T A T T G C C A T G C C A T G A A G T T T T G A G A A T A G C A 501
435 T C A T G T C A T C A C T C A A C C A C C C T C A C A T A T T G C A T C C A T G A A G T G T T T T G A G A A C A G C A 494
502 G C A A G A T T G A T T G T C A T G A G T A T C C A G C C G A G C G A T C T G A T G A T T A C A T C A G T G 561
495 G C A A G A T C G T G A T G C T C A T G A G T A T C C A G C C G G G C G A C C T T A T G A C T A C A T C A G C G 554
562 A G C G G C C A C G G C T G A G T A G C G G A C C C A G G A T T T T T C C G A C A G A T C G T G T G C C C 621
555 A G C G G A G A C A G C T C A G T A G C G G A G T A G G A T T T T T C C G G A G A T C G T C T G C C G 614
622 T G C A T A C T C C C A C C A A G A G G A T C G T T C A C G A G A T C T C A A G T G G A A A A C A T C C T T C 681
615 T G C A C T A T T G C C A T C A G A C A G A G T T G T C C A C C G A G A T C T C A A G C T G G A A A C A T C C T C T 674
682 T A G A T G C A A T G A A A C A A G A T T G C T A C T T G G C C T C C A A C C T G T A C C A A A G 741
675 T G A T G C C A A T G G A A T A C A A G A T T G C T A C T T G G C C T C C A A C C T C A C A C C T C A C A A G 734

742 G C A A G T T C C T C C A G A G T T C T G T G G A G C C C T C T C T A C G C C T C G C C T G A G A T A G T C A A C G 801
735 G C A A G T T C C T G C A G A C A T T C T G T G G A G C C C C T C T A T G C C T C G C A G A T T G T C A A T G 794
802 G G A A G C C C T A T G T G G G C C C A G A G T G G A C A G C T G T C T C T G G G C G T T C T C C T G T A C A T C C 861
795 G G A A G C C C T A C A C A G A G C C C A G A G T G G A C A G C T G T C C C T G G G T G T T C T C C T C T A C A T C C 854
862 T G T G A T G C A C A C A T G C C C C T T T T G A C G G G A G A T A T A A A C A C A T G T G A A G A A A T C A 921
855 T G T G A T G C A C A C A T G C C C C T T T G A T G G G C A T A C C A T A G A T C C T A G T G A A A C A G A T C A 914
922 G T A A C G G G C T T A C C G T G A G C C C C A A G C G C C G A T G C C T G T G C C T A C T G C G T G G C 981
915 G C A A C G G G C C T A C C G G A G C C A C C T A A A C C C T T G A T G C C T G T G G C C T A T C C G T G G C 974
982 T G T T A A T G T G A A C C C C A C C C G T C G G G C C A C A C T G G A G A T G T A G C A G T C A T T G T G G G 1041
975 T G T T G A T G T G A A C C C C A C C C C G C C G G C C A C C C T G G A G A T G T G G C C A G T C A C T G T G G G 1034
1042 T C A A C T G G G G T T A C A C A C C G G A G T C G G G A A C A G A A G C C C T G C T G A G G T G G G C A C C 1101
1035 T C A A C T G G G G C T A C G C C A C C C G A G T G G A G A G A G G C T C C G C A T A G A G G T G G G C A C C 1094
1102 C T A G T G T G A C T T T G C C G G C C T C C A T G C G A C T G T T A C G T C G C T C C T C G C G C C C C 1161
1095 C T G C A G T G A C T C T G C C G C C C T C C A T G C T G A C T G G C T C C G G C G T T C C T C C G C C C C 1154
1162 T C C T G G A A T G G A G C C A A G G T G T G A G C T T C T T C A A G C A G C A C G T G C C G G A G G T G G A A 1221
1155 T C C T G G A A T G G G C C A A G G T G T G A G C T T C T T C A A G C A G C A T G C A C C T G T G G G G A A 1214
1222 G C A C T G T A C C T G G G C T G G A G C G C A C A T T C T T A A G A A G T C C C A A A G A G A A T G A C A 1281
1215 G C A C C A C C C T G G C C T G G A G C G C C A G C A T T C G C T C A A G A A G T C C C A A A G A G A A T G A C A 1274
1282 T G C C T C A A A T C T G C A A G T G A C C C G G C T G A G A T A C C T T C T C C C C C T G G C A A G A G C A 1341
1275 T G C C C A G T C T C C A C A G T G A C A C G C T G A T G A C A C T G C C C A T C G C C T T G G C A A G A G C A 1334
1342 G C C T T A A G T T C C G A A A G C A T T C T C A G A A A A A G T C C T T A C C T C G T C A G G G A G G T A C 1401
1335 A C C T A A G T G C C A A A G G C A T T C T C A A G A A A G G T G T C A G C C T C T G C A A A A G G G T A C 1394
1402 A G A G A C C C T C A G A A C T C A G A C C G T G C C T G A T A C T C C A G G C A C C T G T C C C T G C T G 1461
1395 A G A G A C C C T C G G A G C T C A G C C C A A T C C C T G C A G C C C A G G G C A G G C T G C C C ----- 1448
1462 T A T C C C T G C T C C C A A G A A A G G C A T C C T T A A A A A G T C T G A C A G C G T G A A T C T G G T T A C T 1521
1449 --- C G C T G C T C C C A A G A A G G C A T T C T C A G A A G C C C G A C A G C G G A G T C T G G C T A C T 1505
1522 A C T C C T C T C A G A C C C A G C A G T C T G G G A A C T T T A G A C G C C A G T A G T G T T T G T G A 1581
1506 A C T C C T C T C C C A G C C A G T A A T C T G G G A G C T C T T G G A C G C A G C A G C G T G T T T G T G A 1565
1582 G T G G G A C C C C T G G A G A C A G T C C C A G C G T T C A G G C T C C T C C C A C C G A A G 1641
1566 G T G G G A T C C C A A G A G A G A A G C C T C C C A G C T C C C A G C T G C T C C C A T C A T C A A A G 1625
1642 G C A T T C T C A A A C T C A A T G G C A A G T T C C C C G C A C A C C C T T A G A A G G C A C T A C C C C T A G C A 1701
1626 G C A T C C T C A A C T C A A T G G C A A G T T C T C C A G A C A G C C T T G A G C T C G G G C C C C A C C A 1685
1702 C T T T G G C T C C C T G A C C A A C T G G C C C T C C C A T C C T G A G C C C G G C C A G C C G C C C T 1761
1686 C T T C G G C T C C C T G A T A A C T C G C C C A C C T C G C C C C C T G G C C C C G G C C A G C C G C C C T 1745
1762 C A G G G C T G T G A G T A G A G A C A C A T C T C T C C T C C G A G T C C T T T G A C C A A T T G G A C T T G C 1821
1746 C A G G G C T G T G A G C G A G A C A G A T C C T G T C C T G A G T C C T T T G A C C A G C T G A C T T G C 1805
1822 C T G A A C G T C T C C C G A A A C C C A C C A C T A G G G G C T G T G T C T G T G G A C A A C C T G A G G G G C 1881

Db 1806 CTGAACGGCTCCAGAGCCCCCACTGCGGGGCTGTGTCTGTGACAACTCAGGGC 1865
Qy 1882 TTGAGGACCTCCCTCAGAG-----GTCTGAAGCGATGTGCGAGATCCT 1929
Db 1866 TTGAGGAGCCCCCTCAGAGGGCCCTGGAAGCTGCCGTGAGGCGCTGGCGGAGATCCTT 1925
Qy 1930 TGGGGGATAGCTGTTTCTTCTGACAGACTGCCAAGAGGTGACTGACAGCCTACAGACAAG 1989
Db 1926 TGGGGGACAGCTGTTTCTTCTGACAGACTGCCAAGAGGTGACAGCCTACCGACAG 1985
Qy 1990 CCTAGGAATCTGCTAAAGCTCAGCTGAGAAAGGAGATGTTGCTTCTAGTATGGGGTAG 2049
Db 1986 CACTGAGGGTCTGCTCAAAGCTCACTGAGTGGAGTAGGCAATGCCCCAG-CCGGGTGAG 2044
Qy 2050 GCTCTGAGAGGGTTTGACAGAGGAACCTGGGTGCGATTCTCC 2092
Db 2045 GCTCTGAGTGCAGCTGGTTGCACCCCGAGGGGAGATGCTTTC 2087

RESULT 10

AD020171
ID AD020171 standard; cDNA; 3443 BP.

XX AC AD020171;

XX XX 12-AUG-2004 (first entry)

XX DE Human PRO polynucleotide #540.

XX KW Human; PRO; gene; ss; immune related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW renal disease; demyelinating disease; central nervous system;
KW peripheral nervous system; demyelinating polyneuropathy;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.

XX OS Homo sapiens.

XX PN WO2004043361-A2.

XX XX 27-MAY-2004.

XX PF 06-NOV-2003; 2003WO-US035268.

XX PR 08-NOV-2002; 2002US-0425235P.

XX XX (GETH) GENENTECH INC.

XX PA Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;

XX XX WPI; 2004-420067/39.

XX DR P-PSDB; ADO20172.

XX PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.

XX PS Claim 1; SEQ ID NO 1136; 1731pp; English.

XX CC The invention relates to human PRO polypeptides and the polynucleotides
XX encoding them. The polypeptides and polynucleotides are useful for
XX treating and diagnosing immune related disorders in mammals. The immune
XX related disorders include systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic
XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
XX mellitus, immune-mediated renal disease, demyelinating diseases of the

CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polynucleotide of
CC the invention.

XX SQ Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;

Query Match 47.4%; Score 1374.2; DB 12; Length 3443;
Best Local Similarity 81.6%; Pred. No. 9.5e-294;
Matches 1651; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

Qy 82 CTACTGTCGCCACCCACCTCCACCTCGGGTCCCCGACCATCGAGTGGTGGCTTAC 141
Db 87 CTACTGATTCCCTGCGGCTTGTCTCACCCTCTGCTCGCATGAGTCTGCTTTCG 146
Qy 142 TCCAGCGCCGAGCAGGCTCCCTCGGCTCCGCTCGGCTCGGAGAGCGCCGCGCGC 201
Db 147 CGCGGGCTCCGGCCCACTCCCTCGGCGCAGACTA-----GCCGCGCGC 194
Qy 202 TGGCGGACGGGCTCATCAAGTCGCTAAACCTCTGATGAAGAAGCAGCGGTGAAGCGC 261
Db 195 TGGCGGAGGGCTGATCAAGTCGCCCAAGCCCTTAATGAAGAAGCAGCGGTGAAGCGC 254
Qy 262 ACCATCAAAACAAACCTCGCGCACCGCTACGAGTTCCTGGAGACGCTGGCAAGGCA 321
Db 255 ACCACCAAGACAAACCTCGCGCACCGCTACGAGTTCCTGGAGACCTGGCAAGGCA 314
Qy 322 CTTACGGGAAGGTGAAGAGGACGAGAGAGCTCGGGGCTCTGTTGGCCATCAGTCCA 381
Db 315 CTTACGGGAAGGTGAAGAGGCGCGGAGAGCTCGGGGCGCTGGTGGCCATCAAGTCAA 374
Qy 382 TCAGGAAAGACAAATCAAGATGAGCAGGATCTGCTGCACATACGAGGAGATTGAGA 441
Db 375 TCCGGAAGACAAATCAAGATGAGCAGGATCTGATGCACATACGAGGAGATTGAGA 434
Qy 442 TCATGTTTCACTCAACCCACCATCATTCGCCATCCATGAAGTGTGTTGAGAATAGCA 501
Db 435 TCATGTCATCACTCAACCCCTCACATCATTCGCCATCCATGAAGTGTGTTGAGAATAGCA 494
Qy 502 GCAAGATTGTGATTGTGATGGAGTATGCCAGCGGAGCGATCTGTATGATTACATCAGT 561
Db 495 GCAAGATCGTGTGATCGTATGGAGTATGCCAGCGGAGCGACCTTTATGATACATCAGC 554
Qy 562 AGCGGCCAGCGCTGAGTGAGCGGAGCGCAGGCAATTTCTCCGACAGATCGTGTGCCC 621
Db 555 AGCGGACAGCTCAGTGAGCGGAGAGTAGGATTTCTTCCGCGAGATCGTCTGCGCG 614
Qy 622 TGCACTACTGCCACCAAGACGGGATCGTTTCCACCGAGATCTCAAGCTGGAAAAATCCTTC 681
Db 615 TGCACATTGSCCATCAGACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCT 674
Qy 682 TAGATGCCATGGAACATCAAGATTGCTGACTTTGGCTTCCACCTCGAGATAGTCAACG 741
Db 675 TGGATGCCAATGGGAATATCAAGATTGCTGACTTCGAGCTCTCCAACTCTACCATCAAG 734
Qy 742 GCAAGTTTCTCCAGAGCTTCTGTGGAGCGCTCTCTACGCTCGCTCGAGATAGTCAACG 801
Db 735 GCAAGTTTCTGAGACATTTCTGTGGAGCGCTCTATGCTCGCCAGAGATTGTCAATG 794
Qy 802 GGAAGCCCTATGTGGGCCACAGAGTGAGACAGCTGGTCTCTGGGCGTTCTCTGTACATCC 861
Db 795 GGAAGCCCTACACAGGCGCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCTCTACATCC 854
Qy 862 TGGTGCATGSCCATGCTCCCTTTGAGCGGCGAGATCATAAACACTGGTGAAGCAATCA 921
Db 955 TGGTGCATGSCCATGCTCCCTTTGATGGGCGATGACCATAGATCTCTAGTAGTAAACAGATCA 914
Qy 922 GTAACGGGGCTTACCGTGAGCGCCCAAGCGCTCGCATGCTGTGGCTCATCGGTGGC 981
Db 915 GCAACGGGGCTTACCGGAGCGACCTTAACCTCTGTATGCTGTGGCTGATTCGGTGGC 974
Qy 982 TGTTAATGTGTAACCCCGCTCGGGCCCACTGGAGGATGTAGCCAGTCATTGTGGTGG 1041


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Db 975 TGTGATGGTGAACCCCAACCCCGGGCCACCCCTGGAGGATGTGCCAGTCACTGGTGGG 1034
Qy 1042 TCRACTGGGTTACACACCGGAGTCGGGNAACAGGAAGCCCTCGTGAGGGTGGGACC 1101
Db 1035 TCRACTGGGTTACACACCGGAGTCGGGNAACAGGAAGCCCTCGTGAGGGTGGGACC 1094
Qy 1102 CTAGTGTGACTTTGGCGGGCCCTCCATGGCGGACTGGTTACGTGGCTCTCGGCCCCCC 1161
Db 1095 CTGGCAGTGACTTGGCGGGCCCTCCATGGCTGACTGGCTCCGGGTTCTCCCGCCCC 1154
Qy 1162 TCTGGAATGAGAGCAAGGTGTGCAGCTTCTTCAAGCAGCAGCTGCCGGAGGTGGAA 1221
Db 1155 TCTGGAATGAGAGCAAGGTGTGCAGCTTCTTCAAGCAGCAGCTGGTGGGGAA 1214
Qy 1222 GCACTGTACCTGGCTGGAGGCAACATCTCTTAAGNAGTCCGGAAGAGNATACA 1281
Db 1215 GCACACCCCTGGCTGGAGGCGCAGATTCGCTCAAGAAGTCCCGAAGAGNATACA 1274
Qy 1282 TGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGACA 1341
Db 1275 TGGCCAGTCTCTCCACAGTGACAGGCTGATGACATGCCATCGCCCTGGCAAGACA 1334
Qy 1342 GCCTTAAGTCTCGAAGGCAATCTCAAGAAAAGTCTCTACCTCTGTCAGGGAGGTAC 1401
Db 1335 ACCTCAAGCTGCCAAGGCAATCTCAAGAAGAGGTGTGAGCCCTCTGCAGAGGGGTAC 1394
Qy 1402 AGGAGGACCTTCAGAACTCAGACCGGTGCTGATACTCCAGGGCAGCTGTCCCTGCTG 1461
Db 1395 AGGAGGACCTTCGGAGCTCAGCCCAATCCCTGGAGCCAGGGCAGGCTGCC----- 1448
Qy 1462 TATCCTCTGCTCCCAAGGAAAGGCACTCTTAAGAAAGTCTCGACAGCGTGAATCTGGTTACT 1521
Db 1449 ---CGCTGCTCCCAAGAGGCAATCTCAAGAGCCCGACAGCGGAGTCTGGCTACT 1505
Qy 1522 ACTCCTCTCAGAGCCCGAGGAGTCTGGGAACTCTTTAGACGCCAGTGATGTGTTGTGA 1581
Db 1506 ACTCCTCTCCGAGCCCGAGGAGTCTGGGAGTCTTTGGACGCGAGGCGAGCTGTTGTGA 1565
Qy 1582 GTGGGAGCCCGTGAGCAGAGTCTCCACAGGCTTCAGGGCTCTCCTCCACGCAAGG 1641
Db 1566 GTGGGATCCAGGAGCAGAGCTCCGCAAGCTTCAGGGCTCTCCTCCATCGCAAG 1625
Qy 1642 GCATTTCAAACTCAATGGCAAGTTCTCCGCAAGCTTTAGAGGCACTACCCCTAGCA 1701
Db 1626 GCATTTCAAACTCAATGGCAAGTTCTCCGCAAGCTTTGGAGCTCGCGGCCCCACCA 1685
Qy 1702 CTTTGGCTCTCGGACCAACTGGCTCTCTCCATCTCAGCGCCGCGCCAGCGCCCT 1761
Db 1686 CTTTGGCTCTCGGATGATGATCGCCCACTCGCCCTCTGGCCCGGGCCAGCGACCT 1745
Qy 1762 CAGGGGCTGTGAGTGAGCAGACATCTCTCTCCGAGTCTTTGACCAATTGACATTGC 1821
Db 1746 CAGGGGCTGTGAGCAGCAGACATCTCTCTCTGAGTCTTTGACACAGTGGACTTGC 1805
Qy 1822 CTGAACGCTTCTCCGAAACCCCACTGAGGGGCTGTGTCTGTGGACAACCTGAGGGGGC 1881
Db 1806 CTGAACGCTTCTCCGAGCCCACTGCGGGGCTGTGTCTGTGGACAACCTCAGCGGC 1865
Qy 1882 TTGAGCAGCTCTCTCAGAAG-----GTCTGAGCAGTGTGTGAGGATTCCT 1929
Db 1866 TTGAGGAGCCCTCTCAGAGGGCCCTTGAAGTGTCTGAGGGCGTGGCGCAGGATCTTT 1925
Qy 1930 TGGGGGATAGTGTCTTCTCTGACAGCTGCCAAGAGGTGACTGACGCTTACAGACAAG 1989
Db 1926 TGGGGGACAGTGTCTTCTCTGACAGCTGCCAGGAGGTGACAGCACTTACGACAGG 1985
Qy 1990 CCTAGGAATCTGCTAAAGCTCAGTTGAGGAAGGAGATGGTGCCCTAGTATGGGGTAG 2049
Db 1986 CACTGAGGGTCTGCTCAAGCTCACTGAGTGGAGTAGGCAATGGCCCGAG-CCCGGTGAG 2044
Qy 2050 GCTCTGAGAGGGTTGAGAGGAAACCTGGGTGGATTCCTCC 2092
Db 2045 GCTCTGAGTGCAGTGTGTTGCACCCCGAGGGGAGATGCTCTTC 2087
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RESULT 11

ADJ96554
ID ADJ96554 standard; DNA; 3463 BP.

XX AC ADJ96554;
XX 06-MAY-2004 (first entry)

XX Human calcium/calmodulin-dependent protein kinase NuaK2 DNA SeqID 11.

DE gene; ds; kinase; human; SNP; single nucleotide polymorphism;
XX tyrosine protein kinase; serine/threonine protein kinase; PTK; STK;
XX tyrosine protein kinase; cancer; immune-related disease; cardiovascular disease;
KW brain; neuronal associated disease; metabolic; inflammatory disorder;
KW cytosolic; neuroprotective; immunomodulator; antiinflammatory;
KW calcium/calmodulin-dependent protein kinase; NuaK2.

OS Homo sapiens.
OS 68.

XX Key Location/Qualifiers
PH variation /*tag= a
FT /*tag= a
FT variation replace(1727,a)
FT /*tag= b
FT /*tag= b
FT variation replace(1727,a)
FT /*tag= b
FT variation replace(1727,a)
FT /*tag= b

XX WO2004006838-A2.

XX 22-JAN-2004.

XX 15-JUL-2003; 2003WO-US021730.

XX 15-JUL-2002; 2002US-0395632P.

XX (SUGEN-) SUGEN INC.

XX Whyte D, Manning G, Caenepeel S;

XX WPI; 2004-122753/12.

XX P-PSDB; ADJ96620.

XX New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.

XX Example 1; SEQ ID NO 11; 366pp; English.

XX This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytosolic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polynucleotide sequence is a human kinase DNA sequence
CC of the invention.

XX Sequence 3463 BP; 732 A; 1057 C; 919 G; 755 T; 0 U; 0 Other;

XX Query Match 47.4%; Score 1374.2; DB 12; Length 3463;
XX Best Local Similarity 81.6%; Pred. No. 9.6e-294;
XX Matches 1651; Conservative 0; Mismatches 338; Indels 34; Gaps 4;

Qy 82 CTACTCTCGCCGACCCCACTCCACCTCGCGGTCCCGCACCATGAGTGGTGGCCTTAC 141

Genetic disorder.
 XX Homo sapiens.
 XX US2004053250-A1.
 XX 18-MAR-2004.
 XX 21-NOV-2002; 2002US-00302172.
 XX 05-MAR-2001; 2001US-00799451.
 XX 05-MAR-2002; 2002WO-US005095.
 XX 20-AUG-2002; 2002US-00225251.
 XX (TANG/) TANG Y T.
 XX (XUE/) XUE A.
 XX (DRMA/) DRMANAC R T.
 XX Tang YT, Xue A, Drmanac RT;
 XX WPI; 2004-238579/22.
 XX New isolated arginine-rich protein-like polynucleotides and polypeptides,
 XX useful for diagnosing and/or treating conditions associated with aberrant
 XX activity of the arginine-rich polypeptides, such as cancer and
 XX inflammation.
 XX Disclosure; SEQ ID NO 215; 51pp; English.
 XX The invention relates to an isolated polynucleotide. The methods and
 XX compositions of the present invention are useful for the diagnosis and/or
 XX treatment of diseases or conditions associated with aberrant expression
 XX or activity of the arginine-rich protein-like polypeptides, such as
 XX cancer and inflammation. They can also be used in forensics, gene
 XX mapping, identification of mutations responsible for genetic disorders,
 XX and in assessing biodiversity. The present sequence represents a novel
 XX human arginine-rich protein cDNA.
 XX Sequence 2501 BP; 525 A; 788 C; 728 G; 460 T; 0 U; 0 Other;
 XX
 XX Query Match 47.3%; Score 1372.2; DB 12; Length 2501;
 XX Best Local Similarity 81.6%; Pred. No. 2.4e-293;
 XX Matches 1649; Conservative 0; Mismatches 338; Indels 34; Gaps 4;
 XX
 XX 82 CTACTGCTGCGGACCACTCCACCTCGCGTCCCGCACCACCTGGAGTTCGGTCCCTTAC 141
 XX 65 CTATTGATTCCCTGCGCGCTTGGCTCACCTCTGCTCGCCATGGAGTGGTGGTTTCG 124
 XX 142 TCAGAGCGCGGAGCGAGGCTCCCTCGGCGCTCCGCGCTCGGAGAGCGCGCGCGCG 201
 XX 125 CGCGGCGCTCGGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 172
 XX 202 TGGGAGCGGCTCATCAAGTGGCTTAACTCTGTGTAAGAGAGCGGCGTGAAGCGG 261
 XX 173 TGGCGGAAGGCGTATCAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 232
 XX 262 ACCATCAACAACAACCTCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 321
 XX 233 ACCACCAAGAGCAACCTCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 292
 XX 322 CCTACGGGAAGGTGAAGAGGCGGAGAGAGTCTCGGCGCGGCGGCGGCGGCGGCGGCG 381
 XX 293 CCTACGGGAAGGTGAAGAGGCGGCGGAGAGTCTCGGCGCGGCGGCGGCGGCGGCGG 352
 XX 382 TCAGGAAGACAAATCAAGATGAGCAGATCTGCTGCAATACGAGGAGGAGATTGAGA 441
 XX 353 TCCGGAAGAGCAAAATCAAGATGAGCAGATCTGCTGCAATACGAGGAGGAGATTGAGA 412
 XX 442 TCATGCTTCACTCAACACCCACATCATTTGCCATCCATGAAGTCTTTGAGAATAGCA 501
 XX 413 TCATGTCATCACTCAACACCCACATCATTTGCCATCCATGAAGTCTTTGAGAATAGCA 472
 XX 502 GCAAGATTGATTGATGAGATGATGCCAGCGAGCGGATCTGTATGATTATCATCAGTG 561
 XX
 XX Db 473 GCAAGATCGTATCGTATGAGATATGCCAGCGCGGCGGCGGCGGCGGCGGCGGCGG 532
 XX Qy 562 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 621
 XX Db 533 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 592
 XX Qy 622 TGCACTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 681
 XX Db 593 TGCACTACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 652
 XX Qy 682 TAGATGCCAATGGAATATCAAGATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 741
 XX Db 653 TGATGCCAATGGAATATCAAGATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 712
 XX Qy 742 GCAAGTTCTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 801
 XX Db 713 GCAAGTTCTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 772
 XX Qy 802 GGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 861
 XX Db 773 GGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 832
 XX Qy 862 TGGTGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 921
 XX Db 833 TGGTGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 892
 XX Qy 922 GTAAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 981
 XX Db 893 GCAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 952
 XX Qy 982 TGGTGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1041
 XX Db 953 TGGTGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1012
 XX Qy 1042 TCAACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1101
 XX Db 1013 TCAACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1072
 XX Qy 1102 CTAGTGGTGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1161
 XX Db 1073 CTGGCGAGTGCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1132
 XX Qy 1162 TCCGCGAGAGTGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1221
 XX Db 1133 TCCGCGAGAGTGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1192
 XX Qy 1222 GCACTGTACTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1281
 XX Db 1193 GCACCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1252
 XX Qy 1282 TGGCTCAAAATCTGAAAGTGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1341
 XX Db 1253 TGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1312
 XX Qy 1342 GCCTTAAGCTTCCGGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1401
 XX Db 1313 ACCTCAAGCTGCCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1372
 XX Qy 1402 AGGAGGACCGCTCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1461
 XX Db 1373 AGGAGGACCGCTCAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1426
 XX Qy 1462 TATCCCTGTCCCAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1521
 XX Db 1427 ---CCCTGTCTCCCAAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1483
 XX Qy 1522 ACTCTCTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1581
 XX Db 1484 ACTCTCTCCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1543
 XX Qy 1582 GTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1641

Db 1544 GTGGGGATCCCAAGGAGCAGAGGCTCCGCAAGCTTCAGGGCTGCTCTCTCCATCGCAAG 1603
Qy 1642 GCATTCTCAAACTCAATGGCAAGTTCTCCGCGCAGAGCTTAGAGGCACTACCCCTAGCA 1701
Db 1604 GCATCTCAAACTCAATGGCAAGTTCTCCGCGCAGAGCTTAGAGCTCGGGCCCCACCA 1663
Qy 1702 CCTTTGGCTCCCTGGACCAACTGSCCTCTCTCCCATCTCGACGCCCGGCCCGCCCT 1761
Db 1664 CCTTCGGCTCCCTGGATGAATGSCCCCACTGCTGCCCTCTGGCCCGGGCCAGCGACCT 1723
Qy 1762 CAGGGCTGTGAGTGAGGACAGCATCTGTCTCTCCGAGTCTTTGACCAATTTGACTTGC 1821
Db 1724 CAGGGCTGTGAGTGAGGACAGCATCTGTCTCTCTGAGTCTTTGACCAATTTGACTTGC 1783
Qy 1822 CTGAAGCTCTTCCGGAACCCCACTGAGGGGCTGTGTCTGTGGAACCTGAGGGGC 1881
Db 1784 CTGAGCGCTCCGAGACCCCACTGCGGGCTGTGTCTGTGGAACCTGAGGGGC 1843
Qy 1882 TTGAGCAGCTCTCTCAGAAG-----GTCTGAAGCGATGTGTGCGAGGATCTCT 1929
Db 1844 TTGAGGAGCCCTCTCAGAGGGCCCTGGAAGCTGCTGAGGCGCTGCGCGAGGATCTT 1903
Qy 1930 TGGGGATAGTGTCTTTCTGTGACAGCTGCCAAGAGGTGACTGTGAGCTTACAGCAAG 1989
Db 1904 TGGGGACAGTGTCTTTCTGTGACAGCTGCCAGAGGTGACAGCGACCTTACCGACAG 1963
Qy 1990 CCTTAGGAATCTGCTCAAGCTCAGCTGAGGAGGAGATGCTGCCCTAGTATGGGTAG 2049
Db 1964 CACTGAGGGTCTGCTCAAGCTCACCTGAGTGGAGTAGGCAATGCCCCAG-CCCGGTGAG 2022
Qy 2050 GCTCTGAGAGGGTTTTCAGAGGAACCTCGGTGCTCGATTCCT 2090
Db 2023 GCTCTCAGATGCAGCTGTTGCAACCCCGAGGGGAGATGCTCT 2063

RESULT 13
AB211333
ID AB211333 standard; cdna; 2043 BP.
XX
AC AB211333;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 215.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR P-PSDB; ABP69116.
XX

PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.

XX Claim 1; SEQ ID NO 215; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB211119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2043 BP; 418 A; 659 C; 592 G; 374 T; 0 U; 0 Other;

Query Match 47.3%; Score 1371.8; DB 6; Length 2043;
Best Local Similarity 82.3%; Pred. No. 2.8e-293;
Matches 1625; Conservative 0; Mismatches 317; Indels 33; Gaps 3;

Qy 82 CTACTGCTGCCCGACCCCACTCCACCTCGCGGTCCCGCACCATCGAGTCGGTGGCTTAC 141
Db 65 CTATTGATTCCCTGCGCCCTTGCTCACTCTGCTGCGCATGAGTCGCTGGTTTCG 124
Qy 142 TCCAGCGCCGACGAGGCTCCCTCGGCTCCGCTCGGAGAGCGCCGCGCGC 201
Db 125 CGCGGGCTCCGCGCCCACTCCCTCGCGCGCAGAGCTA-----GCCGCGCGC 172
Qy 202 TGGCGGACGGCTCATAGTCGCTTAAACCTCTGATGAGAGACAGCGCGTGAAGCGGC 261
Db 173 TGGCGGAGGGCTGATCAAGTCCGCCCAAGCCCTTAATGAAGAAGAGCGCGTGAAGCGGC 232
Qy 262 ACCATCACAAACAAACCTCGCGCACCGCTTACAGTTCTCTGGAGAGCGCTGGCAAGGGCA 321
Db 233 ACCACCAACAGCACACCTCGCGCACCGCTTACAGTTCTCTGGAGAGCGCTGGCAAGGGCA 292
Qy 322 CTACGGGAAGGTGAAGAAGGACGAGAGAGCTCGGGGCGCTCTGGTGCCCATCAAGTCCA 381
Db 293 CCTACGGGAAGGTGAAGAAGGCGCGGGAGAGCTCGGGGCGCTCTGGTGCCCATCAAGTCCA 352
Qy 382 TCAGGAAGACAAATCAAGATGAGCAGGATCTGCTGCACATACGAGGGGAGATTGAGA 441
Db 353 TCCGGAAGGACAAATCAAGATGAGCAGGATCTGATGACATACGAGGGGAGATTGAGA 412
Qy 442 TCATGCTTTCACCTCAACCCACCCACATCATTTCCCATTCATGAAGTGTGTTGAGAATAGCA 501
Db 413 TCATGCTTTCACCTCAACCCACCCACATCATTTCCCATTCATGAAGTGTGTTGAGAATAGCA 472
Qy 502 GCAAGATTGTGATTGTGATGAGATATGCCAGCGCGAGCGGATCTGTATGATTATCATCATG 561
Db 473 GCAAGATTGTGATTGTGATGAGATATGCCAGCGCGAGCGGATCTGTATGATTATCATCATG 532
Qy 562 AGCGGCCACGGCTGAGTGAGCGGAGCGCCAGGCAATTTCTTCCGACAGATCGTCTGCGCC 621
Db 533 AGCGGCCACGGCTGAGTGAGCGGAGCGGAGCGGATCTGTATGATTATCATCATG 592
Qy 622 TGCACTACTGCCACCAAGACGGGATCGTTCAACCGAGATCTCAAGCTGGAAACATCCTTC 681
Db 593 TGCACTACTGCCACCAAGACGGGATCGTTCAACCGAGATCTCAAGCTGGAAACATCCTTC 652
Qy 682 TAGATGCCAATGGAACATCAAGATTGTGACTTTTGGCTCTTCCAACTCTACCAAAAG 741
Db 653 TGGATGCCAATGGAATATCAAGATTGTGACTTTTGGCTCTTCCAACTCTTACCATCAAG 712

QY 742 GCAAGTTCCTCCAGACGTTCTGTGGAGCCCTCTCTACGCTCGCCTGAGATAGTCAACG 801
Db 713 GCAAGTTCCTCCAGACATCTGTGGAGCCCTCTCTATGCTTCGCCAGAGATTGTCAATG 772
QY 802 GGAAGCCCTATGTGGGCCAGAGGTGGACAGCTGTCTCTGGGGTCTCTCTGTACATCC 861
Db 773 GGAAGCCCTACACAGGCCACAGGTGGACAGCTGTCTCTGGGTCTCTCTGTACATCC 832
QY 862 TGGTGCATGGACCATGCTTTGACGGGCAAGGATATATAAACAATGTTGAAGCAAAATCA 921
Db 833 TGGTGCATGGACCATGCTTTGATGGGCATGACCAATAAGATCTTAGTGAACAGATCA 892
QY 922 GTAACGGGGCTTACCGTAGCGGCCCAAGCCGTCGATGCTGTGGCTGATCGGTGGC 981
Db 893 GCAACGGGGCTTACCGGAGCCCACTAAACCTCTGTATGCTGTGGCTGATCGGTGGC 952
QY 982 TGTAAATGGTGAACCCCAACCCGTCGGGCCACACCTGGAGGATGTAGCCAGTCAATTTGGTGGG 1041
Db 953 TGTGATGGTGAACCCCAACCCGTCGGGCCACACCTGGAGGATGTGGCCAGTCACTTGGTGGG 1012
QY 1042 TCAACTGGGGTTACACACCGGAGTGGGGGAACAGGAAGCCCTCGTGAGGGTGGGCACC 1101
Db 1013 TCAACTGGGGTTACCGCACCCGAGTGGGAGACAGGAGGCTCCGCATGAGGGTGGGCACC 1072
QY 1102 CTAGTGTGACTTTGGCGGGCTCCATGGCGGACTGTTACGTCGCTCTCGCGGCCCC 1161
Db 1073 CTGCACTGACTCTGCGCGCCCTCCATGGCTGACTGGCTCCGGGTTCTCTCGCGCCCC 1132
QY 1162 TCCTGGAGATGGAGCAAGGTGTGCAGCTTCTTCAAGACAGCAGCTGCGCGGAGGTGGAA 1221
Db 1133 TCCTGGAGATGGGGCAAGGTGTGCAGCTTCTTCAAGACAGCAGTGCACCTGGTGGGGAA 1192
QY 1222 GCATCTGACTGGCTGGAGGGCAACATCTCTTAAGAGTCCCGAAGAGAGATGACA 1281
Db 1193 GCACACCTCTGGCTGGAGGGCCAGCATTCGCTCAAGAAGTCCCGAAGAGAGATGACA 1252
QY 1282 TGGCTCAAAATCTCAAGGTGACCCGCTGAGGATACCTCTTCTCGCCCTGGCAAGAGCA 1341
Db 1253 TGGCCAGTCTCTCCAGTAGACAGCGTGTATGACCTGCCCATCGCCCTGGCAAGAGCA 1312
QY 1342 GCCTTAAGTCTCGAAAGGCATCTCAAGAAAAAGTCTCTACCTCGTCAGGGGAGGTAC 1401
Db 1313 ACCTCAAGTCTGCAAGAGGCATCTCAAGAAAGAGGTGTCAAGCTCTGCAAGAGGGGTAC 1372
QY 1402 AGGAGGACCTTCAGAACTCAGACCGGTGCTGATCTCAGGGCAGCCTGTCTCCTCTG 1461
Db 1373 AGGAGGACCTTCAGGAGCTCAGCCCAATCTCTGCGAGCCCGAGGGCAGGCTGCC- 1426
QY 1462 TATCCCTGCTCCCAAGGAAGGCATCTTAAGAAGTCTCGACAGCGTGAATCTGTTTACT 1521
Db 1427 ---CCCTGCTCCCAAGAGGGCAATCTCAAGAAGCCCGACAGCGAGTCTGGTACT 1483
QY 1522 ACTCTCTCCAGAGCCCGAGGAGTCTGGGAACTCTTTAGACGCCAGTGTATGTTGTGA 1581
Db 1484 ACTCTCTCCGAGCCCGAGTGAATCTGGGAGCTTTGGACGCGAGCGAGTGTGTTGTA 1543
QY 1582 GTGGGACCCGCTGGAGCAGAGTCTCAAGGCTTCAGGGCTCTCTCTCAACGGAAG 1641
Db 1544 GTGGGATCCCAAGGAGCAGAGCTCCGAAAGTTCAGGGCTGCTCTCTCATCGCAAG 1603
QY 1642 GCATTTCTCAAACTCAATGGCAAGTTCCTCCGCAAGCTTAGAAGGCACTACCCCTAGCA 1701
Db 1604 GCATCTCAAACTCAATGGCAAGTTCCTCCAGACAGCCTTGGAGCTCGCGGCCCCACCA 1663
QY 1702 CTTTGGCTCCTGGACCAACTGCGCTCTCTCCCATCTGAGCCCGCCAGCGCCCT 1761
Db 1664 CTTTGGCTCCTGGATGAATCTGCCCCACCTGCCCCCTTGGCCCGGCGCAGCGACCT 1723
QY 1762 CAGGGCTGTGAGGAGCAGCATCTGCTCCGAGTCTTTGACCAATTGACTTGC 1821
Db 1724 CAGGGCTGTGAGGAGCAGCATCTGCTCTGAGTCTTGTACCACTGACTTGC 1783

QY 1822 CTGAACGCTCTCCGAAACCCCACTGAGGGGCTGTGTCTGTGGACAACCTGAGGGGGC 1881
Db 1784 CTGAACGCTCTCCGAGAGCCCACTGCGGGGCTGTGTCTGTGGACAACCTCAGGGGC 1843
QY 1882 TTGAGCAGCCTCCCTCAGAAG-----GTCTGAAGCGATGTGTGCGAGGAATCCT 1929
Db 1844 TTGAGGAGCCCTCTCAGAGGGCCCTGGAAGCTGCTCTGAGGCGCTGCGGAGGATCCTT 1903
QY 1930 TGGGGGATAGCTGCTTTTCTTCTGACAGACTGCCAAGAGGTGACTGACGCTTACAGACAAG 1989
Db 1904 TGGGGGACAGCTGCTTTTCTTCTGACAGACTGCCAAGAGGTGACAGCGACCTACGACAGG 1963
QY 1990 CCTAGGAATCTGCTCAAGCTCAGCTGAGGAAGGAGATGCTGCCCTAGTATGG 2044
Db 1964 CACTGAGGGTCTGCTCAAGACTCACCTGAGTGGAGTAGGCAATGCCCCAGCCCGG 2018

RESULT 14
AAD26459
ID AAD26459 standard; cDNA; 3360 BP.
XX AAD26459;
AC AC
DT 26-MAR-2002 (first entry)
XX
XX Human kinase PKIN-12 cDNA.
DE
XX Human; kinase; PKIN-12; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
CDS 181..1965
FT /*tag= a
FT /product= "Human PKIN-12 protein"
XX
XX W0200196547-A2.
XX
XX 20-DEC-2001.
XX
XX 14-JUN-2001; 2001WO-US019444.
XX
XX 15-JUN-2000; 2000US-0212073P.
PR 23-JUN-2000; 2000US-0213467P.
PR 30-JUN-2000; 2000US-0215651P.
PR 07-JUL-2000; 2000US-0216605P.
PR 13-JUL-2000; 2000US-0218372P.
PR 25-AUG-2000; 2000US-0228056P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H, Lal P, Bandnan O, Borowsky M, Au-Young J, Lu Y;
PI Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DM, Greenwald SR;
PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang Y;
PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
DR WPI: 2002-090207/12.
DR P-PSDB; AAE16266.
XX
XX New polypeptides, useful for diagnosing, treating or preventing disorders
PT of growth and development, cardiovascular and lipid, and diseases such as

CC electronic format from
CC ftp.segdata.uspto.gov/sequence.html?DocID=20040058355.

XX Sequence 1884 BP; 403 A; 599 C; 548 G; 334 T; 0 U; 0 Other;

Query Match 46.9%; Score 1360.2; DB 12; Length 1884;
Best Local Similarity 84.2%; Pred. No. 9.9e-291;
Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;

Qy	169	CCTCGGCGCTCGGAGAGCGCGCGCGCTGGCGGAGCGGCTCATCAAGTCGCGCTA	228
Db	35	CCACTCCCTCGGCGCGAGAGCTAGCCCGCGCTGGCGGAGGCGCTGATCAAGTCGCGCA	94
Qy	229	AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCAACCATCAAAACAAACCTCGGCGACC	288
Db	95	AGCCCTTAATGAAGAAGCAGCGGTGAAGCGGCAACCATCAAAACAAACCTCGGCGACC	154
Qy	289	GCTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACGGAGGTGAAGAGCGACGAG	348
Db	155	GCTACGAGTTCCTGGAGACGCTGGGCAAGGCGACCTACGGAGGTGAAGAGCGCGGG	214
Qy	349	AGAGCTGGGCGCTCTGGTCCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC	408
Db	215	AGAGCTGGGCGCTCTGGTCCCATCAAGTCCATCAGGAAGACAAATCAAGATGAGC	274
Qy	409	AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCCGCCACA	468
Db	275	AGGATCTGATGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCCGCCACA	334
Qy	469	TCATTGCGATCCATGAAGTGTGAGAAATAGCAGCAAGATTGATGTCTATGAGATGATG	528
Db	335	TCATTGCGATCCATGAAGTGTGAGAAATAGCAGCAAGATTGATGTCTATGAGATGATG	394
Qy	529	CCAGCGAGGCGATCTGTATGATTACATCAGTGAGCGGCACCGCTAGTGAGCGGACG	588
Db	395	CCAGCGAGGCGATCTGTATGATTACATCAGTGAGCGGCACCGCTAGTGAGCGGACG	454
Qy	589	CCAGCGATTTCTCCGACAGATCGTGTCTGCCCTGCATCTAGTCCACAGAAACGGGATCG	648
Db	455	CTAGCGATTTCTCCGCGAGATCGTGTCTGCCCTGCATCTAGTCCACAGAAACGGGATG	514
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2005, 11:04:39 ; Search time 8911.77 Seconds
(without alignments)
11866.113 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est2:*
- 3: gb_hc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2865.8	98.8	2899	3 AK004737	AK004737 Mus muscu
2	2865.8	98.8	3098	3 AK033672	AK033672 Mus muscu
3	2804.4	96.6	2869	3 AK034082	AK034082 Mus muscu
4	1776	61.2	1896	9 AY399041	AY399041 Mus muscu
5	1264	43.6	1887	9 AY399039	AY399039 Homo sapi
6	951.4	32.8	1887	9 AY399040	AY399040 Pan trogl
7	721	24.8	746	6 B1653092	B1653092 603300616
8	720	24.8	795	6 CA319312	CA319312 UI-M-PWO-
9	714	24.6	727	7 CF729223	CF729223 UI-M-PWO-
10	700.2	24.1	932	4 BG915967	BG915967 602815231
11	688	23.7	705	6 CF726196	CF726196 UI-M-PWO-
12	683.6	23.6	726	6 CB248251	CB248251 UI-M-PWO-
13	672	23.2	672	7 CO424322	CO424322 UI-M-HU0-
14	667.4	23.0	716	7 CO041415	CO041415 UI-M-PWO-
C 15	663	22.8	986	7 CF584809	CF584809 AGENCOURT
16	660.8	22.8	816	4 B1143828	B1143828 602907107
C 17	655.4	22.6	704	7 CO041178	CO041178 UI-M-PWO-
18	654	22.5	893	2 BF785290	BF785290 602108490
19	653.2	22.5	713	2 BB625283	BB625283 602108490
20	652.4	22.5	655	7 CK781308	CK781308 UI-M-G10-
21	651.6	22.5	805	4 EG174288	EG174288 602334589
22	646	22.3	646	4 BG694881	BG694881 NISC_lv09
23	645.8	22.3	948	2 BF789245	BF789245 602105144
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25	639	22.0	669	2 BB078728	BB078728 BB078728
26	627.6	21.6	782	7 CN261003	CN261003 170004247
27	626	21.6	939	2 BE912458	BE912458 60166074
28	624.6	21.5	1069	4 BM927376	BM927376 AGENCOURT
29	615.6	21.2	1022	5 BQ062868	BQ062868 AGENCOURT
30	608	21.0	608	7 CK625537	CK625537 mj10904.Y
31	600.8	20.7	616	4 B1647932	B1647932 603276014
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35	596	20.5	674	5 BQ445704	BQ445704 UI-M-ERO-
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43	556	19.2	556	6 BY704937	BY704937 BY704937
44	556	19.2	556	6 CA535696	CA535696 C0222H05-
45	554.8	19.1	558	8 BH116351	BH116351 RPCI-24-2

ALIGNMENTS

RESULT 1	AK004737	2899 bp	linear	HTC 03-APR-2004
LOCUS	Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200013B22 product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.1-) [Homo sapiens], full insert sequence.	AK004737	2899 bp	AK004737
DEFINITION	HTC; CAP trapper.	AK004737	2899 bp	AK004737
ACCESSION	Mus musculus (house mouse)	AK004737	2899 bp	AK004737
VERSION	Mus musculus	AK004737	2899 bp	AK004737
KEYWORDS	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mus.	AK004737	2899 bp	AK004737
SOURCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mus.	AK004737	2899 bp	AK004737
ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mus.	AK004737	2899 bp	AK004737
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	AK004737	2899 bp	AK004737
AUTHORS	Carninci, P. and Hayashizaki, Y.	AK004737	2899 bp	AK004737
TITLE	High-efficiency full-length cDNA cloning	AK004737	2899 bp	AK004737
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	AK004737	2899 bp	AK004737
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REFERENCE	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	AK004737	2899 bp	AK004737
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	AK004737	2899 bp	AK004737
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	AK004737	2899 bp	AK004737
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	AK004737	2899 bp	AK004737
MEDLINE	20499374	AK004737	2899 bp	AK004737
PUBMED	11042159	AK004737	2899 bp	AK004737
REFERENCE	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	AK004737	2899 bp	AK004737
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	AK004737	2899 bp	AK004737
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MEDLINE	20530913	AK004737	2899 bp	AK004737
PUBMED	11076861	AK004737	2899 bp	AK004737
REFERENCE	4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	AK004737	2899 bp	AK004737
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium	AK004737	2899 bp	AK004737
TITLE	Functional annotation of a full-length mouse cDNA collection	AK004737	2899 bp	AK004737
JOURNAL	Nature 409, 685-690 (2001)	AK004737	2899 bp	AK004737
REFERENCE	5	AK004737	2899 bp	AK004737

AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2899)
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanganaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT On Dec 10, 2002 this sequence version replaced gi:12836134. Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGCGCGCGCACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGAGCGCGCGCACTCGAGTTTCTTTTCTTTTNN 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOUR.

FEATURES

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QY	1351	TTCCGAAAGGCATTCTCAAGAAAGTCTCTACCTCGTCAGGGGAGGTACAGAGGACC	1410
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Db	1502	CAGAGCCACGAGTCTGGGGAACTCTTAGACGCCAGTGTGTGTGTGAGTGGGACC	1561
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QY	1831	TTCCCGAAACCCACTGAGGGGTGTGTCTGTGGACAACTGAGGGGCTTGTAGCAGC	1890
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QY	2011	TCAGCTGAGGAAGGAGATGCTGCCCTAGTATGGGTAGGCTCTGAGAGGTTTGAGAG	2070
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QY	2311	CAACCAACAGGGTTAGAACCCCTGACTTCTCTGGAGGTAAATGTGTAGTACTGTCATTTAT	2370
Db	2282	CAACCAACAGGGTTAGAACCCCTGACTTCTCTGGAGGTAAATGTGTAGTACTGTCATTTAT	2341
QY	2371	TAGAGAGGAACAGCCTCTGGTTTCCATCTCTGCTGCTGTCATCTCAAGACCTGGAA	2430
Db	2342	TAGAGAGGAACAGCCTCTGGTTTCCATCTCTGCTGCTGTCATCTCAAGACCTGGAA	2401
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QY	2551	TTTCTCAGGCCAACGGACCTAGAAATGTGCTGACTTATTTATTTTGTGATCTCACT	2610
Db	2522	TTTCTCAGGCCAACGGACCTAGAAATGTGCTGACTTATTTATTTTGTGATCTCACT	2581
QY	2611	TCGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG	2670
Db	2582	TCGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG	2641
QY	2671	CAATAATGGAATGCTGTGTTCTTGGGAACTCCACTGTGCCACTGAAGTTTATGTACAGA	2730
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QY	2731	GAAGTATTTGGCAATGATGTCCTCTATTCAAGGGGGGTGGGGCGTTTTTCAAAATGAT	2790
Db	2702	GAAGTATTTGGCAATGATGTCCTCTATTCAAGGGGGGTGGGGCGTTTTTCAAAATGAT	2761
QY	2791	GTCTTGAGCACTGTCTGGATTGAGTCTCCAGTCCCTTTCACACCAAGGCTGGCCACCTC	2850
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RESULT 2

AK033672

LOCUS

DEFINITION

AK033672 3098 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male cecum cDNA, RIKEN full-length enriched
library, clone:9130215K18 product:weakly similar to PROBABLE
SERINE/THROMBIN-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) (Homo
sapiens), full insert sequence.

ACCESSION

AK033672

VERSION

AK033672.1

GI:26329364

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

REFERENCE

1

AUTHORS

Carninci, P. and Hayashizaki, Y.

TITLE
JOURNAL
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PUBMED
REFERENCE
AUTHORS

High-efficiency full-length cDNA cloning
99279253
10349636
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Please visit our web site for further details.
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URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Location/Qualifiers
1. .3098
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ORIGIN

Query Match 98.8%; Score 2865.8; DB 3; Length 3098;
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Qy 91 CCGAGCCCACTCCACCTCCGGTCCCGCCACCATGAGTCTGGTGGCTTACTCCAGCGCC 150
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Qy 151 CGAGCCAGGCTCCCTCGGCTCCGCTCGGCTCGGAGAGCGCCCGCGCTCGCGGACG 210
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Qy 211 GGCTCATCAAGTCCGCTAACTCTGATGAGAGAGCGCGGTGAGCGGACCATCACA 270
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QY 391 ACATAATCAAGATGAGCAGGATCTGTGCACATACGAGGGGAGATTGAGATCATGTCTT 450
DB 366 ACAAAATCAAGATGAGCAGGATCTGTGCACATACGAGGGGAGATTGAGATCATGTCTT 425
QY 451 CACTCAACCCACCCACATCATTCGCCATCCATGAA-----G 486
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VERSION AY399041.1 GI:39755030
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1896)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1896)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
ADAMS,M.D. and CARGILL,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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genomic survey sequence.
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VERSION AY399039
KEYWORDS
SOURCE GSS.
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS
TITLE
1 (bases 1 to 1887)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2' (bases 1 to 1887)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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DB	1115	ATTGCTTCAAGAAG	TCCCGCAAGGAGAATGACATGG	CGCCAGTCTCTCTCCACAGTGACACGG	1174
QY	1309	CTGAGGATACCTCTT	CTCGCCCTGGCAAGAGCAGCCTTA	GCTTCCGAAAGGCATTTCTCA	1368
DB					
DB	1175	CTGATGACACTGCC	CCATCGCCCTGGCAAGAGCAACCTCA	AGCTGCCAAAGGCGCATTTCTCA	1234
QY	1369	AGAAAAAGTCCCTT	ACCTCGTCAGGGAGGTACAGGAGG	AGCCCTCAGGAACTCAGACCGG	1428
DB					
DB	1235	AGAAGAGGTGTCA	GCTCTTCGCAAGGGGTACAGGAGG	AGCCCTCCGGAGCTCAGCCCAA	1294
QY	1429	TGCCTGATATCTCA	GAGGAGCCTGTCTCCCTGTGTTAT	CTCTGCTCCCAAGGAAAGGCATCC	1488
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DB	1295	TCCCTGGAGGCCA	GAGGAGGCTGCC-----CCCTGCT	CCCCCAAGAGGGGCATTC	1345
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DB	1346	TCAGAAGCCCCG	ACAGCGGAGTCTGGCTACTACTCT	CTCTCCGAGCCCAGTGAATCTG	1405
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QY	1609	CACAGGCTTCAGG	CTCTCTCACCGCAAGGGCATTTCA	AACTCAATGGGCAAGTTCT	1668
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QY	1669	CCGCAAGCTTTAGA	AGGCACTACCCCTAGCACCTTTGG	CTCCCTCGACCAACTGSCCT	1728
DB					
DB	1526	CCAGACAGCCTTG	AGACTCGCGGCCCCACCA	CTTCGGCTCCTCGATGAATCTCGCC	1585
QY	1729	CCTTCCCATCTTG	ACCGCGGCCACGCGCCCTCAGGG	GGCTGTGAGTGAGSACAGCATCC	1788
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DB	1646	TGTCCTCTGAGT	CTCTTTGACACAGCTGACATTGG	CTCTGAAACGCGCTCCAGAGCCCCCACTGC	1705
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ACCESSION	AY399040		
VERSION	AY399040.1	GI:39755029	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Pan troglodytes		
REFERENCE	1 (bases 1 to 1887)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003)		
PUBMED	Science 302 (5652), 1960-1963 (2003)		
REFERENCES	1 (bases 1 to 1887)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003)		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
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Best Local Similarity	60.1%;	Pred. No. 4e-213;	
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Qy	229	AACCTTGTATGAAGAAGCAGCGGCTGAAGCGGACCATCATCAACAACAACCTCGCGCAC	288
Db	95	AGCCCTTAATGAAGAAGCAGCGGCTGAAGCGGACCATCAACAACAACCTCGCGCAC	154
Qy	289	GCTACGAGTTCCTGGAGACGCTGGCAAGGCGACCTACGGGAAGGTTGAAGAAGCGCAG	348
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Qy	349	AGAGCTCGGGCGCTCTGGTGGCCATCAAGTTCATCAGGAAGGACAAATCAAAAGATGAGC	408
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Qy	409	AGGATCTGTGCATACGAGGAGATTGAGATCATGTCTTCACTCAACACCCGCCACA	468
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455 NNN 514
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1175 CTGATGACTGCCCCATCGCCCTGGCAAGAGAGACCTTCAAGTGGCCAAAGGGATTTCTCA 1234
1369 AGAAAGAGTCTCTTACCTCGCTCAGGGAGGTACAGGAGGACCTCTCAGGAATCTCAGACCGG 1428
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1429 TGCTGTATCTCAGGCGCAGCTGTCTCCCTGTATCTCTGCTTCCCTGCTCCCAAGAAAGGATCC 1488
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2017 GA 2018
1886 GA 1887

RESULT 7
BI653092
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI653092 746 bp mRNA linear EST 12-SEP-2001
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mRNA sequence.
BI653092
BI653092.1 GI:15567328
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC <http://mgi.nhl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLML1866 row: p column: 04
High quality sequence stop: 746.

FEATURES
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 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lother Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

ORIGIN

Query Match 24.8%; Score 721; DB 4; Length 746;
 Best Local Similarity 98.0%; Pred. No. 7.7e-159;
 Matches 730; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 UI-M-FW0-cbz-i-16-0-UI.r1 NIH BMAP_FW0 Mus musculus cDNA clone
 IMAGE:6816569 5', mRNA sequence.
 CA319312
 ACCESSION
 CA319312.1 GI:24537436

KEYWORDS

SOURCE
 ORGANISM

EST.
 Mus musculus (house mouse)

Mus musculus

REFERENCE
 1 (bases 1 to 795)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS

TITLE

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. .795

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/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP_FW0"

/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

is AGCGAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN

Query Match 24.8%; Score 720; DB 6; Length 795;

Best Local Similarity 96.8%; Pred. No. 1.3e-158;

Matches 765; Conservative 0; Mismatches 0; Indels 25; Gaps 2;

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Db 1 GCGGCTGTGACCTCTGAGCCCGGCTCAGCGCGGCTGCTACTGTGCCGACCCACTC 60

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Db 121 CTTGGGCTTCCGCTTGGGCTCGGAGAGCGCCGCGGCTGGCGGAGGCTCATCAAGT 180

Qy 223 CCGCTAAACCTCTGATGAAGAGCGGCTGAAGCGGACCATCAACAACACCTCGC 282

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Qy 283 GGCACCGCTACAGTTCCTGGAGAGCGTGGCAAGGACCTACGGGAGGTGGAAGG 342

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QY 463 CCACATCATGTGCATCCATGAA-----GTGTTTGAGAAATA 498
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Db 481 GCAGCAAGATTGATGTTGATGAGATGATCCAGCGAGCGGATCTGTATGATATCATCA 540
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CF729223
VERSION CF729223.1 GI:37603391
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
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Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTTTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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ORIGIN

Query Match	Best Local Similarity	24.6%	Score 714;	DB 7;	Length 727;				
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QY	2248	GTCAACCATGACATTTCCCAACCTGTTCTCTGGCTGCACCTTCACATAAGTTTCTGTTTC	2307						
Db	420	GTCAACCATGACATTTCCCAACCTGTTCTCTGGCTGCACCTTCACATAAGTTTCTGTTTC	479						
QY	2308	CATCAACCAACCCAGGGTTAGAACCTTGACTTCTCTGGAGGTAATGTGTAGTACTGCCATT	2367						
Db	480	CATCAACCAACCCAGGGTTAGAACCTTGACTTCTCTGGAGGTAATGTGTAGTACTGCCATT	539						
QY	2368	ATTAGAGAGGAAACAGCTCTGGTTTTCATCTCTGCTGCTGTGCATCTCAAGAACCTGG	2427						
Db	540	ATTAGAGAGGAAACAGCTCTGGTTTTCATCTCTGCTGCTGTGCATCTCAAGAACCTGG	599						
QY	2428	GAAAGACTCGGACCGCTGTTTGAATCTCTCAAGGGGACCCAGATGCCCTGGACCCCATC	2487						
Db	600	GAAAGACTCGGACCGCTGTTTGAATCTCTCAAGGGGACCCAGATGCCCTGGACCCCATC	659						
QY	2488	TTAGATCTCAGAGACTTGAACCTTGAAGCTGTTTCTTAGTACCAGATGTGGATGGATGCT	2547						
Db	660	TTAGATCTCAGAGACTTGAACCTTGAAGCTGTTTCTTAGTACCAGATGTGGATGGATGCT	719						
QY	2548	CTGTTTCT 2555							
Db	720	CTGTTTCT 727							

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RESULT 10
BG915967
LOCUS
DEFINITION
  602815231F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4937647 5',
  mRNA sequence.
ACCESSION
  BG915967
VERSION
  BG915967.1 GI:14296443
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 992)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-rc@mail.nih.gov
  Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
  Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LHAM10871 row: m column: 08
  High quality sequence stop: 695.
  Location/Qualifiers
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      /clone="IMAGE:4937647"
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      /dev stage="5 months"
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      /notes="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;
      Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
      Library constructed by Life Technologies. Investigators
      providing samples: Lothar Hennighausen/Priscilla Furth,
      NIH Reference for transgenic model: Li et al., Cell Growth
      and Differentiation 7, 3-11 (1996)."
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ORIGIN

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Query Match      24.1%; Score 700.2; DB 4; Length 992;
Best Local Similarity 92.2%; Pred. No. 6.6e-154;
Matches 857; Conservative 0; Mismatches 60; Indels 12; Gaps 11;

QY 1931 GGGGATAGCTGCTTTCTCTGACAGACTGCCAAGAGTGCAGCTGCAGCTACAGCAAGC 1990
DB 13 GGGGATAGCTGCTTTCTCTGACAGACTGCCAAGAGTGCAGCTGCAGCTACAGCAAGC 72

QY 1991 CCTAGGAATCTGCTCAAGCTCAGCTGAGGAAGGAGTGCCTCTAGTATGGGTAGG 2050
DB 73 CCTAGGAATCTGCTCAAGCTCAGCTGAGGAAGGAGTGCCTCTAGTATGGGTAGG 132

QY 2051 CTCTGAGAGGTTTGCAGAGGAACCCCTGGTCCGATTCCTCCAGTGAATAGATACATCA 2110
DB 133 CTCTGAGAGGTTTGCAGAGGAACCCCTGGTCCGATTCCTCCAGTGAATAGATACATCA 192

QY 2111 AGGGCTCTAGCTGCAGCTGACTGACCTGAAGATGAGAAATCGCATTTGATGTGG 2170
DB 193 AGGGCTCTAGCTGCAGCTGACTGACCTGAAGATGAGAAATCGCATTTGATGTGG 252

QY 2171 AAAGGAATGGAAACCCCTTGTCTGCCCGAGTGTATAGTGGGGTGCCTGAAGGTGCCTACC 2230
DB 253 AAAGGAATGGAAACCCCTTGTCTGCCCGAGTGTATAGTGGGGTGCCTGAAGGTGCCTACC 312
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QY 2231 TCCTTTGTGCGCATGAGTGCACCCATGACATTTCCACCCCTGTTCTCTGCTGCACCTTC 2290
DB 313 TCCTTTGTGCGCATGAGTGCACCCATGACATTTCCACCCCTGTTCTCTGCTGCACCTTC 372

QY 2291 ACATAAGTTTCTGTTTCCATCAACCAAGGGTTAGAACCTCAGCTTCCTGGGAGGTA-A 2349
DB 373 ACATAAGTTTCTGTTTCCATCANACA-CAGGGTTAGAACCTCAGCTTCCTGGGAGGTACA 431

QY 2350 TGTGTAGTGAATGCCATTTATTTAGAGAGGAACAGCCTCTGGTTTCCATCTCTGCTGCTG 2409
DB 432 TGTGTAGTGAATGCCATTTATTTAGAGAGGAACAGCCTCTGGTTTCCATCTCTGCTGCTG 491

QY 2410 TGCATCTCAAGACCTCGGAGAGCTCGGACCGCTGTTTGAATTCATCTCAAGGGGACCAG 2469
DB 492 TGCATCTCAAGACCTCGGAGAGCTCGGACCGCTGTTTGAATTCATCTCAAGGGGACCAG 551

QY 2470 ATGCCCTCTGACCCCATCTTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTCTAGTACC 2529
DB 552 ATGCCCTCTGGA-CCCATCTTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTCTAGTACC 610

QY 2530 CAGATGTGGA-TGGATGCTCTGTTTCTCAGGCCAACCGGACCTAGAAATGTGCTGCTAT 2588
DB 611 CAGATGTGGA-TGGATGCTCTGTTTCTCAGGCCAACCGGACCTAGAAATGTGCTGCTAT 670

QY 2589 TTATTTTTTTTGATTTCTCACTTCTGTTTGGTTT- -TTTGTGTTGTTGTTGTTTGG 2646
DB 671 NTAATCTCCCGTGATTTCTCACTTCTGTTTCCAGGTCAAAGATCGAGCGGTAGCCCAAGG 730

QY 2647 TTTTAAAGTGAATTTTGGT- -GCTTTCAATAATGTGAATGCTGTGTTCTGGGGAATCCAC 2705
DB 731 TCCTAACGTGCACTTTTGTCTGGCTTTCACCTACTGTGAATGCTGTGTTCTGGG- -ACTCCAC 789

QY 2706 TGTGCCACTGAAGTTTATGTACAGAGAAATTTTGGCAATGATG-TCCCTCTATTTCAGG 2764
DB 790 TGTGCC-CTGAAGTCTAGGTCCGGCGAAAGTTTGGCACTGATGTTTCCCTCTATTTCAGG 848

QY 2765 GGGGTGGGGCGGTTTTTCA-AATGATGCTTTGAGCAGCTGCTGGATTGAGTCTCCAGTC 2823
DB 849 GGGGTGGGGCGGTTTTTCAATGCTGTTTGAAGCAGCTGGTGGATTGCGT-TCCCGTC 907

QY 2824 CTTTACACCCCAAGGCTGCCACCCCTCCC 2852
DB 908 CTTTCAGGCCCAAGGTGGGCCACCCCTGCC 936

RESULT 11
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LOCUS
DEFINITION
  UI-M-GZO-cjp-h-08-0-UI.r1 NIH BMAP_GZO Mus musculus cDNA clone
  IMAGE:30606415 5', mRNA sequence.
ACCESSION
  CF726196
VERSION
  CF726196.1 GI:37600364
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
REFERENCE
  1 (bases 1 to 705)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-rc@mail.nih.gov
  Tissue Procurement: Dr. James Lin University of Iowa
  CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefl.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  Seq primer: pYX-5.
  Location/Qualifiers
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FEATURES

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/mol_type="mRNA"
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/clone="IMAGE:30606415"
/tissue_type="whole eye"
/dev_stage="embryo 12.5, 13.5, 14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_G20"
/notes="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATGAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
```

ORIGIN

Query Match 23.7%; Score 688; DB 7; Length 705;
Best Local Similarity 99.3%; Pred. No. 4.6e-151;
Matches 688; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 31 GCGTCTCGGTCGGCTGTGACCTCGAGCCGCGCTCAGCGCGCTGCTACTGCTG 90
DB 13 GCGTCTCGGTCGGCTGTGACCTCGAGCCGCGCTCAGCGCGCTGCTACTGCTG 72

QY 91 CCCGACCACTCCACCTCGCGCTCCCGCACCATGAGTGGTGGCTTACTCCAGCGCC 150
DB 73 CCCGACCACTCCACCTCGCGCTCCCGCACCATGAGTGGTGGCTTACTCCAGCGCC 132

QY 151 CGAGCCAGGCTCCCTCGGCTCCGCTCGGCTCGGAGAGGCGCGCGCTGCGGAGC 210
DB 133 CGAGCCAGGCTCCCTCGGCTCCGCTCGGAGAGGCGCGCGCTGCGGAGC 192

QY 211 GGCTCATCAAGTCCCTAACTCTGATGAGAGAGGCGGTGAAGCGCACCATCACA 270
DB 193 GGCTCATCAAGTCCCTAACTCTGATGAGAGAGGCGGTGAAGCGCACCATCACA 252

QY 271 AACACAACTCGCGCACCGCTTACGAGTTCCTGGAGAGCGCTGGGCAAGGCACTTACGGGA 330
DB 253 AACACAACTCGCGCACCGCTTACGAGTTCCTGGAGAGCGCTGGGCAAGGCACTTACGGGA 312

QY 331 AGGTGAAGAGGCAAGAGAGCTCGGGCGTCTGGTGGCCATCAATCCATCAGGAAG 390
DB 313 AGGTGAAGAGGCAAGAGAGCTCGGGCGTCTGGTGGCCATCAATCCATCAGGAAG 372

QY 391 ACAAATCAAGATGACGAGATCTGTCACATACGAGGAGATTCATGATCCTT 450
DB 373 ACAAATCAAGATGACGAGATCTGTCACATACGAGGAGATTCATGATCCTT 432

QY 451 CACTCAACACCCCAACATCATTCATGAGTGTGAGATGAGAGGAGATTCATG 510
DB 433 CACTCAACACCCCAACATCATTCATGAGTGTGAGATGAGAGGAGATTCATG 492

QY 511 TGATTGTATGAGATGATCCAGCGGAGCTGTTATGATTAATCATCAGTGGCGGAC 570
DB 493 TGATTGTATGAGATGATCCAGCGGAGCTGTTATGATTAATCATCAGTGGCGGAC 552

QY 571 GGCTGAGTGGCGGAGCGGAGATTCCTCCAGAGATCTGCTGCGCTGCACTACT 630
DB 553 GGCTGAGTGGCGGAGCGGAGATTCCTCCAGAGATCTGCTGCGCTGCACTACT 612

QY 631 GCCACCAAGAGGATCGTTCCAGCGATCTCAAGCTGGAAACATCTCTTAGATGCA 690

Db 613 GCCACCAAGAGGATCGTTCCAGCGATCTCANGCTGAANACATCTCTTAGATGCA 672

QY 691 ATGGAACATCAAGATTCGCTGACTTTGGCTCT 723

Db 673 NTGGAACATCAAGATTCGCTGACTTTGGCTCT 705

RESULT 12

LOCUS CB248251 726 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-FD0-byi-a-21-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone

ACCESSION IMAGE:5718428 5', mRNA sequence.

VERSION CB248251

KEYWORDS CB248251.1 GI:28386432

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 726)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.
Location/Qualifiers
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/clone="IMAGE:5718428"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F00"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 23.6%; Score 683.6; DB 6; Length 726;
Best Local Similarity 98.8%; Pred. No. 5.1e-150;
Matches 720; Conservative 0; Mismatches 5; Indels 4; Gaps 3;

QY 922 GTAAACGGGCTTAC-CGTGAGCGCCAGCCGCTCCGCTGCTGCGCTGATCCGCTGG 980

DB 1 GTAAACGGGCTTACNCGTGAGCGCCAGCCGCTCCGCTGCTGCGCTGATCCGCTGG 60

QY 981 CTGTTAATGTGTAACCCCGCTCGGGCCACACTGAGGATGTAGCAGTCTATTGCTGG 1040


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Db      61  CTGTTAATGTGAACCCACCCCGTCGGGCCACACTGGAGGATGTAGCAGTCATTGGTGG 120
QY      1041 GTCAACTGGGTTACACCAACCGAGTGGGAAACAGAAAGCCCTGCGTGGAGTGGGCAC 1100
Db      121  GTCAACTGGGTTACACCAACCGAGTGGGAAACAGAAAGCCCTGCGTGGAGTGGGCAC 180
QY      1101 CCTAGTGGTGAATTTGGCGGGCTCCATGCGGACCTGGTTACGTGCTCTCGCGCCCC 1160
Db      181  CCTAGTGGTGAATTTGGCGGGCTCCATGCGGACCTGGTTACGTGCTCTCGCGCCCC 240
QY      1161 CTCCTGAGAAATGAGCAAGGTGTGACGTCTTCAAGCAGACAGTGCCTGGAGGTGGA 1220
Db      241  CTCCTGAGAAATGAGCAAGGTGTGACGTCTTCAAGCAGACAGTGCCTGGAGGTGGA 300
QY      1221 AGCACTTACTGGCTGGAGCGCAATCTTTAAGAGTCCGAGAGGTGGA 1280
Db      301  AGCACTTACTGGCTGGAGCGCAATCTTTAAGAGTCCGAGAGGTGGA 360
QY      1281 ATGGCTCAAAATCTGCAAGGTGACCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGC 1340
Db      361  ATGGCTCAAAATCTGCAAGGTGACCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGC 420
QY      1341 AGCCTTAAGTCTCGAAAGGATCTCAAGAAAGTCTTACCTCGTCAGGGAGGTA 1400
Db      421  AGCCTTAAGTCTCGAAAGGATCTCAAGAAAGTCTTACCTCGTCAGGGAGGTA 480
QY      1401 CAGGAGACCTCAGGAACCTAGACCGGTGCTGATCTCCAGGCGAGCTGTCCCTGCT 1460
Db      481  CAGGAGACCTCAGGAACCTAGACCGGTGCTGATCTCCAGGCGAGCTGTCCCTGCT 540
QY      1461 GTATCCCTGCTCCCAAGGAAGGATCTTAAGAGTCTCGACAGCTGAATCTGGTTAC 1520
Db      541  GTATCCCTGCTCCCAAGGAAGGATCTTAAGAGTCTCGACAGCTGAATCTGGTTAC 600
QY      1521 TACTCTCTCAGAGCCAGCAGTCTGGGAACTCTTAGACGCGCAGTGTGTTGTG 1580
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QY      1581 AGTGGGACCCGTTGAGCAGAGTCTCCAGAGCTTCAGGGCTCTCCCTCCACCGCAAG 1640
Db      661  AGCGNGA--CCGTGGAGCAGAA--TCTCAGGCTTCAGGGCTCTCTCCACCGCAAG 717
QY      1641 GGCATTCTC 1649
Db      718  GGCATTCTC 726

RESULT 13
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LOCUS      672 bp      mRNA      linear      EST 06-JUL-2004
DEFINITION      UI-M-HUO-cqx-a-14-0-UI.r1 NIH_BMAP_HU0 Mus musculus cDNA clone
IMAGE:30665389 5', mRNA sequence.
ACCESSION      CO424322.1 GI:49670481
VERSION        CO424322.1
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 672)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@email.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

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      /dev_stage="newborn ( 1, 5, 15 days )"
      /lab_host="DH10B (T1 phage resistant)"
      /clone_lib="NIH_BMAP_HU0"
      /note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AATAATTACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN
Query Match      23.2%; Score 672; DB 7; Length 672;
Best Local Similarity 100.0%; Pred. No. 2.7e-147;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      913  AGCAATCAGTAACGGGGCTTACCGTAGCGCGCCAGCGCTCGATCGCTGTGGCTGA 972
Db      1    AGCAATCAGTAACGGGGCTTACCGTAGCGCGCCAGCGCTCGATCGCTGTGGCTGA 60
QY      973  TCCGGTGGCTGTTAATGTTGAACCCACCCGTCGGGCCACACCTGGAGGATGTAGCCAGTC 1032
Db      61  TCCGGTGGCTGTTAATGTTGAACCCACCCGTCGGGCCACACCTGGAGGATGTAGCCAGTC 120
QY      1033 ATTGTGGGTCAAATCGGGTTACACCCGAGTTCGGGAAACAGGAAGCCCTCGGTGAG 1092
Db      121  ATTGTGGGTCAAATCGGGTTACACCCGAGTTCGGGAAACAGGAAGCCCTCGGTGAG 180
QY      1093 GTGGGCAACCTAGTGTGCTTTGGCGGGCTTCATGGGAGTGGTACGTGCTCT 1152
Db      181  GTGGGCAACCTAGTGTGCTTTGGCGGGCTTCATGGGAGTGGTACGTGCTCT 240
QY      1153 CGCGCCCTCTCTGGAGAAATGGAGCCAAAGTGTGCAGCTTCTTCAAGCAGCAGTGC 1212
Db      241  CGCGCCCTCTCTGGAGAAATGGAGCCAAAGTGTGCAGCTTCTTCAAGCAGCAGTGC 300
QY      1213 GAGGTGGAAGCACTGTACTTGGGCTGGAGCGGCAACATTTCTTTAAGAAAGTCCCGAAAG 1272
Db      301  GAGGTGGAAGCACTGTACTTGGGCTGGAGCGGCAACATTTCTTTAAGAAAGTCCCGAAAG 360
QY      1273 AGAATCAGATGCTCAAAATCTGCAAGTGAACCCGCTGAGGATACCTCTTCTCGCCCTG 1332
Db      361  AGAATCAGATGCTCAAAATCTGCAAGTGAACCCGCTGAGGATACCTCTTCTCGCCCTG 420
QY      1333 GCAAGAGCAGCTTAAAGCTTCCGAAAGGATTTCTCAAGAAAGTCTCTTACCTCGTCAG 1392
Db      421  GCAAGAGCAGCTTAAAGCTTCCGAAAGGATTTCTCAAGAAAGTCTCTTACCTCGTCAG 480
QY      1393 GGGAGTACAGGAGGACCTCAGGAACCTCAGACCGGTGCTGTATCTCCAGGGCAGCTG 1452
Db      481  GGGAGTACAGGAGGACCTCAGGAACCTCAGACCGGTGCTGTATCTCCAGGGCAGCTG 540
QY      1453 TCCTCTCTGTATCCCTGCTCCCAAGGAAAGGATCTTAAAGAGTCTCCAGCAGCGTGAAT 1512
Db      541  TCCTCTCTGTATCCCTGCTCCCAAGGAAAGGATCTTAAAGAGTCTCCAGCAGCGTGAAT 600
QY      1513 CTGGTTACTACTCTCTCCAGAGCCAGCGAGTCTGGGGAACCTCTTTAGACGCCAGTGATG 1572

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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

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High quality sequence stop: 347.

FEATURES

Location/Qualifiers

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1..986

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/lab host="DH10B"

/clone_lib="NIH_MGC_137"

/note="Organ: pancreas; Vector: pSPORT1; Site 1: SalI;
Site 2: NotI; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
islets 1 MIS1-A, and Kaestner ngn3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 22.8%; Score 663; DB 7; Length 986;
Best Local Similarity 96.2%; Pred. No. 3.e-145;
Matches 709; Conservative 0; Mismatches 24; Indels 4; Gaps 3;

Qy 2166 TGTGGAAGGAATGGGAACCTTCTGCCGAG-TGTTATAGTGGGTGGCCCTGAAGGTG 2224
Db |||
Qy 738 TGGAAAGGAATGGGAACCTTCTGCCGAGTGTATAGTGGGTGGCCCTGAAGGTG 679
Db |||
Qy 2225 CCTACCTCCTTTGTGCC--ATGAGTGTACCCATGACATTTCCACCCCTGTCTCTGGCT 2282
Db |||
Qy 678 CCTACCTCCTTTGTGCCATGAGTGTACCCATGACATTTCCACCCCTGTCTCTGGGT 619
Db |||
Qy 2283 GCACCTTCACATAGTTTCTCTTCCATCAACACACAGGTTAGAACCTTGACTTCCTGG 2342
Db |||
Qy 618 GCACCTTCACATAGTTTGTGTTTCCATCACCACACAGGTTAGAACCTTGACTTCCTGG 559
Db |||
Qy 2343 GAGTAAATGTGTAGTGTGCTGCATTTATTAGAGAGGAACAGCCTCTGGTTCCATCTCT 2402
Db |||
Qy 558 GAGTAAATGTGTAGTGTGCTGCATTTATTAGAGAGGAACAGCCTCTGGTTCCATCTCT 499
Db |||
Qy 2403 GCTGCTGTGATCTCAAGACCTGGGAAGCTGGGACCGCTGTTGACTTCACTCAAGG 2462
Db |||
Qy 498 GCTGCTGTGATCTCAAGACCTGGGAAGCTGGGACCGCTGTTGACTTCACTCAAGG 439
Db |||
Qy 2463 GGACCAAGATCCCTGGACCCCATCTTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTC 2522
Db |||
Qy 438 GGACCAAGATCCCTGGACCCCATCTTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTC 379
Db |||
Qy 2523 TAGTACCAAGATGGATGTGCTCTGTTTTCAGGCCAACGGGACCTAGATGTGCTG 2582
Db |||
Qy 378 TAGTACCAAGATGGATGTGCTCTGTTTCTCAGGCCACCGGGCCCTAGAATGTGCTG 319
Db |||
Qy 2583 ACTTATTTATTTTGTGATCTCACTCTGTTTTTTGG-TTTTGTGTTGTTGTTGT 2641
Db |||
Qy 318 ACTTATTTATTTTGTGATCTCACTCTGTTTTTTGGTTTTTGTGTTGTTGT 259
Db |||
Qy 2642 TTTTGTGTTTAAAGTAAATTTGTGCTTTCAATAATGTAATGCTGTGTTCTGGGAACT 2701
Db |||
Qy 258 TTTTGTGTTTAAAGTAAATTTGTGCTTTTCAATAATGTAATGCTGTGTTCTGGGAACT 199
Db |||
Qy 2702 CCACTGTGCCACTGAAGTTATGTACAGAGAATTTTGGCAATGATGTCCTCTATTCA 2761
Db |||
Qy 198 CCACTGTGCCACTGAAGTTATGTACAGAGAATTTTGGCAATGATGTCCTCTATTCA 139
Db |||
Qy 2762 AGGGGGGTGGGGGGTTTTTCAATGATGCTTTGAGCACTGTCTGATTGAGTCTCCAG 2821
Db |||
Qy 138 AGGGGGGTGGGGGGTTTTTCAATGATGCTTTGAGCACTGTCTGATTGAGTCTCCAG 79
Db |||
Qy 2822 TCCTCTTACACCAAGGCTGGCCACCCCTCCCTCATCTTTCATCTGTGTGGCCAAAAA 2881
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Db 78 TCCTCTTACACCAAGGCTGGCCACCCCTCCCTCATCTTTCATCTGTGTGGCCAAAAA 19
Qy 2882 AAAAAAAAAAAAAAAAAA 2898
Db 18 AAAAAAAAAAAAAAAAAA 2

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Job time : 8923.77 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:22:58 ; Search time 159.178 Seconds
(without alignments)
1422.048 Million cell updates/sec

Title: US-09-980-464-11

Perfect score: 3293

Sequence: 1 MESVALLQRPSQAPSALA.....DCQSVTAAYRQALGICSKLS 631

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3293	100.0	631	4	AAB50056 Murine Ly
2	3068.5	93.2	630	5	Aae19885 Rat SNF1/
3	2824.5	85.8	628	4	Aam93360 Human pol
4	2824.5	85.8	628	4	Abu53319 Human cel
5	2824.5	85.8	628	5	Adp69116 Human pol
6	2824.5	85.8	628	5	Aau79652 Human pro
7	2824.5	85.8	628	7	Adf76965 Novel hum
8	2824.5	85.8	628	8	Adl30886 Human pro
9	2824.5	85.8	628	8	Adl25362 Human SNA
10	2824.5	85.8	628	8	Adl14161 Novel hum
11	2824.5	85.8	628	8	Ado20172 Human pro
12	2824.5	85.8	672	8	Adj96620 Human cal
13	2800	85.0	629	4	Aab65632 Novel pro
14	2800	85.0	629	8	Adi29239 Human MAR
15	2720.5	82.6	594	5	Aae16266 Human kin
16	2590	78.7	611	6	Abp96085 Human pro
17	2416.5	73.4	534	4	Aab71959 Human TGF
18	1781.5	54.1	406	5	Abp51382 Human MDD
19	1781.5	54.1	406	5	Abp51482 Human pro
20	1699.5	51.6	661	4	Aae07847 Human pro
21	1699.5	51.6	661	4	Aae07846 Human pro
22	1699.5	51.6	661	7	Adc38421 Human pro
23	1699.5	51.6	661	8	Adj75331 Marker ge
24	1699.5	51.6	661	8	Adl25353 Human ARK
25	1699.5	51.6	661	8	Adq19734 Human sof

ALIGNMENTS

RESULT 1

AAB50056
ID AAB50056 standard; protein; 631 AA.

XX AC AAB50056;

XX DT 19-MAR-2001 (first entry)

XX DE Murine Lymph node Stromal cell kinase 1.

XX KW Murine; Lymph node Stromal cell kinase; MUSK-1; autoimmune disorder;
wound healing; periodontal disease; inflammatory disease; tumour;
infection; allergy.

XX OS Mus musculus.

XX PN WO200073468-A1.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US014696.

XX PR 28-MAY-1999; 99US-0136781P.

XX (IMMV) IMMUNEX CORP.

XX PI Bird TA, Virca GD, Martin U, Anderson DM;

XX DR WPI; 2001-061546/07.

XX DR N-PSDB; AAC90433.

XX PT Novel murine and human kinase nucleic acids useful for treating
inflammations, infections, tumors, allergies, autoimmune diseases, and
for stimulating or suppressing immune responses.

XX PS Claim 10; Page 94-96; 106pp; English.

XX CC The present sequence is Murine Lymph node Stromal cell kinase 1 (MUSK-1).
This protein is useful for treating a variety of disorders listed in the
disclosure of the specification, including autoimmune disorders, allergic
reactions, myeloid or lymphoid cell deficiencies, wound healing, and
tissue repair and replacement, burns, incisions and ulcers, periodontal
disease, inflammatory diseases, tumours and bacterial, viral or fungal
infection

XX SQ Sequence 631 AA;

Query Match 100.0%; Score 3293; DB 4; Length 631;

```

Best Local Similarity 100.0%; Pred. No. 9.5e-281;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESVALLORPSQAPSASALASASAPLADGLIKSPKPLMKQAVKRRHHKINLHRYEFL 60
Db 1 MESVALLORPSQAPSASALASASAPLADGLIKSPKPLMKQAVKRRHHKINLHRYEFL 60
Qy 61 ETLGKGTGKVKKARESSGRIVAKTSIRKDKIKDEQDLHTRREIETMSSLNHPHIIAH 120
Db 61 ETLGKGTGKVKKARESSGRIVAKTSIRKDKIKDEQDLHTRREIETMSSLNHPHIIAH 120
Qy 121 EVFENSISKIVIMEYASRGDLYDIYSERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL 180
Db 121 EVFENSISKIVIMEYASRGDLYDIYSERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL 180
Qy 181 KLENILLDANGNIKIADFGCLNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPVEDSWSL 240
Db 181 KLENILLDANGNIKIADFGCLNLYHKGFLOTFCGSPLYASPEIVNGKPYVGPVEDSWSL 240
Qy 241 GVLLYILVHGTMPDGDQDKTLVKQISNGAYREPPKPSDACGLIRWLLMVPNTPRATLLED 300
Db 241 GVLLYILVHGTMPDGDQDKTLVKQISNGAYREPPKPSDACGLIRWLLMVPNTPRATLLED 300
Qy 301 VASHWVNWGTYTGVGEALREGCHPSGDFGRASMDWLRSSRPILLENGAKVCSEFFKQ 360
Db 301 VASHWVNWGTYTGVGEALREGCHPSGDFGRASMDWLRSSRPILLENGAKVCSEFFKQ 360
Qy 361 HVPGGSTVPGLEQRHSLKSKRKNENDMAQNLOQDPAEDTSSRPKSSILKPKGILKKSS 420
Db 361 HVPGGSTVPGLEQRHSLKSKRKNENDMAQNLOQDPAEDTSSRPKSSILKPKGILKKSS 420
Qy 421 TSSEVEQDPELRPVPDTPGQPVAVSLLPRKGLKKSRORESGYTSSPEPSGELLDD 480
Db 421 TSSEVEQDPELRPVPDTPGQPVAVSLLPRKGLKKSRORESGYTSSPEPSGELLDD 480
Qy 481 ASDVFSVSDPVEQKSPQASGILLHRKGLKNGKFSRTALRGTTPTFGSLDQLASSHPA 540
Db 481 ASDVFSVSDPVEQKSPQASGILLHRKGLKNGKFSRTALRGTTPTFGSLDQLASSHPA 540
Qy 541 ARPSRPSGAVSEDSILSESDQDLPERLPETPLRGCVSDNLRGLRQPPSEGLKRWQ 600
Db 541 ARPSRPSGAVSEDSILSESDQDLPERLPETPLRGCVSDNLRGLRQPPSEGLKRWQ 600
Qy 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631
Db 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631

RESULT 2
AAE19885
ID AAE19885 standard; protein; 630 AA.
XX
AC AAE19885;
XX
DT 18-JUN-2002 (first entry)
XX
DE Rat SNF1/AMPK-Related Kinase (SNARK) protein.
XX
KW Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes;
KW glucose deprivation; lipid metabolism; therapy; lipoprotein disorder;
KW hyperglycaemic; drug screening; hypoglycaemia.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Binding-site 63..89
FT Domain /note= "Protein kinase ATP-binding region signature"
FT Domain 137..140
FT Active-site /note= "Serine/threonine kinase catalytic domain"
FT Active-site 175..187
FT Domain /note= "Serine/threonine protein kinase active-site"
FT Domain 297..300
FT /note= "Serine/threonine kinase catalytic domain"

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FT Domain 335..338
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 381..384
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 422..425
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 468..471
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 517..520
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 601..604
FT /note= "Serine/threonine kinase catalytic domain"
FT Domain 608..611
FT /note= "Serine/threonine kinase catalytic domain"
XX
W0200212456-A2.
14-FEB-2002.
02-AUG-2001; 2001WO-CA001109.
03-AUG-2000; 2000US-0222850P.
12-MAR-2001; 2001US-0274613P.
28-MAR-2001; 2001CA-02340783.
(ONEO-) 1149336 ONTARIO INC.
Drucker DJ, Rosen CF, Lefebvre DL;
WPI; 2002-241747/29.
N-PSDB; AAD31710.
AMPK (AMP-activated protein kinase)-related kinase, designated SNARK
polypeptides and polynucleotides, useful for treating or preventing
diabetes, or other disorders of lipoprotein production leading to
increased levels of cholesterol.
Claim 1; Fig 2; 94pp; English.

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The invention relates to an AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polynucleotides. SNARK (SNF1/AMP-activated protein kinase) is involved in stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK stimulates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted to have insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipoprotein production leading to increased levels of cholesterol or triglycerides. SNARK or its variants may be administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as diabetes. SNARK antibodies are used to modulate SNARK activity either in vivo for therapeutic purposes, or in vitro, for drug screening and related investigational purposes. SNARK antagonists may be administered to increase fuel production. decrease glucose uptake and increase levels of blood glucose in a patient suffering from hypoglycaemia. The present sequence is rat SNARK protein

Sequence 630 AA;

```

Query Match 93.2%; Score 3068.5; DB 5; Length 630;
Best Local Similarity 94.0%; Pred. No. 5.9e-261;
Matches 593; Conservative 12; Mismatches 25; Indels 1; Gaps 1;

```

```

Qy 1 MESVALLORPSQAPSASALASAPLADGLIKSPKPLMKQAVKRRHHKINLHRYEFL 60
Db 1 MESVALLORPSQAPSASALASAPLADGLIKSPKPLMKQAVKRRHHKINLHRYEFL 60
Qy 61 ETLGKGTGKVKKARESSGRIVAKTSIRKDKIKDEQDLHTRREIETMSSLNHPHIIAH 120
Db 61 ETLGKGTGKVKKARESSGRIVAKTSIRKDKIKDEQDLHTRREIETMSSLNHPHIIAH 120

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```
QY 121 EVFENSKIIVMEYASRGDLYVYSERPRLSERDARHFFRQIVSALHYCHONGIVHRDL 180
Db 121 EVFENSKIIVMEYASRGDLYVYSERPRLSERDARHFFRQIVSALHYCHONGIVHRDL 180
QY 181 KLENILLDANGNIKIADPGSLNLYHKGFQTCGSPLYASPEIVNGKPYVGPVDSWSL 240
Db 181 KLENILLDANGNIKIADPGSLNLYHKGFQTCGSPLYASPEIVNGKPYVGPVDSWSL 240
QY 241 GVLlyILVHGTMPPDGDHKTIVKQISNGAYREPPKPSDACGLIRWLLMNPTRATLED 300
Db 241 GVLlyILVHGTMPPDGDHKTIVKQISNGAYREPPKPSDACGLIRWLLMNPTRATLED 300
QY 301 VASHWVNWGYTTGVGQEQALREGGHPGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Db 301 VASHWVNWGYTTGVGQEQALREGGHPGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
QY 361 HVPGGGTVPLRGHSLKSRKENDMAQNIQDPAEDTSRRPKSILKPKGLKKSS 420
Db 361 HVPGGGTVPLRGHSLKSRKENDMAQNIQDPAEDTSRRPKSILKPKGLKKSS 420
QY 421 TSSGEVQEDPQELRPVDPDTPQVPVAVSLPRKGIKKSRQRESGYSSPEPSGELLDD 480
Db 421 TSSGEVQEDPQELRPVDPDTPQVPVAVSLPRKGIKKSRQRESGYSSPEPSGELLDD 480
QY 481 ASDVFGSDPVEQKSPQASGLLHHRKGIKNGKFSRTALEGTPSTFGSLDQLASHPA 540
Db 481 AGDVFGSDPVEQKSPQASGLLHHRKGIKNGKFSRTALEGTPSTFGSLDQLASHPA 540
QY 541 ARSRPSGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQEPSEGLKRWQ 600
Db 541 ARSRPSGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQEPSEGLKRWQ 600
QY 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631
Db 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 630

RESULT 3
AAM93360
ID AAM93360 standard; protein; 628 AA.
XX
AC AAM93360;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 2919.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
XX
PR 11-JAN-2000; 2000JP-00118774.
XX
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
DR WPI; 2001-524255/58.
XX
DR N-PSDB; AAK94280.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 2919; 1380pp + Sequence Listing; English.
```

```
XX The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesized by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 628 AA;
```

```
Query Match 85.8%; Score 2824.5; DB 4; Length 628;
Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;
```

```
QY 1 MESVALLQRPSPQASASALASERPLADGLIKSPKPKMKQAVKRHHKHLRHYEFL 60
Db 1 MESVLPARRSGPTFS-----AAELARPLAEGLIKSPKPKMKQAVKRHHKHLRHYEFL 56
QY 61 ETLGKGTGYGVKKARSSGRLVAIKSIRKDKIKDEQDLHRRREIETMSSLNHPHIIAH 120
Db 57 ETLGKGTGYGVKKARSSGRLVAIKSIRKDKIKDEQDLHRRREIETMSSLNHPHIIAH 116
QY 121 EVFENSKIIVMEYASRGDLYVYSERPRLSERDARHFFRQIVSALHYCHONGIVHRDL 180
Db 117 EVFENSKIIVMEYASRGDLYVYSERQQLSERARHFFRQIVSAVHYCHONRVHRDL 176
QY 181 KLENILLDANGNIKIADFGSLNLYHKGFQTCGSPLYASPEIVNGKPYVGPVDSWSL 240
Db 177 KLENILLDANGNIKIADFGSLNLYHQKGFQTCGSPLYASPEIVNGKPYTGPVDSWSL 236
QY 241 GVLlyILVHGTMPPDGDHKTIVKQISNGAYREPPKPSDACGLIRWLLMNPTRATLED 300
Db 237 GVLlyILVHGTMPPDGDHKTIVKQISNGAYREPPKPSDACGLIRWLLMNPTRATLED 296
QY 301 VASHWVNWGYTTGVGQEQALREGGHPGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Db 297 VASHWVNWGYATRVGEQEAPEHGGHPGSDSASASMDWLRSSRPLLENGAKVCSFFKQ 356
QY 361 HVPGGGTVPLRGHSLKSRKENDMAQNIQDPAEDTSRRPKSILKPKGLKKSS 420
Db 357 HAFGGGTTPLERQHSKSRKENDMAQSLHSDTADDTAHRPKSKLKLKPKGLKKVVS 416
QY 421 TSSGEVQEDPQELRPVDPDTPQVPVAVSLPRKGIKKSRQRESGYSSPEPSGELLDD 480
Db 417 ASAEVQEDPPELSPIPASPGQAAP---LLPKKGIKKRQRESGYSSPEPSGELLDD 473
QY 481 ASDVFGSDPVEQKSPQASGLLHHRKGIKNGKFSRTALEGTPSTFGSLDQLASHPA 540
Db 474 AGDVFGSDPVEQKSPQASGLLHHRKGIKNGKFSRTALEGTPSTFGSLDQLASHPA 533
QY 541 ARSRPSGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQEPSEGLKRWQ 596
Db 534 ARSRPSGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQEPSEGLKRWQ 593
QY 597 RWMQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 594 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 628
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```
RESULT 4
ABU53319
ID ABU53319 standard; protein; 628 AA.
XX
AC ABU53319;
XX
DT 14-APR-2003 (first entry)
XX
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Human cell cycle-associated protein from DKFZphtes3_7j3.

Human; gene therapy; vaccine; disease treatment; detection.

Homo sapiens.

WO200112659-A2.

22-FEB-2001.

18-AUG-2000; 2000WO-IB001496.

18-AUG-1999; 99US-0149499P.

28-SEP-1999; 99US-0156503P.

(GEHU-) GERMAN HUMAN GENOME PROJECT.

Wiemann S;

WPI; 2001-327840/34.

N-PSDB; ABX71420.

Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.

Claim 21; Page 943; 1095pp; English.

This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a polypeptide described in the disclosure of the invention

Sequence 628 AA;

Query Match 85.8%; Score 2824.5; DB 4; Length 628;

Best Local Similarity 85.7%; Pred. No. 1.9e-239;

Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;

QY 1 MESVALLQRPQAPASALASESARPLADGLIKSPKPLMKQAVKRRHHKHLRHRYEFL 60

DB 1 MESLVFARRSGPTPS----AAELARPLAELGKSPKPLMKQAVKRRHHKHLRHRYEFL 56

QY 61 ETLLGKTYGKVKARESSGRILVAIKSRKDKIDEQDLHRRRIEIMSSLNHPHIIAIIH 120

DB 57 ETLLGKTYGKVKARESSGRILVAIKSRKDKIDEQDLHRRRIEIMSSLNHPHIIAIIH 116

QY 121 EVFENSISKIVIMYASRGDLYDIYSERPLSERDARHFRQIVSALHYCHONGIVHRDL 180

DB 117 EVFENSISKIVIMYASRGDLYDIYSERQQLSERARHFRQIVSALHYCHONRVHRDL 176

QY 181 KLENILDANGNIKIADFGSLNLYHKGKFLQTCGSPLYASPEIVNGKPYVGEVDSWSL 240

DB 177 KLENILDANGNIKIADFGSLNLYHKGKFLQTCGSPLYASPEIVNGKPYVGEVDSWSL 236

QY 241 GVLIIYLVHGTMPDGDHKTIVKQISNGAYREPPKPSDAGLIRLLWMVNPTRATLED 300

DB 237 GVLIIYLVHGTMPDGDHKTIVKQISNGAYREPPKPSDAGLIRLLWMVNPTRATLED 296

QY 301 VASHWWNVGTYTGVQEQALREGCHPSGDFGRASMDWLRSSRPLLENGAKVCSPFKQ 360

DB 297 VASHWWNVGTYTGVQEQALREGCHPSGDFGRASMDWLRSSRPLLENGAKVCSPFKQ 356

QY 361 HVPGGGTVPLERQHSLSKSRKENDMAQNLQGDPAEDTSRPGKSLKLPKGLKKKS 420

DB 357 HAPGGGTVPLERQHSLSKSRKENDMAQNLQHSADTDTHRPGKSLKLPKGLKKKS 416

QY 421 TSSEGEQEDPQELRPVPTTFQGPVPAVSLPRKGIKKSRQREGSGYSSPEPSGELL 480

Db 417 ASAEGVQEDPELSPIPASFGQAAP----LLPKKGIKKRQREGSGYSSPEPSGELL 473

Qy 481 ASDVFSVSGDFVEQKSPQASGLLHRRKGIKLNKGFSTALEGTTPTFGSLDQLASSHPA 540

Db 474 AGDVFSVSGDFVEQKSPQASGLLHRRKGIKLNKGFSTALEAAPTTFGSLDELAPRPL 533

Qy 541 ARPSRPSGAVSEDSIISSESFQDLDPERLPETPLRGCVSDNLRGLRQPPSEG----LK 596

Db 534 ARASRPSGAVSEDSIISSESFQDLDPERLPETPLRGCVSDNLRGLRQPPSEGPGCLR 593

Qy 597 RWOESLGDSGCSLTDCQEVTAAYRQALGICSKLS 631

Db 594 RWRQDPLGDSGCSLTDCQEVTAAYRQALRVCSKLT 628

RESULT 5

ABP69116

ID ABP69116 standard; protein; 628 AA.

XX AC ABP69116;

XX DT 20-JAN-2003 (first entry)

XX DE Human polypeptide SEQ ID NO 1163.

XX KW Human; genome mapping; gene therapy; food supplement; virus; fungus;

XX KW cell-proliferative disorder; neurodegenerative disease; bacterial;

XX KW Parkinson's disease; Alzheimer's disease; autoimmune disease;

XX KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;

XX KW arthritis; cytostatic; immunomodulator; neotropic; neuroprotective;

XX KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;

XX KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;

XX KW antiarthritic.

XX OS Homo sapiens.

XX PN WO200270539-A2.

XX PD 12-SEP-2002.

XX PF 05-MAR-2002; 2002WO-US005095.

XX PR 05-MAR-2001; 2001US-00799451.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren P;

XX PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

XX PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX DR WPI; 2002-759812/82.

XX DR N-PSDB; ABZ11333.

XX PT New polynucleotides comprising sequences assembled from expressed

XX PT sequence tags (ESTs) useful for treating cell-proliferative,

XX PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet

XX PT or coagulation disorders.

XX PS Claim 9; SEQ ID NO 1163; 1012pp + Sequence Listing; English.

XX CC The invention relates to an isolated polynucleotide (1) comprising a

XX CC nucleotide sequence selected from any of 948 sequences (ABZ11119-

XX CC ABZ12066) or their mature protein coding portion, active domain coding

XX CC protein or complementary sequences. The polynucleotides are useful for

XX CC identifying expressed genes or for physical mapping of human genome. The

XX CC encoded polypeptides (ABP69116-ABP69119) are useful as molecular weight

XX CC markers, as a food supplement, for generating antibodies, in medical

XX CC imaging, screening and diagnostic assays and for treating cell-

XX CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's

XX CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,

XX CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,

XX CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver

CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 628 AA;

Query Match 85.8%; Score 2824.5; DB 5; Length 628;
 Best Local Similarity 85.7%; Pred. No. 1.9e-239;
 Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;

QY 1 MESVALLQRPQAPSASALASASARPLADGLIKSPKPLMKQAVKRRHHKHLRHYEFL 60
 DB 1 MESLVFARRSGPTPS-----AAELARPLAELGKSPKPLMKQAVKRRHHKHLRHYEFL 56
 QY 61 ETLGKGTGKVKKARESSGRVLVAIKSRDKIKDEQDLHLIRREIEMSSLNPHIATIH 120
 DB 57 ETLGKGTGKVKKARESSGRVLVAIKSRDKIKDEQDLHLIRREIEMSSLNPHIATIH 116
 QY 121 EVFENSKIVIMVEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIVHRDL 180
 DB 117 EVFENSKIVIMVEYASRGDLVDYISERQQLSREARHFRQIVSAVHYCHQNRVHRDL 176
 QY 181 KLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPVGVPEVDSWSL 240
 DB 177 KLENILLDANGNIKIADFGLSNLYHQGKFLQTCGSPLYASPEIVNGKPVGVPEVDSWSL 236
 QY 241 GVLLYILVHGTMPDGDHDKTLVKQISNGAYRPPKPSDACGLIRWLLMNPTRATLED 300
 DB 237 GVLLYILVHGTMPDGDHDKTLVKQISNGAYRPPKPSDACGLIRWLLMNPTRATLED 296
 QY 301 VASHWVWVNGYTTGVEQEALREGGHPGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
 DB 297 VASHWVWVNGYATRVGQEPHGGHPGSDSARASMDWLRSSRPLLENGAKVCSFFKQ 356
 QY 361 HVPGGSTVPLERQHSKKSRKENDMAQNQDPAEDTSRPGKSLKLPKGLKKKSS 420
 DB 357 HAPGGGTTPLERQHSKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPGILKKKVS 416
 QY 421 TSSEVEDQQLRPVPTDQGPVPAVLLPRKILKKRSQREGSYSSPEPESGELL 480
 DB 417 ASAGVEDQPELSPISPASGQAAP---LUPKGLKKRSQREGSYSSPEPESGELL 473
 QY 481 ASDVVFVSGDPEVQKSPQASGLLHRRKILKNGKFSRTALEGTPFTFGSLDQLASSHPA 540
 DB 474 AGDVVFVSGDPEKQKPPQASGLLHRRKILKNGKFSQTALAEAPTFTFGSLDELAPRPL 533
 QY 541 ARPSRPSGAVSEDSILSSESFQDLDPRLPPLRCVVDNLRGLQPPSEG---LK 596
 DB 534 ARASRPSGAVSEDSILSSESFQDLDPRLPPLRCVVDNLRGLQPPSEGSGCLR 593
 QY 597 RHWQESLGDSCFSITDCQEVTAAYRQALGTCSLK 631
 DB 594 RWRQDPLGDSFCFLTDCQEVTAAYRQALVCSKLT 628

RESULT 6
 AAU79652
 ID AAU79652 standard; protein; 628 AA.
 XX
 AC AAU79652;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human protein kinase 3700.
 XX
 KW Human; protein kinase 3700; PK; protein phosphorylation; tumorigenesis;
 KW cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma;
 KW tissue repair; tissue regeneration; atherosclerosis; blood-brain barrier;
 KW cell proliferation disorder; cell differentiation disorder; carcinoma;
 KW haematopoietic neoplastic disorder; metastatic disorder; leukaemia;
 KW cytostatic; antiatherosclerotic; enzyme.
 XX

OS Homo sapiens.
 XX
 PN WO200224921-A2.
 XX
 PD 28-MAR-2002.
 XX
 XX 25-SEP-2001; 2001WO-US030115.
 XX
 XX 25-SEP-2000; 2000US-0234922P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Curtis RAJ, Galvin KM;
 XX
 XX WPI; 2002-352007/38.
 XX
 XX N-PSDB; ABK14000.
 DR
 DR
 XX
 PT Use of modulators of activity of 3700 protein for making medicament for
 PT e.g., modulating protein phosphorylation or cell signaling, or for
 PT treating or preventing cellular proliferative and/or differentiative
 PT disorders.
 XX
 PS Claim 19; Fig 1; 115pp; English.

The present invention relates to the isolation of a novel human protein kinase designated 3700, and the polynucleotide sequence encoding it. The invention also describes the use of a modulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a substrate protein. Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylation, cell signalling, tumorigenesis, mitogenesis, transcription of a gene, angiogenesis, tissue repair, tissue regeneration, establishment or progression of atherosclerosis, and signalling across the blood-brain barrier. The polynucleotide and polypeptide molecules for protein kinase 3700 may be used as diagnostic targets and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating, or curing PK-related disorders and cellular proliferative and/or differentiative disorders (e.g. haematopoietic neoplastic disorders, carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700 polynucleotide sequence can be used to express protein kinase 3700, to detect a genetic alteration in a 3700 gene, in chromosome mapping, for tissue typing, in forensic biology, and as surrogate markers. The present sequence represents human protein kinase 3700

Query Match 85.8%; Score 2824.5; DB 5; Length 628;
 Best Local Similarity 85.7%; Pred. No. 1.9e-239;
 Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;

QY 1 MESVALLQRPQAPSASALASASARPLADGLIKSPKPLMKQAVKRRHHKHLRHYEFL 60
 DB 1 MESLVFARRSGPTPS-----AAELARPLAELGKSPKPLMKQAVKRRHHKHLRHYEFL 56
 QY 61 ETLGKGTGKVKKARESSGRVLVAIKSRDKIKDEQDLHLIRREIEMSSLNPHIATIH 120
 DB 57 ETLGKGTGKVKKARESSGRVLVAIKSRDKIKDEQDLHLIRREIEMSSLNPHIATIH 116
 QY 121 EVFENSKIVIMVEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHQNGIVHRDL 180
 DB 117 EVFENSKIVIMVEYASRGDLVDYISERQQLSREARHFRQIVSAVHYCHQNRVHRDL 176
 QY 181 KLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPVGVPEVDSWSL 240
 DB 177 KLENILLDANGNIKIADFGLSNLYHQGKFLQTCGSPLYASPEIVNGKPVGVPEVDSWSL 236
 QY 241 GVLLYILVHGTMPDGDHDKTLVKQISNGAYRPPKPSDACGLIRWLLMNPTRATLED 300
 DB 237 GVLLYILVHGTMPDGDHDKTLVKQISNGAYRPPKPSDACGLIRWLLMNPTRATLED 296
 QY 301 VASHWVWVNGYTTGVEQEALREGGHPGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
 DB 297 VASHWVWVNGYATRVGQEPHGGHPGSDSARASMDWLRSSRPLLENGAKVCSFFKQ 356

297 VASHWVNWGYATRVGEQEPHGGHSGDSARASMDWLRSSRPILLENGAKVCSFFKQ 356
 361 HVPGGSTVPLGRQHSILKSKRKENDMAQNLQDPAEDTSRPOKSSILKPKGILKKSS 420
 357 HAPGGSTTPGLERQHSILKSKRKENDMAQSLHSDTADTAHRPGKSNLKLKPKGILKKVS 416
 421 TSSEVOEDPOELRPVDPDPQVPVAVSLLPRKGLKSKRSRGYSSPSPSSGELL 480
 417 ASAGVQEDPELSPFASPGQAAP---LLPKGLKPKRSGSYSSPSPSSGELL 473
 481 ASDVFGSDPVEOKSPQASGLLHRKGLKNGKFSRTALGTTPTFGSLDOLASSHPA 540
 474 AGDVFGSDPVEOKSPQASGLLHRKGLKNGKFSRTALEAAPTTFGSLDELAPRPL 533
 541 ARPSRPSGAVSEDSILSSESDQLDLPRLPETPLRGCVSDNLRGLQPPSEG---LK 596
 534 ARASRPSGAVSEDSILSSESDQLDLPRLPETPLRGCVSDNLTGLEPSPGSGCLR 593
 597 RWMQESLGDSFSLTDCQEVTAAYRQALGICSKLS 631
 594 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 628

RESULT 7

ADF76965
 ID ADF76965 standard; protein; 628 AA.

AC ADF76965;

XX 26-FEB-2004 (first entry)

XX Novel human secreted and transmembrane protein SeqID 640.

XX human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neuropeptide; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.

XX Homo sapiens.

XX WO2003072035-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005241.

XX 22-FEB-2002; 2002US-0359461P.

PR (GETH) GENENTECH INC.

XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WI, Wu TD;

XX WPI; 2003-721702/68.

DR N-PSDB; ADF76964.

XX New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.

XX Claim 10; SEQ ID NO 640; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neuropeptides and hormones) which are received and interpreted by diverse

CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytostatic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.

XX Sequence 628 AA;

Query Match 85.8%; Score 2824.5; DB 7; Length 628;
 Best Local Similarity 85.7%; Pred. No. 1.9e-239;
 Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;

QY 1 MESVALLORPSQASALASESARPLADGLIKSPKLMKKQAVKRHHKHLRHYEFL 60
 DB 1 MESLVFARRSGPTPS---AAELARPLAELGLIKSPKLMKKQAVKRHHKHLRHYEFL 56

QY 61 ETILGKTYGVKKARESSGRLVAIKIRKDKIKDEQDLHRRREIEIMSSLNHPHIIAIIH 120

DB 57 ETILGKTYGVKKARESSGRLVAIKIRKDKIKDEQDLHRRREIEIMSSLNHPHIIAIIH 116

QY 121 EVFENGSKIIVIMEYASRGDLYDIYSERPLSRDARHFFRQIVSALHYCHQNGIVHRDL 180

DB 117 EVFENGSKIIVIMEYASRGDLYDIYSERQQLSREARHFFRQIVSAVHYCHQNRVHRDL 176

QY 181 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYTGVPEVDSWSL 240

DB 177 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPIVNGKPYTGVPEVDSWSL 236

QY 241 GVLLYILVHGTMPFDGQDHTLVKQISNGAYRPPKPSDACGLIRWLLMWNPTRRATLED 300

DB 237 GVLLYILVHGTMPFDGHDHKLILVKQISNGAYRPPKPSDACGLIRWLLMWNPTRRATLED 296

QY 301 VASHWVNWGYTTGVGEQEAALREGHPGSDFGASMDWLRSSRPILLENGAKVCSFFKQ 360

DB 297 VASHWVNWGYATRVGEQEPHGGHSGDSARASMDWLRSSRPILLENGAKVCSFFKQ 356

QY 361 HVPGGSTVPLGRQHSILKSKRKENDMAQNLQDPAEDTSRPOKSSILKPKGILKKSS 420

DB 357 HAPGGSTTPGLERQHSILKSKRKENDMAQSLHSDTADTAHRPGKSNLKLKPKGILKKVS 416

QY 421 TSSEVOEDPOELRPVDPDPQVPVAVSLLPRKGLKSKRSRGYSSPSPSSGELL 480

DB 417 ASAGVQEDPELSPFASPGQAAP---LLPKGLKPKRSGSYSSPSPSSGELL 473

QY 481 ASDVFGSDPVEOKSPQASGLLHRKGLKNGKFSRTALEGTTPTFGSLDOLASSHPA 540

DB 474 AGDVFGSDPVEOKSPQASGLLHRKGLKNGKFSRTALEAAPTTFGSLDELAPRPL 533

QY 541 ARPSRPSGAVSEDSILSSESDQLDLPRLPETPLRGCVSDNLRGLQPPSEG---LK 596

DB 534 ARASRPSGAVSEDSILSSESDQLDLPRLPETPLRGCVSDNLTGLEPSPGSGCLR 593

QY 597 RWMQESLGDSFSLTDCQEVTAAYRQALGICSKLS 631

DB 594 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 628

RESULT 8
 ADL30886

ID ADL30886 standard; protein; 628 AA.

XX ADL30886;

XX 20-MAY-2004 (first entry)

XX Human protein encoded by a full length cDNA clone SeqID 2919.

QY 61 ETLLKGTGYKVKKARESSGLVAIKSTRKDKIKDEODLLHRRREIETMSSLNPHIIAIIH 120
DB 57 ETLLKGTGYKVKKARESSGLVAIKSTRKDKIKDEODLLHRRREIETMSSLNPHIIAIIH 116
QY 121 EVFENSISKIVMEYASRGDLXYISRPRLSERDARHFFRQIVSALHYCHQNGIVHRDL 180
DB 117 EVFENSISKIVMEYASRGDLXYISERQQLSEREARHFFRQIVSAVHYCHQNRVHRDL 176
QY 181 KLENILLDANGNIKIADFGLSNLVHKGFLOTFCGSPLYASPEIVNGKPYVGPVDSWSL 240
DB 177 KLENILLDANGNIKIADFGLSNLVHQCKFLQTCGSPLYASPEIVNGKPYTGPVDSWSL 236
QY 241 GVLLYILVHGTMPDGDHKLIVKQISNGAYREPKPSDACGLIRWLLMNPTRATLED 300
DB 237 GVLLYILVHGTMPDGDHKLIVKQISNGAYREPKPSDACGLIRWLLMNPTRATLED 296
QY 301 VASHWWNVWYTTGVGQEQALREGGHPGDFGRASMDLRRSRPRLLENGAKVCSPFKQ 360
DB 297 VASHWWNVWYATVVGQEQAPHEGGHPGDSARASMDLRRSRPRLLENGAKVCSPFKQ 356
QY 361 HVPGGGSTVPLERQHLKSKSRKENDMAQNLQSDPAEDTSSRPCKSSKLKPKGILKKKSS 420
DB 357 HAPGGGSTVPLERQHLKSKSRKENDMAQNLSDTADTAHRPGKSNLKLKPKGILKKKVS 416
QY 421 TSSEVEQEDQELRPVPTDQOPVAVSLLPRKGIKKSQRESGYSSPEPSESGLLD 480
DB 417 ASABGVQEDPELSPITPASQQAAP---LIPKGIKKSQRESGYSSPEPSESGLLD 473
QY 481 ASDVVFSGDPEQKSPQASGLLLHRKGIKLNKGFRTALEGTTPTFGSLDQLASSHPA 540
DB 474 AGDVVFSGDPEQKSPQASGLLLHRKGIKLNKGFRTALEGTTPTFGSLDQLASSHPA 533
QY 541 ARPSRPGAVSEDSILSESPDQLDPLRLPETPLRGVSDNLRGLQEPPESEG---LK 596
DB 534 ARASRPGAVSEDSILSESPDQLDPLRLPETPLRGVSDNLRGLQEPPESEGPGSLR 593
QY 597 RWOQESIGDSCFSLTDCQEVTAARQALGICSKLS 631
DB 594 RWRQDPLGDSFSLTDCQEVTAARQALRVCSKLT 628
RESULT 10
ADL14161
XX ID ADL14161 standard; protein; 628 AA.
XX AC ADL14161;
XX XX
XX DT 17-JUN-2004 (first entry)
XX DE Novel human gene 3700 encoded protein.
XX KW cytostatic; cardiac; hypotensive; antiangiinal; osteopathic;
KW antiarthritic; antirheumatic; neuroprotective; antiinflammatory;
KW antiproliferative; antidiabetic; cardiovascular; virucide; analgesic; CNS;
KW angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective;
KW nephrotropic; antithyroid; dermatologic; immunomodulator;
KW cell proliferation disorder; cell differentiation disorder;
KW brain disorder; platelet disorder; breast disorder; colon disorder;
KW kidney disorder; renal disorder; lung disorder; ovarian disorder;
KW prostate disorder; cervical disorder; spleen disorder; thymus disorder;
KW thyroid disorder; testes disorder; hematopoietic disorder;
KW pancreatic disorder; skeletal muscle disorder; skin disorder;
KW dermal disorder; bone metabolism disorder; immune disorder;
KW inflammatory disorder; cardiovascular disorder;
KW endothelial cell disorder; liver disorder; viral disease; pain disorder;
KW metabolic disorder; neurological disorder;
KW central nervous system disorder; erythroid disorder;
KW blood vessel disorder; angiogenic disorder; cancer; heart failure;
KW hypertension; angina; osteoarthritis; rheumatoid arthritis;
KW multiple sclerosis; Crohn's disease; psoriasis; asthma;
KW cell proliferation; cell differentiation; cell growth; cell division;
KW human.

XX OS Homo sapiens.
XX PN US2004058355-A1.
XX PD 25-MAR-2004.
XX PF 25-APR-2003; 2003US-00423543.
XX 30-SEP-1998; 98US-00163821.
PR 27-JAN-1999; 99US-0117580P.
PR 25-MAR-1999; 99US-00276400.
PR 30-JUL-1999; 99US-00365162.
PR 09-SEP-1999; 99US-00392189.
PR 05-OCT-1999; 99US-00412210.
PR 23-NOV-1999; 99US-00448076.
PR 29-FEB-2000; 2000US-0186061P.
PR 28-APR-2000; 2000US-0200688P.
PR 19-MAY-2000; 2000US-0205447P.
PR 30-JUN-2000; 2000US-00608921.
PR 31-JUL-2000; 2000US-0221925P.
PR 25-SEP-2000; 2000US-0234922P.
PR 25-SEP-2000; 2000US-0235035P.
PR 08-NOV-2000; 2000US-0246669P.
PR 09-NOV-2000; 2000US-00711216.
PR 14-NOV-2000; 2000US-0248325P.
PR 15-NOV-2000; 2000US-0248893P.
PR 22-DEC-2000; 2000US-0257511P.
PR 05-JAN-2001; 2001US-0260166P.
PR 28-FEB-2001; 2001US-00797039.
PR 27-APR-2001; 2001US-00845044.
PR 20-JUL-2001; 2001US-00909743.
PR 31-JUL-2001; 2001US-00920346.
PR 13-AUG-2001; 2001US-00928531.
PR 14-AUG-2001; 2001US-00929218.
PR 15-AUG-2001; 2001US-0312539P.
PR 25-SEP-2001; 2001US-00963159.
PR 08-NOV-2001; 2001US-0008016.
PR 13-NOV-2001; 2001US-00012055.
PR 15-NOV-2001; 2001US-00003690.
PR 30-JAN-2002; 2002US-00060763.
PR 25-MAR-2002; 2002US-00105989.
PR 12-APR-2002; 2002US-00121911.
PR 12-AUG-2002; 2002US-00217168.
PR 22-OCT-2002; 2002US-00278036.
PR 02-JAN-2003; 2003US-00336489.
PR 03-JAN-2003; 2003US-00336153.
XX XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Kapeller-Libermann R, Hunter JJ, Meyers RE, Rudolph-Owen LA;
PI Curtis RAJ, Olandt PJ, Tsai F, Galvin KM, Chun M, Williamson MJ;
PI Silos-Santiago I, Bandaru R;
XX WPI; 2004-268788/25.
XX N-PSDB; ADL14160, ADL14162.
XX New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529,
PT 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593,
PT nucleic acid molecules and proteins, useful for treating, e.g. cancer,
PT heart failure and angina.
XX Claim 4; SEQ ID NO 44; 139pp; English.
XX The invention describes an isolated 21910, 56634, 55053, 2504, 15977,
XX 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217,
CC 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising
CC any one of 40 nucleotide sequences (I). The nucleic acid molecules and
CC polypeptides are useful for diagnosing and treating a subject having a
CC disorder, or a subject at risk of developing a disorder, which is
CC associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,
CC 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983,
CC m1983, 38555 or 593 activity, such as cellular proliferative and/or

CC differentiative disorders, brain disorders, platelet disorders, breast
CC disorders, colon disorders, kidney (renal) disorders, lung disorders,
CC ovarian disorders, prostate disorders, cervical disorders, spleen
CC disorders, thymus disorders, thyroid disorders, testes disorders,
CC hematopoietic disorders, pancreatic disorders, skeletal muscle disorders,
CC skin (dermal) disorders, disorders associated with bone metabolism,
CC immune, e.g. inflammatory disorders, cardiovascular disorders,
CC endothelial cell disorders, liver disorders, viral diseases, pain
CC disorders, metabolic disorders, neurological or central nervous system
CC disorders, erythroid disorders, blood vessel disorders or angiogenic
CC disorders (all claimed), e.g. cancer, heart failure, hypertension,
CC angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's
CC disease, psoriasis, or asthma. The nucleic acid molecules and
CC polypeptides are also useful as modulating agents in regulating a variety
CC of cellular process, e.g. cell proliferation, differentiation, growth and
CC division. This is the amino acid sequence of a novel human protein of the
CC invention. Note: The sequences given in the specification are also
CC available in electronic format from
CC ftp.segdata.uspto.gov/sequence.html?docID=20040058355.
XX
SQ Sequence 628 AA;

Query Match 85.8%; Score 2824.5; DB 8; Length 628;
Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;
QY 1 MESVALLQRPQSAPASALASASARPLADGLIKSPKMKQAVKRRHHKHLNRHYEFL 60
Db 1 MESLVFARRSGTPS-----AELARPLAEGLIKSPKMKQAVKRRHHKHLNRHYEFL 56
QY 61 ETLGKGTGYGVKKARESSGRGLVAIKSRKDKIKDEQDLHRRREIEMSSLNPHIAT 120
Db 57 ETLGKGTGYGVKKARESSGRGLVAIKSRKDKIKDEQDLHRRREIEMSSLNPHIAT 116
QY 121 EVFENSSKIVIVMEYASRGDLYDIISERPLSRDARHFRQIVSALHYCHQIVHRDL 180
Db 117 EVFENSSKIVIVMEYASRGDLYDIISERQQLSREARHFRQIVSAVHYCHQIVHRDL 176
QY 181 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPVGVDEDSWSL 240
Db 177 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYTGVDEDSWSL 236
QY 241 GVLLYLIVHGTMPDGDHKLTVKQISNGAYRPPKPSDACGLIRWLLMVNPTRRATLED 300
Db 237 GVLLYLIVHGTMPDGDHKLTVKQISNGAYRPPKPSDACGLIRWLLMVNPTRRATLED 296
QY 301 VASHWWNWCYTTGCGEALREGCHPSGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Db 297 VASHWWNWCYTRVGEQAPHEGCHPSGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 356
QY 361 HVPGGGSTVPLERQHSKKSRKENDMAQNLQGDPAEDTSRPGKSSLKLPKGLKKSS 420
Db 357 HAPGGGSTVPLERQHSKKSRKENDMAQSLHSDTADTAHRPKSNLKLPGILKKVS 416
QY 421 TSSEGVQEDPOELRPVPTDTPQVPVAVSLLPKGLKKSRQSGYYSPPESGESGLLD 480
Db 417 ASAEQVEDDPPELSPASPQAP---LLPKGILKKRQSGYYSPPESGESGLLD 473
QY 481 ASDVFSVGDPEQKSPQASGLLHRRKILKNGKFSSTALETGTPFTGSLDQLASHPA 540
Db 474 AGDVFSVGDPEQKPPQASGLLHRRKILKNGKFSQTALEAAPTFTGSLDELAPRPL 533
QY 541 ARSPRSGAVSSEDSILSSSEFDQLDLPERLPETPLRGCVSDNLRGLQEPSESG---LK 596
Db 534 ARSPRSGAVSSEDSILSSSEFDQLDLPERLPETPLRGCVSDNLTGLEPPSGPGSCLR 593
QY 597 RWMQESLGDSCFSLTDCQEVTAAYRQALGCSKLS 631
Db 594 RWRQDPLGDSCFSLTDCQEVTAAYRQALVCSKLT 628

RESULT 11
ADO20172

ID ADO20172 standard; protein; 628 AA.
XX
AC ADO20172;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #540.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN WO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003WO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX
XX WPI: 2004-420067/39.
DR N-PSDB; ADO20171.
XX
PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX
PS Claim 7; SEQ ID NO 1080; 1731pp; English.
XX
CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
SQ Sequence 628 AA;

Query Match 85.8%; Score 2824.5; DB 8; Length 628;
Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;
QY 1 MESVALLQRPQSAPASALASASARPLADGLIKSPKMKQAVKRRHHKHLNRHYEFL 60
Db 1 MESLVFARRSGTPS-----AELARPLAEGLIKSPKMKQAVKRRHHKHLNRHYEFL 56
QY 61 ETLGKGTGYGVKKARESSGRGLVAIKSRKDKIKDEQDLHRRREIEMSSLNPHIAT 120
Db 57 ETLGKGTGYGVKKARESSGRGLVAIKSRKDKIKDEQDLHRRREIEMSSLNPHIAT 116
QY 121 EVFENSSKIVIVMEYASRGDLYDIISERPLSRDARHFRQIVSALHYCHQIVHRDL 180
Db 117 EVFENSSKIVIVMEYASRGDLYDIISERQQLSREARHFRQIVSAVHYCHQIVHRDL 176

QY 181 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWSL 240
DB 177 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWSL 236
QY 241 GVLLYILVHGTMPDQGHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 300
DB 237 GVLLYILVHGTMPDQGHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 296
QY 301 VASHWWNVWYTTGCVGQEQALREGGHPGSDGFRASMDWLRSSRPILLENGAKVCSFFKQ 360
DB 297 VASHWWNVWYATRVGQEQAPHEGGHPGSDSARASMDWLRSSRPILLENGAKVCSFFKQ 356
QY 361 HVPGGGTVPGLEERQHSLLKSKRKENDMAQNLQGDPAEDTSSRPCKSSIKLPKGLKKSS 420
DB 357 HAPGGGTTTGLERQHSLLKSKRKENDMAQNLQGDPAEDTSSRPCKSSIKLPKGLKKSS 416
QY 421 TSSEGEQEDPQELRPVDPDTPGQPVAVSLLRKGLKKRQRESGYSSPEPSSGELL 480
DB 417 ASAEVQEDPPELSPIPASPGQAAP---LLPKGILKKRQRESGYSSPEPSSGELL 473
QY 481 ASDVVFVSGDPVEOKSPQASGLLHRKGLKLGKFSRTALEGTTPTFGSLDQLASSHPA 540
DB 474 AGDVVFVSGDPKEQKPPQASGLLHRKGLKLGKFSRTALEGTTPTFGSLDQLASSHPA 533
QY 541 ARPSRPSGAVSEDSILSSESFDQLDLPRLPETPLRGCVSDNLRGLEQPPSEG---LK 596
DB 534 ARASRPSGAVSEDSILSSESFDQLDLPRLPETPLRGCVSDNLRGLEQPPSEG---LK 593
QY 597 RWOQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
DB 594 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 628

RESULT 12

ADJ96620
ID ADJ96620 standard; protein; 672 AA.
XX AC ADJ96620;
XX DX 06-MAY-2004 (first entry)
XX DE Human calcium/calmodulin-dependent protein kinase NuaK2 protein SeqID 77.
XX KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
XX KW PK; STK; gene therapy; cancer; immune-related disease;
XX KW cardiovascular disease; brain; neuronal associated disease; metabolic;
XX KW inflammatory disorder; cytosolic; neuroprotective; immunomodulator;
XX KW antiinflammatory; enzyme; calcium/calmodulin-dependent protein kinase;
XX KW NuaK2.
XX OS Homo sapiens.
XX OS 72.
XX PN WO2004006838-A2.
XX PD 22-JAN-2004.
XX PF 15-JUL-2003; 2003WO-US021730.
XX PR 15-JUL-2002; 2002US-0395632P.
XX PA (SUGEN-) SUGEN INC.
XX PI Whyte D, Manning G, Caenepeel S;
XX DR WPI; 2004-122753/12.
XX DR N-PSDB; ADJ96554.
XX PT New nucleic acid molecule encoding a kinase polypeptide, useful for
XX PT preparing a composition for treating diseases or disorders, e.g., cancer,
XX PT or neurological, immunological or inflammatory disorders.
XX PS Claim 1; SEQ ID NO 77; 366pp; English.

XX This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytosolic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
CC of the invention.

SQ Sequence 672 AA;

Query Match 85.8%; Score 2824.5; DB 8; Length 672;
Best Local Similarity 85.7%; Pred. No. 2.1e-239;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;

QY 1 MESVALLQRFQSPASALASERPLADGLIKSPKPLMKKQAVKRHHKHLRHYEFL 60
DB 45 MESLVFARRSGPTPS-----AAELARPLAEGLIKSPKPLMKKQAVKRHHKHLRHYEFL 100
QY 61 ETLLGKTYGVKKARESSGRVLAIKIRKDKIKDEQDQLHRRREIEMSSLNHPHITAIH 120
DB 101 ETLLGKTYGVKKARESSGRVLAIKIRKDKIKDEQDQLHRRREIEMSSLNHPHITAIH 160
QY 121 EVFENSISKIVIMVEYASRGDLYDIYSERPLSRDARHFFRQIVSALHYCHQNGIVHRDL 180
DB 161 EVFENSISKIVIMVEYASRGDLYDIYSERQQLSREARHFFRQIVSALHYCHQNGIVHRDL 220
QY 181 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWSL 240
DB 221 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWSL 280
QY 241 GVLLYILVHGTMPDQGHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 300
DB 281 GVLLYILVHGTMPDQGHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 340
QY 301 VASHWWNVWYTTGCVGQEQALREGGHPGSDGFRASMDWLRSSRPILLENGAKVCSFFKQ 360
DB 341 VASHWWNVWYATRVGQEQAPHEGGHPGSDSARASMDWLRSSRPILLENGAKVCSFFKQ 400
QY 361 HVPGGGTVPGLEERQHSLLKSKRKENDMAQNLQGDPAEDTSSRPCKSSIKLPKGLKKSS 420
DB 401 HAPGGGTTTGLERQHSLLKSKRKENDMAQNLQGDPAEDTSSRPCKSSIKLPKGLKKSS 460
QY 421 TSSEGEQEDPQELRPVDPDTPGQPVAVSLLRKGLKKRQRESGYSSPEPSSGELL 480
DB 461 ASAEVQEDPPELSPIPASPGQAAP---LLPKGILKKRQRESGYSSPEPSSGELL 517
QY 481 ASDVVFVSGDPVEOKSPQASGLLHRKGLKLGKFSRTALEGTTPTFGSLDQLASSHPA 540
DB 518 AGDVVFVSGDPKEQKPPQASGLLHRKGLKLGKFSRTALEGTTPTFGSLDQLASSHPA 577
QY 541 ARPSRPSGAVSEDSILSSESFDQLDLPRLPETPLRGCVSDNLRGLEQPPSEG---LK 596
DB 578 ARASRPSGAVSEDSILSSESFDQLDLPRLPETPLRGCVSDNLRGLEQPPSEG---LK 637
QY 597 RWOQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
DB 638 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 672

RESULT 13

AAB65632
ID AAB65632 standard; protein; 629 AA.
XX AC AAB65632;
XX DT 27-MAR-2001 (first entry)

CC of a test compound and in gene therapy. The present sequence is human
CC PKIN-12 protein
XX

SQ Sequence 594 AA;

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Query Match      82.6%; Score 2720.5; DB 5; Length 594;
Best Local Similarity 87.3%; Pred. No. 2.6e-230;
Matches 521; Conservative 22; Mismatches 47; Indels 7; Gaps 2;

Qy 39 MKQAVRHHHKNLRHRYELETGLGTYGKVKKARESSGRLVAIKSIRKDKIKDEODL 98
Db 1 MKQAVRHHHKNLRHRYELETGLGTYGKVKKARESSGRLVAIKSIRKDKIKDEODL 60

Qy 99 LHIREIEIMSSLNHPHIIAIHEVFENSKKIIVMEYASRGDLVDYISERPLSERDARH 158
Db 61 MHIREIEIMSSLNHPHIIAIHEVFENSKKIIVMEYASRGDLVDYISERQQLSREARH 120

Qy 159 FFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKTADFGLSNLYHKGFQFCGSP 218
Db 121 FFRQIVSALHYCHQNRVVHRDLKLENILLDANGNIKTADFGLSNLYHQGKFLQTF 180

Qy 219 YASPEIVNGKPYGVPEVDSWSLGLVLLYLVHGTWPFQDQHTLVKQISNGAYREP 278
Db 181 YASPEIVNGKPYGVPEVDSWSLGLVLLYLVHGTWPFQDQHTLVKQISNGAYREP 240

Qy 279 DACGLIRWLLMVNPTTRATLEDVASHWVNWNGYTTGVGEQALREGGHPGDFGRAS 338
Db 241 DACGLIRWLLMVNPTTRATLEDVASHWVNWNGYATRVGEQAPHEGGHPGSDSAR 300

Qy 339 WLRSSRPILLENGAKVCSFFKQHVPGGGSTVPGLEHSLKSKRKENDMAQNLOGDPA 398
Db 301 WLRSSRPILLENGAKVCSFFKQHAPGGGTTTPGLEHSLKSKRKENDMAQSLHSD 360

Qy 399 TSSRPKSSLLPKGIILKKSTSSGEVQEDPQELRPVDPDPGQPVPAVSLIPKGI 458
Db 361 TAHRPGKSNLKPGLIILKKVSASAEVQEDPPELSPIPASPGQAP---LLPKGI 417

Qy 459 SRQESGYSSPEPSESGELLDSDFVSGDPVQKSPQASGLLHRRKGIILKNGKFS 518
Db 418 PRQESGYSSPEPSESGELLDSDFVSGDPKQKPPQASGLLHRRKGIILKNGKFS 477

Qy 519 ALEGTTPSTFGSLDQLASSHPAARPSGAVSEDSILSSSEFPQDLPERLPETPLRG 578
Db 478 ALELAAPTTFGSLDELAPRPLARASRPSGAVSEDSILSSSEFPQDLPERLPETPL 537

Qy 579 VSDNLRGLQPPSEG---LKRWWQSLGDSCEFLTDCEVTAAYQALGICSKLS 631
Db 538 VSDNLTGLBEPPEPGSCLRWRQDPLGDSCEFLTDCEVTAAYQALRVCSKLT 594
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Search completed: January 22, 2005, 06:38:26
Job time : 165.178 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:30:32 ; Search time 40.6867 Seconds
(without alignments)
1028.511 Million cell updates/sec

Title: US-09-980-464-11
Perfect score: 3293
Sequence: 1 MESVALLQRPQSPASALA.....DCQEVTAAYRQALGICKLS 631

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3293	100.0	631	4	US-09-579-664B-11
2	3293	100.0	631	4	US-10-355-975A-11
3	3278.5	99.6	630	4	US-10-355-975A-38
4	703.5	21.4	729	2	US-08-677-298-2
5	703.5	21.4	729	4	US-09-523-849-33
6	694.5	21.1	713	4	US-09-538-092-1022
7	691.5	21.0	793	4	US-09-523-849-32
8	688	20.9	745	4	US-09-523-849-36
9	680	20.6	724	4	US-09-984-890-2
10	680	20.6	724	4	US-10-274-194-2
11	677.5	20.6	722	4	US-09-984-890-4
12	677.5	20.6	722	4	US-10-274-194-4
13	675	20.5	779	4	US-08-817-832B-31
14	673.5	20.5	722	4	US-08-817-832B-32
15	653	19.8	604	4	US-09-523-849-35
16	648.5	19.7	633	3	US-08-557-006C-43
17	648.5	19.7	633	4	US-09-538-092-212
18	648.5	19.7	633	4	US-09-633-328B-3
19	648.5	19.7	633	4	US-09-824-735-3
20	648.5	19.7	1203	4	US-09-799-875-5
21	645.5	19.6	512	4	US-09-633-328B-2
22	636.5	19.3	552	4	US-09-824-735-4
23	635.5	19.3	345	3	US-09-101-146-1
24	635.5	19.3	776	4	US-09-523-849-34
25	631	19.2	511	4	US-09-633-328B-4
26	628.5	19.1	552	4	US-09-538-092-1212
27	625.5	19.0	418	4	US-09-248-796A-18441

28	625	19.0	257	3	US-09-101-146-6	Sequence 6, Appl
29	623.5	18.9	552	3	US-08-557-006C-40	Sequence 40, Appl
30	619.5	18.8	257	2	US-07-857-224B-25	Sequence 25, Appl
31	613.5	18.6	778	4	US-10-116-326-2	Sequence 2, Appl
32	613.5	18.6	778	4	US-10-003-690-2	Sequence 2, Appl
33	599.5	18.2	668	4	US-09-930-181-2	Sequence 2, Appl
34	549	16.7	1064	4	US-09-538-092-154	Sequence 154, App
35	547	16.6	703	4	US-10-116-326-6	Sequence 6, Appl
36	528.5	16.0	603	4	US-09-930-181-17	Sequence 17, Appl
37	525	15.9	260	2	US-07-857-224B-28	Sequence 28, Appl
38	522	15.9	776	1	US-08-198-446B-17	Sequence 17, Appl
39	522	15.9	776	2	US-08-870-693-17	Sequence 17, Appl
40	522	15.9	821	1	US-08-198-446B-6	Sequence 6, Appl
41	522	15.9	821	2	US-08-870-693-6	Sequence 6, Appl
42	519	15.8	391	4	US-09-248-796A-18435	Sequence 18435, A
43	515.5	15.7	160	4	US-09-270-767-32886	Sequence 32886, A
44	514	15.6	915	4	US-09-538-092-63	Sequence 63, Appl
45	513	15.6	260	2	US-07-857-224B-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-579-664B-11
; Sequence 11, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-579-664B-11

Query Match	100.0%;	Score	3293;	DB	4;	Length	631;
Best Local Similarity	100.0%;	Pred. NO.	2.2e-277;	Mismatches	0;	Indels	0;
Matches	631;	Conservative	0;	0;	0;	Gaps	0;
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Db	1	MESVALLQRPQSPASALASARPLADGLIKSPKPLMKKQAVKRHHKHLRHYEFL	60				
Qy	61	ETLGKGYGVKKARSSGRGLVAIKIRKDKIKDEQLLHRRREIETMSSLNHPHIIAIIH	120				
Db	61	ETLGKGYGVKKARSSGRGLVAIKIRKDKIKDEQLLHRRREIETMSSLNHPHIIAIIH	120				
Qy	121	EVFENSSKIVIVMEYASRGDLYISERPLSRDARHFRQIVSALHYCHQNGIVHRDL	180				
Db	121	EVFENSSKIVIVMEYASRGDLYISERPLSRDARHFRQIVSALHYCHQNGIVHRDL	180				
Qy	181	KLENILLDANGNKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWSL	240				
Db	181	KLENILLDANGNKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWSL	240				
Qy	241	GVLLYLIVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRLLMVNPTRRATLED	300				
Db	241	GVLLYLIVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRLLMVNPTRRATLED	300				
Qy	301	VASHWWNVGYYTGVGEQEAALREGGHPGDFGRASMDWLRSSRPILLENGAKVCSPFKQ	360				
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Qy 361 HVPGGSTVPLGRQHSLKSKRKENDMAQNLDQPAEDTSRPGKSSLLPKGILKKSS 420
Db 361 HVPGGSTVPLGRQHSLKSKRKENDMAQNLDQPAEDTSRPGKSSLLPKGILKKSS 420
Qy 421 TSSEVOEDPQELRPVPTPGQVPVAVSLLPRKILKKRSQREGSYSSPPSPSGELL 480
Db 421 TSSEVOEDPQELRPVPTPGQVPVAVSLLPRKILKKRSQREGSYSSPPSPSGELL 480
Qy 481 ASDVVFSGDPVEOKSPQASGLLHRKILKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Db 481 ASDVVFSGDPVEOKSPQASGLLHRKILKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Qy 541 ARPSRPSGAVSEDSILSSESFDQLDPERLPETPLRGCVSDNLRGLQEPSEGLKRWQ 600
Db 541 ARPSRPSGAVSEDSILSSESFDQLDPERLPETPLRGCVSDNLRGLQEPSEGLKRWQ 600
Qy 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631
Db 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631

RESULT 2
US-10-355-975A-11
; Sequence 11, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355.975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975A-11

Query Match 100.0%; Score 3293; DB 4; Length 631;
Best Local Similarity 100.0%; Pred. No. 2.2e-277; Indels 0; Gaps 0;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MESVALLQRPSPQASALASESARPLADGLIKSPKPLMKKQAVKRHHKHNLRHYEFL 60
Qy 61 ETLGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
Db 61 ETLGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
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Db 121 EVFENSISKIVMEYASRGDLYDIISERPLSRDARHFFRQIVSALHYCHQNGIVHRDL 180
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Db 181 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVEDWSL 240
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Db 241 GVLLYILVHGTMPDQDHTLVKQISNGAYREPPEKPSDACGLIRWLLMNPTRATLED 300
Qy 301 VASHWWNVGTYTTCVGQEQALREGGHPGSGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Db 301 VASHWWNVGTYTTCVGQEQALREGGHPGSGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
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Db 361 HVPGGSTVPLGRQHSLKSKRKENDMAQNLDQPAEDTSRPGKSSLLPKGILKKSS 420
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Db 421 TSSEVOEDPQELRPVPTPGQVPVAVSLLPRKILKKRSQREGSYSSPPSPSGELL 480
Qy 481 ASDVVFSGDPVEOKSPQASGLLHRKILKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Db 481 ASDVVFSGDPVEOKSPQASGLLHRKILKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Qy 541 ARPSRPSGAVSEDSILSSESFDQLDPERLPETPLRGCVSDNLRGLQEPSEGLKRWQ 600
Db 541 ARPSRPSGAVSEDSILSSESFDQLDPERLPETPLRGCVSDNLRGLQEPSEGLKRWQ 600
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Db 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631

RESULT 3
US-10-355-975A-38
; Sequence 38, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355.975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975A-38

Query Match 99.6%; Score 3278.5; DB 4; Length 630;
Best Local Similarity 99.8%; Pred. No. 4.1e-276;
Matches 630; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MESVALLQRPSPQASALASESARPLADGLIKSPKPLMKKQAVKRHHKHNLRHYEFL 60
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Db 61 ETLGKGTGKVKKARESGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
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Db 121 EVFENSISKIVMEYASRGDLYDIISERPLSRDARHFFRQIVSALHYCHQNGIVHRDL 180
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Db 181 KLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVEDWSL 240
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Db 241 GVLLYILVHGTMPDQDHTLVKQISNGAYREPPEKPSDACGLIRWLLMNPTRATLED 300
Qy 301 VASHWWNVGTYTTCVGQEQALREGGHPGSGDFGRASMDWLRSSRPLLENGAKVCSFFKQ 360
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Qy 361 HVPGGSTVPLGRQHSLKSKRKENDMAQNLDQPAEDTSRPGKSSLLPKGILKKSS 420
Db 361 HVPGGSTVPLGRQHSLKSKRKENDMAQNLDQPAEDTSRPGKSSLLPKGILKKSS 419

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DB 420 TSSEVEDQELAPVPTTQGPVAVSLPRKGIKKRSQREGSYSSPEPSGELL 479
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DB 480 ASDVFVSGDPVEQKSPQASGLLHRRKGIKKRSQREGSYSSPEPSGELL 539
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DB 540 ARPSRPGAVSEDSILSESFQDLDPRLPPLRGCVSDNLRGLQEPSEGLKRWQ 599
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DB 600 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 630

RESULT 4

US-08-677-298-2
; Sequence 2, Application US/08677298
; Patent No. 5863729
; GENERAL INFORMATION:
; APPLICANT: Pivnick-Worms, Helen
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1
; TITLE OF INVENTION: KINASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,298
; FILING DATE: 09-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 9-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-677-298-2

Query Match 21.4%; Score 703.5; DB 2; Length 729;
Best Local Similarity 35.1%; Pred. No. 3.4e-52;
Matches 195; Conservative 76; Mismatches 180; Indels 105; Gaps 18;
QY 57 YEFLETGKGTGKVKKARE--SSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPH 115
DB 56 YRLKTKTGKGNFAKVLARHILTGREVAIKIDKTLQ--NPTSLOKLFRVIRIMKILNHPN 114
QY 116 IIAIHEVFENSSKIVIMVEASRGDLYDIYSERPLSRDARHPFRQIVSALHYCHQNGI 175
DB 115 IVKLFEVETIEKTLVLYMEYASGGEVFDYLVHGRMKEKARSFRQIVSAVQYCHQKRI 174
QY 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPIVNGKPYVGPEV 235
DB 175 VHRDLKAENLLDADNMNIKIADFGFSNEFTVGGKLDTCGSPPPYAAPELFGKKYDGPV 234

QY 236 DMSLGLVLLYLVHGTMPFPDQDHKTLVKQISNGAYREPPKPSDAC--GLIRWLLMVNPT 294
DB 235 DVMSLGLVLLYLVHGTMPFPDQDHKTLVKQISNGAYREPPKPSDAC--GLIRWLLMVNPT 294
QY 295 RATLEDVASHWVNWGVTGVEQEAALREGHSGDFGRASMDWLRSSRPLENGAKV 354
DB 295 RGLEQIMKDRWINAGH-----BEDELKPFVPELDISDQKRIDIM-----V 336
QY 355 CSFFKQHVPGGSGTVPCGLERQHSLSKSRKENDMAQNL---QGDPAEDTSRPGKSSLKLP 411
DB 337 GMYSQB-----ELQESLSKMKYDEITATYLLLRKSELDASDSSSSSLNLSLA 385
QY 412 KGILKKKSTSSGE-----VQ---EDQELRPVDPDTPGQVPVAVSLPRK-----GIL 456
DB 386 KVRPSSDLNNTGQSPHHKQVRSVSSSQKORRYSDHAGPAIPSVVAVPKRSQTSTABDGL 445
QY 457 KK---SQRES-----GYSSPEPSESSEGLLDASDVFVSGDPVEQKSPQ 497
DB 446 KEDGISRSKSSGSAVGKGIAPASPMGNASNPKNADIPERKKSSTV-----PSSNT 497
QY 498 ASGLLLHRK-----GILKNGKFSRTALEGTTPTSTFGSLDQLASSH---PAA 541
DB 498 ASGMTRNTYVCERTADRHSHVIQ--NGKENSTIPDQRTP-----VASTHSISSAA 548
QY 542 RPSR---PSGAVSEDS 554
DB 549 TPDRIREFRGTASRST 564

RESULT 5

US-09-523-849-33
; Sequence 33, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scaccheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 33
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g3089349
US-09-523-849-33

Query Match 21.4%; Score 703.5; DB 4; Length 729;

Best Local Similarity 35.1%; Pred. No. 3.4e-52;
Matches 195; Conservative 76; Mismatches 180; Indels 105; Gaps 18;
QY 57 YEFLETGKGTGKVKKARE--SSGRLVAIKSIRKDKIKDEQDLHRRREIEMSSLNHPH 115
DB 56 YRLKTKTGKGNFAKVLARHILTGREVAIKIDKTLQ--NPTSLOKLFRVIRIMKILNHPN 114
QY 116 IIAIHEVFENSSKIVIMVEASRGDLYDIYSERPLSRDARHPFRQIVSALHYCHQNGI 175
DB 115 IVKLFEVETIEKTLVLYMEYASGGEVFDYLVHGRMKEKARSFRQIVSAVQYCHQKRI 174
QY 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPIVNGKPYVGPEV 235
DB 175 VHRDLKAENLLDADNMNIKIADFGFSNEFTVGGKLDTCGSPPPYAAPELFGKKYDGPV 234
QY 236 DMSLGLVLLYLVHGTMPFPDQDHKTLVKQISNGAYREPPKPSDAC--GLIRWLLMVNPT 294

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Db 235 DVMSGLVILTVLTVSGSLPFDGQNLKELRVRVLRKYRIPFYMSTDCENLLKRFVLVLPK 294
Qy 295 RATLEDVASHWVNWGTYTGVGEQALREGCHPGDFGRASMDWLRSSRPILLENGAKV 354
Db 295 RGTLEQIMKDRWINAGH-----EDELKPFVEPELDSQKRIDIM-----V 336
Qy 355 CSFPKOHVPGGGSTVPGLEHQHSLKSKRKNENDMAQNL-----QGDPAEDTSSRPCKSS 407
Db 337 GMGYSQE-----EQESLSKWKYDEITATYLLLRKSKSEVFPSSDLNNSQGS- 384
Qy 412 KGLLKKSSSSSGE-----VQ---EDPQLRFPVDTQPQVPAVSLLPK-----GIL 456
Db 386 KVRPSSDLNNSGTGSPHHKQVRSVSSQKQRRYSDHAGPAIPSVVAYPKRSQTSADGDL 445
Qy 457 KK---SRQRES-----GYVSSPPSSGELLSDASDVFSVGDVPVEQKSPQ 497
Db 446 KEDGISRSKSSGSAVGKGIAPASPM--LGNASPNKADIPERKKSSTV-----PSSNT 497
Qy 498 ASGULLHRK-----GILKNGKFSRTALEGTTPTSTFGSLDQLASSH---PAA 541
Db 498 ASGWMTRNTYVCSERTTDRHSVIQ-NGKENSTIPDQRTF-----VASTHSISSAA 548
Qy 542 RPSR---PSGAVSEDS 554
Db 549 TPDRIFRPGTASRST 564
```

```
RESULT 6
US-09-538-092-1022
; Sequence 1022, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1022
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022
```

```
Query Match 21.1%; Score 694.5; DB 4; Length 713;
Best Local Similarity 34.5%; Pred. No. 2e-51;
Matches 191; Conservative 75; Mismatches 171; Indels 117; Gaps 17;

Qy 57 YEFLETGKTYGKVKARE--SSGRLVAIKSIRKDKIDQDLHIREIEMSLNHPH 115
Db 56 YRLKTTGKGNFAVKLARHLTGREVAIKIDTQL-NPTSLQKLFREVRIMKILNHPN 114

Qy 116 IIAIHEVFENSSKIVIMEYASRGDLYISERPLSERDARHFFRQIVSALHYCHONGI 175
Db 115 IVKLFEVETOKTLYLIMEYASGGKVFDFYLAHGRMKEKARSFRQIVSAVQCHOKRI 174

Qy 176 VHRDLKLENLLDANGNIKIADFGLSNLYHKGLQTFCGSPLYASPEIVNGKPYGVPEV 235
Db 175 VHRDLKAENLLDADNMKIADFGSNEFTVGGKLDTFCGSPPYAAPELFQGGKYDGPV 234

Qy 236 DWSLGLVLLYILVHGTWMPFDGQDKHTLVKQISNGAYREPPEKPSDAC-GLIRWLLMVPTR 294
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Db 235 DVMSGLVILTVLTVSGSLPFDGQNLKELRVRVLRKYRIPFYMSTDCENLLKRFVLVLPK 294
Qy 295 RATLEDVASHWVNWGTYTGVGEQALREGCHPGDFGRASMDWLRSSRPILLENGAKV 354
Db 295 RGTLEQIMKDRWINAGH-----EDELKPFVEPELDSQKRIDIM-----V 336
Qy 355 CSFPKOHVPGGGSTVPGLEHQHSLKSKRKNENDMAQNL-----QGDPAEDTSSRPCKSS 407
Db 337 GMGYSQE-----EQESLSKWKYDEITATYLLLRKSKSEVFPSSDLNNSQGS- 384
Qy 408 LKLPKGLKKSSTSGEVEDPQELRFPVDTQPQVPAVSLLPK-----452
Db 385 ---PHHKVQRSVSS-----QKQRRYSDHAGPGIPSVVAYPKRSQTSADSLKEDG 433
Qy 453 -----KGLKKSQRESGYVSSPPSSGELLSDASDVFSVGDVPVEQKSPQAS 499
Db 434 ISSRKSTGSAVGKGIAPASPM--LGNASPNKADIPERKKSSTV-----PSSNTAS 483
Qy 500 GLLLRK-----GILKNGKFSRTALEGTTPTSTFGSLDQLASSH---PAARP 543
Db 484 GWMTRNTYVCSERTTDRHSVIQ-NGKENSTIPDQRTF-----VASTHSISSAATP 534
Qy 544 SR---PSGAVSEDS 554
Db 535 DRIRFRPGTASRST 548

RESULT 7
US-09-523-849-32
; Sequence 32, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scaccheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g2052189
US-09-523-849-32
```

```
Query Match 21.0%; Score 691.5; DB 4; Length 793;
Best Local Similarity 35.6%; Pred. No. 4.3e-51;
Matches 187; Conservative 76; Mismatches 189; Indels 73; Gaps 14;

Qy 57 YEFLETGKTYGKVKARE--SSGRLVAIKSIRKDKIDQDLHIREIEMSLNHPH 115
Db 60 YRLQKTGKGNFAVKLARHLTGREVAIKIDTQL-NPTSLQKLFREVRIMKILNHPN 118

Qy 116 IIAIHEVFENSSKIVIMEYASRGDLYISERPLSERDARHFFRQIVSALHYCHONGI 175
Db 119 IVKLFEVETOKTLYLIMEYASGGEVDFYLAHGRMKEKARAKFRQIVSAVQCHOKCI 178

Qy 176 VHRDLKLENLLDANGNIKIADFGLSNLYHKGLQTFCGSPLYASPEIVNGKPYGVPEV 235
Db 179 VHRDLKAENLLDADNMKIADFGSNEFTVGNKLDTFCGSPPYAAPELFQGGKYDGPV 238

Qy 236 DWSLGLVLLYILVHGTWMPFDGQDKHTLVKQISNGAYREPPEKPSDAC-GLIRWLLMVPTR 294
Db 239 DVMSGLVILTVLTVSGSLPFDGQNLKELRVRVLRKYRIPFYMSTDCENLLKRLVLPK 298
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```
QY 402 RPKSSSLKPKGI-----LKKKSTSSGE-----VQEDPQELRPV 436
Db 387 SAPSPSHKQVRSVSNPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEEDRESGRKA 446
QY 437 PDT---PGQVPVAVSLPRKGIKKSQRSGYSSPESESGELLDASDFVSGDPVEQ 493
Db 447 SSTAKVPASPLP-----GLERKK-----TTPTSTNSVLSTSTN-----RSR 483
QY 494 KSPQASGLLHRKGIKILK---NGKFSRTALEGTTPTSTFGSLDQLASSHPAA-RPSRPSGA 549
Db 484 NSP-----LLERASLGQASIQNGKDS-TAPQ-RVPVAPSPSAHNISSSGGAPDRTNPRGV 536
QY 550 VSEDSILSS---ESFDQLDLPERL-PETP 574
Db 537 SSRSTFHAGQLRQVRDQONLPGYVTPASP 565

RESULT 10
US-10-274-194-2
; Sequence 2, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-194-2
```

```
Query Match 20.6%; Score 680; DB 4; Length 724;
Best Local Similarity 32.0%; Pred. No. 3.7e-50;
Matches 201; Conservative 99; Mismatches 195; Indels 134; Gaps 25;

QY 6 LLORPSQAPSASALASESARPLADGLIKSPKPLMKQAVKRRHHKHLRHR-----YEFL 60
Db 11 LNERDTEQPTLGHLS-----KPSKSNMIRGNSATSDEQPHIGNYRL 56
QY 61 ETLGKTYGKVKKARE-SSGRLVAIKSIRKDKIKDQDLHIREIIEIMSLNHPHIIAI 119
Db 57 KTIKGNFAKVKLARHILTGKEVAVKIIDKTQL-NSSSLQKLPREVIRIMKVLNHPNIVKL 115
QY 120 HEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFFRQIVSALHYCHONGIVHRD 179
Db 116 FEVIETETKTLVMEYASGGEVFDYLVNAGRWKKEARAKFRQVVSAYQVCHQKFIHRD 175
QY 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPEDVSW 239
Db 176 LKAENLLDADNMKIADFGFSNEFTFGNKLDTCGSPPYAAPELFQKKYDGEVDVWS 235
QY 240 LGVLLYLIVHGTMPDQDQHTLVKQISNGAYRPPKPSDAC-GLIRWLLMWNTRATL 298
Db 236 LGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMTDCEMLKKFLINPSKRGTL 295
QY 299 EDVASHWVWNGYTTGVGEQALREGHPSGDFGRASMDWLRSSRPLLENGAKVCSFF 358
Db 296 EQIMKDRMWNVGH-----EDDELKPYVEPLFDYKDP-----RTELMSVG- - - - -YT 338
QY 359 KQHPVGGSTVPGLERQHSLLKSKKENDMA-----QNLOD-----PAED-TSS 401
Db 339 REEI-----QDSLQVQRYNEVMATVLLGYKSSSELEGDTITLKRPSADLTNS 386
QY 402 RPKSSSLKPKGI-----LKKKSTSSGE-----VQEDPQELRPV 436
Db 387 SAPSPSHKQVRSVSNPKQRRFSDQAGPAIPTNSYSKKTQSNNAENKRPEEDRESGRKA 446
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QY 437 PDT---PGQVPVAVSLPRKGIKKSQRSGYSSPESESGELLDASDFVSGDPVEQ 493
Db 447 SSTAKVPASPLP-----GLERKK-----TTPTSTNSVLSTSTN-----RSR 483
QY 494 KSPQASGLLHRKGIKILK---NGKFSRTALEGTTPTSTFGSLDQLASSHPAA-RPSRPSGA 549
Db 484 NSP-----LLERASLGQASIQNGKDS-TAPQ-RVPVAPSPSAHNISSSGGAPDRTNPRGV 536
QY 550 VSEDSILSS---ESFDQLDLPERL-PETP 574
Db 537 SSRSTFHAGQLRQVRDQONLPGYVTPASP 565

RESULT 11
US-09-984-890-4
; Sequence 4, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-984-890-4
```

```
Query Match 20.6%; Score 677.5; DB 4; Length 722;
Best Local Similarity 32.9%; Pred. No. 6.1e-50;
Matches 201; Conservative 92; Mismatches 203; Indels 115; Gaps 24;

QY 6 LLORPSQAPSASALASESARPLADGLIKSPKPLMKQAVKRRHHKHLRHR-----YEFL 60
Db 11 LNERDTEQPTLGHLS-----KPSKSNMIRGNSATSDEQPHIGNYRL 56
QY 61 ETLGKTYGKVKKARE-SSGRLVAIKSIRKDKIKDQDLHIREIIEIMSLNHPHIIAI 119
Db 57 KTIKGNFAKVKLARHILTGKEVAVKIIDKTQL-NSSSLQKLPREVIRIMKVLNHPNIVKL 115
QY 120 HEVFENSSKIVIVMEYASRGDLVDYISERPLSRDARHFFRQIVSALHYCHONGIVHRD 179
Db 116 FEVIETETKTLVMEYASGGEVFDYLVNAGRWKKEARAKFRQIVSAYQVCHQKFIHRD 175
QY 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPEDVSW 239
Db 176 LKAENLLDADNMKIADFGFSNEFTFGNKLDTCGSPPYAAPELFQKKYDGEVDVWS 235
QY 240 LGVLLYLIVHGTMPDQDQHTLVKQISNGAYRPPKPSDAC-GLIRWLLMWNTRATL 298
Db 236 LGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMTDCEMLKKFLINPSKRGTL 295
QY 299 EDVASHWVWNGYTTGVGEQALREGHPSGDFGRASMDWLRSSRPLLENGAKVCSFF 358
Db 296 EQIMKDRMWNVGH-----EDDELKPYVEPLFDYKDP-----RTELMSVG- - - - -YT 338
QY 359 KQHPVGGSTVPGLERQHSLLKSKKENDMA-----QNLOD-----PAED-TS 400
Db 339 REEI-----QDSLQVQRYNEVMATVLLGYKSSSELEGDTITLKRPSADLTNS 386
QY 401 SRPKSSSLKPKGIKKSSTSGEVEDQELRPVDPDTPGQVPAVSLPRKGIKLSR 460
Db 387 SAPSPSH-----KQVRSVSA-----NPKQRR-----SSDQAVPAI---PTSNSYSKKT 426
QY 461 QRESGYSSPESESGELLDASDFVSGDP-VEQK-----SPOASGL-----LL 503
Db 427 QSNNAENKRPEETGRKASSTAKVPASPLRGLRDKTTPTSTNSVLSTSTNSRNSPL 486
```

Qy 504 HRKGLKL---NGKFSRTALEGTTPTSTFGSLDQLASSHPAA-RPSRPSGAVSEDSILSS- 558
Db 487 DRASLGQASTQNGKDS-TAPO-RVFPVAPSAHNISSSSGAPDRTNFRPGVSSRSTFFHAGQ 544
Qy 559 --ESFDQDLDP 567
Db 545 LRQVRDQONLP 555

RESULT 12
US-10-274-194-4
; Sequence 4, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001306DIV
; CURRENT APPLICATION NUMBER: US/10/274,194
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-274-194-4

Query Match 20.6%; Score 677.5; DB 4; Length 722;
Best Local Similarity 32.9%; Pred. No. 6.1e-50;
Matches 201; Conservative 92; Mismatches 203; Indels 115; Gaps 24;

Qy 6 LLQRPQAPSASALASESARPLADGLIKSPKPLMKQAVKHHHKNLHRH-----YEFL 60
Db 11 LNERDTQPTLGLHDS-----KPSKSNMLGRNSATADQPHIGNRLL 56

Qy 61 ETLGKTYGVKKARE-SSGRLVAIKSIRKDKINDEQDLHLHIREIEMSLNHPHIAI 119
Db 57 KTIGKGNFAVKLARHLITGKEVAVKIIDKTQL-NSSSLQKLPREVRIMKVLNHPNIVKL 115

Qy 120 HEVFNSSKIVIVMEYASRGDLYDIYSERPLSRDARHFRQIVSAHYCHQNGI 179
Db 116 FEVIETKTYLYLMEYASGGEVFDYLVAGHMKKEARAKFRQIVSAVQYCHOKFI 175

Qy 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPVDSWS 239
Db 176 LKAENLLDADNMNIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFGKKYDGEVDVWS 235

Qy 240 LGVLLYLIVHGTMPFDQDQDKHTLVKQISNGAYREPFPKPSDAC-GLIRWLLMVPTRATL 298
Db 236 LGVILYTLVSGSLPFDGQNLKELRERVLRGKRIPIFYMWSTDCENLLKKFLILNPSKGTLL 295

Qy 299 EDVASHWVWNGYTTGVGEQALREGGHPGDPGRASMDWLRRSRPPLLENGAKVCSFF 358
Db 296 EQIMKDRMNVGH-----EDDELKPYEPLPDYKDP-----RRTLELWSMG-----YT 338

Qy 359 KOHVPGGGSTVGLERHSLKSKSKENDMA-----QNLOQD-----PAED--TS 400
Db 339 REEL-----QDSLVGRQYNEVMATYLLGYKSELEGGDTTLKRPSPADLTNS 386

Qy 401 SRFGKSLKLPKGLKKKSSSTSGEVEDPQELRFPVDPFTGQPPVAVSLLPRKGLKKSR 460
Db 387 SAPSPH-----KVQSVSA-----NPKQR-----SSDQAVAI---PTSNSYSKKT 426

Qy 461 QRESGYSSPEPSSEGLLDASDVFSVGGDP-VBOK-----SPQASGL-----LL 503
Db 427 QSNNAENKRPETEGRKASSTAKVPASPLPGLDRKTTTPSTNSVLSTSTNSRNSPLL 486

Qy 504 HRKGLKL---NGKFSRTALEGTTPTSTFGSLDQLASSHPAA-RPSRPSGAVSEDSILSS- 558
Db 487 DRASLGQASTQNGKDS-TAPO-RVFPVAPSAHNISSSSGAPDRTNFRPGVSSRSTFFHAGQ 544

Qy 559 --ESFDQDLDP 567
Db 545 LRQVRDQONLP 555

RESULT 13
US-08-817-832B-31
; Sequence 31, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/BP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 779 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-832B-31

Query Match 20.5%; Score 675; DB 4; Length 779;
Best Local Similarity 35.4%; Pred. No. 1.1e-49;
Matches 186; Conservative 75; Mismatches 191; Indels 74; Gaps 15;

Qy 57 YEFLTLGKTYGVKKARE-SSGRLVAIKSIRKDKINDEQDLHLHIREIEMSLNHPH 115
Db 46 YRLQKTIGKGNFAVKLARHVLTCREVAVKIIDKTQL-NPTSLQKLPREVRIMKILNHPN 104

Qy 116 IIAIHEVFNSSKIVIVMEYASRGDLYDIYSERPLSRDARHFRQIVSAHYCHQNGI 175
Db 105 IVKLFVETETKTYLYLMEYASGGEVFDYLVAGHMKKEARAKFRQIVSAVQYCHOKCI 164

Qy 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPV 235
Db 165 VHRDLKLENILLDANGNIKIADFGSNEFTVGNGKLDTCGSPPYAAPLFGKKYDGEV 224

Qy 236 DWSLGLVLLYLIVHGTMPFDQDQDKHTLVKQISNGAYREPFPKPSDAC-GLIRWLLMVP 293
Db 225 DVMSLGVILYTLVSGSLPFDGQNLKELRERVLRGKRIPIFYMWSTDCENLLKKFLILNPI 284

Qy 294 RRATLEDVASHWVWNGYTTGVGEQALREGGHPGDPGRASMDWLRRSRPPLLE-NGA 352
Db 285 KRGLSBOIMKDRMNVGH-----EBELKPYSPPELDLNDAKRIDINMTVMTGPARDEINDA 339

Qy 353 KVCSEFFKQ-----HVPGGGSTVGLERHSLKSKSKENDMAQNLOQDPAEDT 399
Db 340 LVQSKYDEVWATYLLGRKPPEEGGESLSSG-----NLQSRSPSSDLNNSTLQSPAH-- 393

Qy 400 SSRPGKSSLLKPKGLKKKSSSTSGEVEDPQELRFPVDPFTGQPPVAVSLLPR-KGILK 457

Db 394 -----LKQRTISANQKQ-----RRFSDHAGSIPPAVSYTKRPQANSV 432
Qy 458 KSRQRE-----SGYSSP--PPSSGELLDDASDVFSVGDVPEQKSPQ 497
Db 433 ESEQKEWMDKTARRLGSTTVGSKSEVTSPLVGPDRKSSAGPSNNVYSGGSMTRNTY 492
Qy 498 ASGULLHRKGLKNGKFSRTALEGTTPTSTFGSLDQLASSHPPAARP 543
Db 493 VCERSTORYAALONGRSSLSMEMSASSSTGS--TVASAGPSARP 536
RESULT 14
US-08-817-832B-32
; Sequence 32, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: NO. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-817-832B-32

Query Match 20.5%; Score 673.5; DB 4; Length 722;
Best Local Similarity 31.3%; Pred. No. 1.4e-49;
Matches 208; Conservative 88; Mismatches 212; Indels 157; Gaps 25;
Qy 6 LLQRPQASASALASARPLADGLIKSPKPLMKQAVKRHHKHLRHR-----YEFL 60
Db 11 LNERDTEQPTGLHDS-----KPSKSNLNRGNSATSADQPHIGNYRL 56
Qy 61 ETGLKGYTKVKKARE--SSGRLVAIKIRKDKIDQDLHIREIIMSLNPHIIAI 119
Db 57 KTIGKGNFAKVKARHLITGKEVAVKIDKTLQ--NSSSLQKLFREVRIMKVLNHPNIVKL 115
Qy 120 HEVPENSSKIVIMVEYASRGDLYDYSERPLSRDARHFRQIVSALHYCHQNGIVHRD 179
Db 116 FEVIETETKLYLVMVEYASGGEVFDYLVHAGMKKEARFRQIVSAVQVCHHKFIVHRD 175
Qy 180 LKLENILLDANGNIKIADFGSLNLYHKGFELQTFCGSPLYASPIVNGKPYVGPEDVDSWS 239
Db 176 LKAENLLDADNMNIKIADFGSNEFTFGNKLDTFCGSPPYAAPLFGQKGYDGPEDVDSWS 235
Qy 240 LGVLLYLVHGTMPDFDQDQDKLYVKQISNGAYRPPKPSDAC--GLIRWLLMVPNTRATL 298
Db 236 LGVILYLVSGSLPFDGQNLKELRERVLRGKIRIPFFYMTDCENLLKFKLILNPSKRGTL 295

Qy 299 EDVASHWVWN-----WGYTTG----- 314
Db 296 EQIMKORWMMVGHEDDELKPYVEPLPDYKDPRTTELMMVSMGYTREETQDSLGVQRYNEVM 355
Qy 315 -----VGEQBALREGG-----HPSGDFGRASMDWLRSSRPLLENGAKVCSPFKQHVP 363
Db 356 ATVLLGLGYSSELEGGDTITLKPRPSADLTNSSAPSPSHKQVRSVSNP-----KQR-R 407
Qy 364 GGGSTVPGLERQHSLSKKSRKENDMAQNLOQDPAEDTSSRPGKSLKLP-----KGILKKKS 419
Db 408 SSDQAVPAIPTNSYSKKTQSN-----NAENKRPDEETGRKASSTAKVPASPLPGLDRKKT 463
Qy 420 -----STSSGEVQEDPQELRPVDPDPGPVPAVSLPRKILKKSRQRESGYSS 469
Db 464 TPTPSTNSVLSTSTNSRNSP-----LLDRASLGQASIQ--NGKDST 503
Qy 470 -----PEPSSGELLDDASDVFSVGDVPEQKSPQ--ASGLLHHRKGLKNGKFSRTALEG 522
Db 504 APQRPVPAFPSAHNISS-----SGAPDRTNFPRGVSSRSTFHA-----GQLRQVRDQ 552
Qy 523 TPTSTFGSLDQLASSHPPAARPSPRGAVSEDSILS--SESFQDLDLPERLPETPLRCVSV 580
Db 553 NLP--FGVTPASPSPSHGSHQGRG--PSG-----SIFSKFTSKFVRRLNE--PESKDR 598
Qy 581 VDNLR 585
Db 599 VETLR 603
RESULT 15
US-09-523-849-35
; Sequence 35, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosetti, Roberta
; APPLICANT: Scacchi, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 35
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 g2564680
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 52, 291, 354
; OTHER INFORMATION: unknown or other
; US-09-523-849-35
Query Match 19.8%; Score 653; DB 4; Length 604;
Best Local Similarity 33.0%; Pred. No. 6.2e-48;
Matches 190; Conservative 76; Mismatches 206; Indels 104; Gaps 19;
Qy 57 YEFLETGKGYTKVKKARE--RESSRLVAIKIRKDKID--EQDLHIREIIMSLN 113
Db 63 YKIITLKGKGNFAKVKARHLITGKEVAVKIDKTLNITARQKLY---REVNMKKLNH 119
Qy 114 PHIIATHEVPENSSKIVIMVEYASRGDLYDYSERPLSRDARHFRQIVSALHYCHQNG 173
Db 120 FNVRLQLQVIESERTLYLVMVEYSGGELFNLYLNGMRERDARVLRQLVSAIEYCHSK 179
Qy 174 GIVHRDLKLENILLDANGNIKIADFGSLNLYHKGFELQTFCGSPLYASPIVNGKPYVGP 233


```

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
180 SIVHRDLKAEULLLDQQMKLIAOFGFSTTFEPKAPLETFCGSPPYAAPELFKGKYSGP 239 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
234 EYDSWSLGLVLIYLHVHTMPDGDQHDHKTIVKOJISNGAYREPPKPSDAC--GLIRWLILMWP 292 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
240 EYDSWSLGLVLIYLVSGSLPDFDGTINLKELDRVLRGKRVYPYVSIECSLRKFVLVLP 299 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
293 TRRATYLEVA SHWVNMGYYTTGVGEQBALREGGHGDFGRASMDWLRRSRRLLENGA 352 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
300 TORTSLSAVMADRWIMNMGYEQGCG--LRPFQBPQMIDLHDVNRLSLLSNMGHKPRDVKQSJK 358 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
353 K-----VCSFPKHVPGGGSTVPCGLRQHSLKKSRKENDMAQNLOQDPADTSSRPCKS 406 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
359 NOKFPDDIYCAIMLDLVAKPRSTACSEKSGSF-----ETPTAMPQSS 401 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
407 SLUKPKG-----ILKKKSSTSSEVGQEDP-----QELRPVDPDTQPQPVAVSL 449 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
402 RIPVFIAIPNTVISQVTFFALDKSTPNRPGATSTRPMAPRIANALTPELUTPP----- 453 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
450 LPRKGIL----KKSQRQESGYSSPEPS--ESELGLDASDFVSGDPVBQKSPQASGLIL 503 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
454 -PKYICCSASKAANPRSEPSISIQSAMPKG-----VGSFVDVKT-----TLL 497 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
504 HRKGILKLNKFSRTALEGTTPTFTGSLDQLASHHPARP-SRPSGAIVESILSESFD 562 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
498 SAQRKLAVNHKLT-----SASHQIRSPITQSSSQASECTRTPTTHFE 539 Db

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
563 QLDELPERLPEPTPLRGCVSVDMRLGLEOPPS-EGIKR 597 Qy

||||||| ||:||| :||||| | : ||||| ||:||| :||| |
540 MLD-----STSTPLKVLKLVAS--NSQTPTSTEMINR 569 Db

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Search completed: January 22, 2005, 06:44:54
Job time : 43.6867 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:29:16 ; Search time 38.5452 Seconds
(without alignments)
1575.104 Million cell updates/sec

Title: US-09-980-464-11
Perfect score: 3293
Sequence: 1 MESVALLQRPSPASALA.....DCOEVTAAVQALGICSKLS 631

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	888	27.0	1558	2 T29253	hypothetical prote
2	694.5	21.1	713	2 S27966	probable serine/th
3	689	20.9	745	2 G01025	probable serine/th
4	686.5	20.8	774	2 I48609	probable serine/th
5	669	20.3	1192	2 T18611	protein H39823.1
6	667	20.3	1246	2 G89287	hypothetical prote
7	664	20.2	1398	2 T13741	serine/threonine-s
8	649.5	19.7	512	2 T52633	serine/threonine-s
9	648.5	19.7	633	1 A26030	gik protein - chic
10	648	19.7	798	2 JC7500	probable serine/th
11	641	19.5	504	2 T10449	serine/threonine-s
12	639.5	19.4	512	1 JC1446	serine/threonine-s
13	631	19.2	511	1 A56009	serine/threonine-s
14	630.5	19.1	552	1 S51025	hydroxymethylglut
15	627.5	19.1	602	2 S72513	POG2 protein - yea
16	623.5	18.9	552	1 A53621	hydroxymethylglut
17	622	18.9	562	2 T29858	hypothetical prote
18	621	18.9	472	2 B90100	SNF-related kinase
19	620	18.8	504	2 T07415	probable serine/th
20	612	18.6	481	2 I49072	protein kinase - m
21	610	18.5	473	1 S59941	serine/threonine-s
22	599	18.2	512	2 T07788	probable serine/th
23	596.5	18.1	887	2 T20941	hypothetical prote
24	594.5	18.1	576	2 T41587	probable carbon ca
25	587.5	17.8	622	1 S44859	serine/threonine-s
26	583.5	17.7	891	2 A38903	protein kinase 1 -
27	581.5	17.7	891	2 T40503	protein kinase kin
28	579	17.6	510	2 T04145	serine/threonine p
29	570	17.3	502	1 A41361	serine/threonine-s

SNF1-related prote
serine/threonine-s
serine/threonine-s
serine/threonine-s
probable protein k
serine/threonine-s
p69Bg3 protein - A
GIN4 protein - yea
protein kinase KIN
probable serine/th
probable serine/th
probable protein k
hypothetical prote
SNF1-related prote
probable protein k

ALIGNMENTS

RESULT 1

T29253
hypothetical protein B0496.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29253
R;Murray, J. J. Le, T. T.
Submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid B0496.
A;Reference number: Z20596
A;Accession: T29253
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1558 <MUR>
A;Cross-references: EMBL:U58749; PIDN:AAB00636.1; GSPDB:GN00022; CESP:B0496.3
A;Experimental source: strain Bristol N2; clone B0496
C;Genetics:
A;Gene: CESP:B0496.3
A;Map position: 4
A;Introns: 55/1; 100/3; 141/1; 226/3; 298/1; 468/3; 502/2; 609/3; 656/3; 795/3; 843/2; 9

Query Match	27.0%	Score	888	DB	2	Length	1558
Best Local Similarity	37.0%	Pred. No.	2.1e-28				
Matches	230	Conservative	73	Mismatches	214	Indels	104
Gaps	15						
Qy	54	RHRYELETGKTYGKVKARESS-GRVVAIKSKDKIKQDQDLHIREIEMSLN	112				
Db	72	KHRFEITKLGSGTYGKVSLAYDHKFDREAVAVKLKKSADLVIRIRREIRMSALN	131				
Qy	113	HPHIIAIEHVEFENSKITIVMEYASRGDLVDYISERPLSERDARHFFROIVSALHYCHQ	172				
Db	132	HPNIIQIYEVFNKDKIILVMEYSSGGELYDYVRCGSLPEAEARRIFQITSAVLCHK	191				
Qy	173	NGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVG	232				
Db	192	HRVAHRDLKLENILLDQNNAKIADFGLSNYPADKLLTTFCCGSPLYASPEIINGTYKG	251				
Qy	233	PEVDSLSGLVLLIYLVHGTMPFDGQDHKTIVKQISNGAYREPPKPSDACGLIRLLMVP	292				
Db	252	PEVDCSLGLITLTVYSGMPFDGRDNRMVROIKRGAYPEPETPTASTASMLIRLVNP	311				
Qy	293	TREATLEDVASHVMVNGVYTTGV-----GQREALREG	324				
Db	312	ERRATIFDASHWMLNLENMVPVQELPENQIIDHTPLTERETMIVQDLADSDQVMEF	371				
Qy	325	GHPSGDGFRASMDWLR-----SSRPLENGAKVCSFFKQHVPGGGSV	369				
Db	372	GHLSSTRRKIEDFRIRREAEFEFNDSVPKPPKARKTDBLTGCKISKEQPEEMKSAEKL	431				
Qy	370	PGLERQHS-----LKKSRK-ENDMAQNIQGDPAEDTSRRPGKSLKLPKGLIKKK	418				
Db	432	RGVKEEKPKVVDPDNDPLERLQIENRLQONKDKKAAKTSARVETVKLK-----EVK	485				

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QY 419 SSTSSGEVQSDPQELRPVPTPGQVPVAVSILPRKGLKKSRQESGYSPSPSESGEL 478
Db 486 KEKSPQOQDPKTPAR-----GTSKPADGRAP-SFVVPKDRPBT-----SEPERPRTRPH 534
QY 479 LDASDFVFSQDPVEQKSPQASGLLHLHKGILKLN--GKFSRTALEGTTPTSTFGSLDQLAS 536
Db 535 LTASAVRIETDSLNLMLNQV--LEQMEKGPVNLNIARIKAHPLYDTRPVVKELLESIIA 592
QY 537 SHPAARSPRSGAVSDESILSSSFDQL-----DLPERLPETPARGCVSVNLRGLEPPS 592
Db 593 AQPEPVQKQTSKVVEQQTFRQNTLTRKKKEDPLEEPIEVP-----SPS 637
QY 593 EGLK-RWW-----QESLG 604
Db 638 RKMKEPWHVSVEVCMKNESVG 658

RESULT 2
S27966
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - human
N;Alternate names: protein p78
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C;Accession: S27966
R;Maheshwari, K.K.; Som, S.; Parsa, I.
submitted to the EMBL Data Library, January 1992
A;Description: Sequence of a cDNA encoding 78kD marker protein lost in chemically induced
A;Reference number: S27966
A;Accession: S27966
A;Molecule type: mRNA
A;Residues: 1-713 <MAH>
A;Cross-references: UNIPROT:P27448; EMBL:M80359; NID:g189511; PID:AAAS9991.1; PID:g1895
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;54-307/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif

Query Match 21.18; Score 694.5; DB 2; Length 713;
Best Local Similarity 34.5%; Pred. No. 4.9e-21;
Matches 191; Conservative 75; Mismatches 171; Indels 117; Gaps 17;

QY 57 YEFLTLGKGTGKVKKARE--SSGLVAIKSIRKDKIKDEQDLHHRREIEIMSSLNHPH 115
Db 56 YRLTKTGKNFAKVKLARHLITGREVAIKIIDTQL-NPTSLOKLFREVRIMKVLNHPN 114
QY 116 IIAIHEVFENSXKIVIMEYASRGDLYDISERPLSERDARHFFRQIVSALHYCHQNGI 175
Db 115 IVKLFVETQKTLYLIMEYASGGKVFYDLVAHGRMEKEARSFRQIVSAVQYCHQKRI 174
QY 176 VHRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPV 235
Db 175 VHRDLKAENLLDADNMNIKIADFGFNEFTVGGKLDTCGSPPYAAPELFGKKYDGPV 234
QY 236 DWSLGLVLLYLHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC--GLIRWLLMVNPT 294
Db 235 DWSLGLVLLYLVSGSLPFDGQNLKELRERVLRGKRIPIPFYMTDCENLKKRFLVLPK 294
QY 295 RATLEDVASHWVNWGYTTGVGEQALREGGHPGDFGRASMDWLRSSRPLLENGAKV 354
Db 295 RGTLEQIMKDRWINAGH-----EDELKPFVPELDISDQKIDIM-----V 336
QY 355 CSFPKQHVPGGTVPGLEHRSQHLKKSRKENDMAQNL-----QCPAEDTSSRPCKSS 407
Db 337 GMGYSQSE-----ETQESLKMKYDEITATYLLGRKSEVFRPSSDLNNSTQGS- 384
QY 408 LKLPKGLIKKKSSSTSGVEQEDPQELRPVPTPGQVPVAVSLLPR-----452
Db 385 ---PHHKVQSVSS-----QKQRYSDHAGPGIPSVVAYPKRSQTSADSLKEDG 433
QY 453 -----KGILKKSRQESGYSPSPSESGELLDASDVVFSGDPVEQKSPQAS 499
Db 434 ISSRKSTGSAVGGKGIAPSPM--LGNASPNKADIPERKKSIV-----PSSNTAS 483
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QY 500 GLLLRHK-----GILKNGKSRTALEGTTPSTFGSLDQLASSH---PAARP 543
Db 484 GGMTRRTYVCSRTTDDRHSHVIQ-NGKENSTIPDQRT-----VASTHSSAATP 534
QY 544 SR---PSGAVSEDS 554
Db 535 DRIRPRGTASRST 548

RESULT 3
G01025
serine/threonine protein kinase - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G01025
R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-745 <NAV>
A;Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C;Superfamily: protein kinase homology
F;18-271/Domain: protein kinase homology <KIN>

Query Match 20.9%; Score 689; DB 2; Length 745;
Best Local Similarity 33.2%; Pred. No. 8.4e-21;
Matches 189; Conservative 92; Mismatches 176; Indels 112; Gaps 20;

QY 57 YEFLTLGKGTGKVKKARE--SSGLVAIKSIRKDKIKDEQDLHHRREIEIMSSLNHPH 115
Db 20 YRLTKTGKNFAKVKLARHLITGREVAIKIIDTQL-NSSSLOKLFREVRIMKVLNHPN 78
QY 116 IIAIHEVFENSXKIVIMEYASRGDLYDISERPLSERDARHFFRQIVSALHYCHQNGI 175
Db 79 IVKLFVETQKTLYLIMEYASGGVFDYLVHGRMKKEARAKFRQIVSAVQYCHQKFI 138
QY 176 VHRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTCGSPLYASPEIVNGKPYVGPV 235
Db 139 VHRDLKAENLLDADNMNIKIADFGFNEFTVGGKLDTCGSPPYAAPELFGKKYDGPV 198
QY 236 DWSLGLVLLYLHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC--GLIRWLLMVNPT 294
Db 199 DWSLGLVLLYLVSGSLPFDGQNLKELRERVLRGKRIPIPFYMTDCENLKKFLILNPSK 258
QY 295 RATLEDVASHWVNWGYTTGVGEQALREGGHPGDFGRASMDWLRSSRPLLENGAKV 354
Db 259 RGTLEQIMKDRWMNVGH-----EDELKPYVEPLPDYKDP-----RRTLMVSMG--- 303
QY 355 CSFPKQHVPGGTVPGLEHRSQHLKKSRKENDMA-----ONLQGD-----PAED 398
Db 304 --YTREEI-----QDSLVGQRYNEVMATYLLLYGKSELEGDTITLKPRESAD 349
QY 399 -TSSRPCKSSLKPKGI-----LKKKSTSSSGE---VQEDPOE 432
Db 350 LTNSSAQFPHKQVRSVANSKORRSDQAGPAIPTSNYSKKTQSNNAENKPEEDRES 409
QY 433 LRFPVPTD---PGQFVPVAVSLLPRKGLKKSRQESGYSPSPSESGELLDASDVVFSGD 489
Db 410 GRKASSTAKVPASPLP-----GLERKK-----TTFTPTNSVLSTSTN----- 447
QY 490 PVQKSPQASGLLHLHKGILKLN---NGKFSRTALEGTTPSTFGSLDQLASSHAAARSRP 546
Db 448 -RSRNSP-----LLEASLGQASIQNGKDSLT-MPGSRASTASAGVSAARPRQHOKSM 500
QY 547 SGAV---SEDSILSSSFDQLDLPRLPE 572
Db 501 SGSVHPNKASGLPPTESNCEVPRPSTAPQ 529

RESULT 4
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148609

probable serine/threonine-specific protein kinase (EC 2.7.1.1-) kem - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C;Accession: I48609; PMID:8358177
R;Ingalls, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A;Title: Enk, a protein kinase with homologs in yeast maps to mouse chromosome 19.
A;Reference number: I48609; MUID:93364122; PMID:8358177
A;Accession: I48609
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-774 <ING1>
A;Cross-references: UNIPROT:Q05512; EMBL:X70764; NID:G57919; PIDN:CAA50040.1; PID:G57920
R;Ingalls, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A;Description: A novel protein kinase with homologues in yeast maps to mouse chromosome
A;Reference number: S31333
A;Accession: S31333
A;Molecule type: mRNA
A;Residues: 1-698, 'K', 700-702, 'GRGLPTAAKASCTSGTCYCAGMAHQART', 731-774 <ING2>
A;Cross-references: EMBL:X70764
C;Genetics:
A;Gene: emk
C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;51-304/Domain: protein kinase homology <KIN>
F;59-67/Region: protein kinase ATP-binding motif

Query Match 20.8%; Score 686.5; DB 2; Length 774;
Best Local Similarity 32.6%; Pred. No. 1.1e-20;
Matches 199; Conservative 90; Mismatches 218; Indels 103; Gaps 20;
6 LLORPSOAPSASALASARPLADGLIKSPKPLMKQAVKHHKHLRHR-----YEFL 60
11 LNERDTQPTGLHDS-----KPSKSNLGRNSATSADQPHIGNVRL 56
61 ETLLGKGTGVKKARE-SSGRLVAIKSIRKDKIDEQDLHRRIRIEMSLNPHIIAI 119
57 KTIGKGNFAKVLARHILTGKVAVKIIDKTQL-NSSSLQKLFREVRIMKVLNHPNIVKL 115
120 HEVFENSKIVIVMEYASRGDLYISERPLSRDARHFRQIVSAHYCHQNGIVHRD 179
116 FEVIETETKLYLVMYASGGVEFDYLVAHGRMKKEARAKFRQIVLHVQVCHQKFIHRD 175
180 LKLENILLDANGNIKIADFGISNLYHKGKFLQTCGSPLYASPEIVNGKPVGPEVDWS 239
176 LKAENLLDAMNIIKIADFGISNLYHKGKFLQTCGSPLYASPEIVNGKPVGPEVDWS 235
240 LGVLLYILVHGTMPDQDQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVPTRATL 298
236 LGVILYTLVSGSLPFDQNLKEURVLRGKYRIPFYMWSTDCENLLKKFLILNPSKGTLL 295
299 EDVASHVWVNGYTTGVGEQALREGHPSGDFGRASMDWLRRSSRPLENGAKVCSFF 358
296 EQIMKDRWN-----VGHED-----DELKPYVEPLLTGP----- 325
359 KQHPVGGGTVPGI-----ERQHSLLKSKRKENDMAQNL-----QCPADETSSRCKSLKL 410
326 RDRVDG-----VNLHTEIQQSLVGQRYNEVMATYLLGLYKSEPEGDTTLKPRPSADL 381
411 PKGILKKKSTSGVEQEDQELRPVDPDTPQCPVAVSLLPRKILKKRSQRSGYVSSP 470
382 TNSAPSPSHKVQSVANPKQR-----SSDQAVPAI-----PTNSYSKKTQSNNAENKRP 434
471 EPESGELLDAQDVVSGDP-VQOK-----SPQASGL-----LHRRGILKL-- 511
435 EETGRKASSTAKVPASFLPCLDRKTTTAPSTNSVLSTSTNSRNSPLLDRAISLQAS 494
512 -NGKFSSTALEGTTPTFGSILDQASSHP-----AARSPSPCAVEDSILSSESF 561
495 QNGKDSLT-MPGRASSTASAAVSAARPROHOKMSASVHPNPKASGLPTES--NCEVP 551

Qy

562 DQLDLPERLP 571

Db

552 RPSTAPQRP 561

RESULT 5

T18611

probable serine/threonine-specific protein kinase (EC 2.7.1.1-), long splice form - Caeno
N;Contains: probable serine/threonine kinase, short splice form
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18611; T18610; T23144; T23143
R;McMurray, A.
submitted to the EMBL Data Library, October 1996

A;Reference number: Z18997

A;Accession: T18611

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1192 <WIL1>

A;Cross-references: UNIPROT:Q9TW45; EMBL:Z81027; PIDN:CAB54179.1; GSPDB:GN00023; CESP:H3

A;Experimental source: clone AH10

A;Accession: T18610

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-487,536-1192 <WIL2>

A;Cross-references: EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b

A;Experimental source: clone AH10

R;McMurray, A.

submitted to the EMBL Data Library, June 1997

A;Reference number: Z19696

A;Accession: T23144

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1192 <WIL3>

A;Cross-references: EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a

A;Experimental source: clone H39E23

A;Accession: T23143

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-487,536-1192 <WIL4>

A;Cross-references: EMBL:Z96102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b

A;Experimental source: clone H39E23

C;Genetics:

A;Gene: CESP:H39E23.1a; CESP:H39E23.1b

A;Map position: 5

A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 535/3; 631/1; 825/2; 914/3; 992

C;Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pro

F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #a

F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splice

Query Match

Best Local Similarity 20.3%; Score 669; DB 2; Length 1192;

Matches 187; Conservative 97; Mismatches 218; Indels 76; Gaps 16;

Qy

11 SOAPSASALASARPLADG-----LIKSPKPLMKQAVKHHKHLRHR 58

Db

113 SGAPASS-GGSSARYSSSSGRSHPTSGSSSSSHARSTQSCMSSRSARRNDQDVHVCKYK 171

Qy

59 FLTLGKGTGVKKARE-SSGRLVAIKSIRKDKIDEQDLHRRIRIEMSLNPHII 117

Db

172 LLKTIGKGNFAKVLARHILTGKVAVKIIDKTAL-NPSSLQKLFREVRIMKVLNHPNIV 230

Qy

118 AIHEVFENSKIVIVMEYASRGDLYISERPLSRDARHFRQIVSAHYCHQNGIVH 177

Db

231 KLYQVMEETQTLVLYVAYSGGVEFDYLVAHGRMKKEARAKFRQIVSAVOYLHRSKNIIH 290

Qy

178 RDLKLENILLDANGNIKIADFGISNLYHKGKFLQTCGSPLYASPEIVNGKPVGPEVDS 237

Db

291 RDLKAENLLDAMNIIKIADFGISNLYHKGKFLQTCGSPLYASPEIVNGKPVGPEVDS 350

Qy

238 WSLGVLLYILVHGTMPDQDQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVPTRRA 296

Db

351 WSLGVLLYILVHGTMPDQDQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVPTRRA 410

Db 568 TGYLNGGVEVDASGILPLPMRYTLP TAASPAPNSCSTSRVGV-----RHSLSSSS 619
Qy 470 P-----EPSESG-----ELLDASDVFVSGDPVEQKSPQASGLLLHR---KGI 508
Db 620 PRSHRPVAISLIDNNPSLANLRCEWMEA-----GGPVGAVGPLASKQLHOTISEFI 674
Qy 509 LKLNKFSRTALEGTT-----PFTGSLDQLASSHPAARSPRPS-----GA 549
Db 675 IKQSTEDCRALLOQSTAVAEKDDPPKAESVGGVPPPASTPTTSSTAGPESGAPCPGE 734
Qy 550 VSEDSI---LSESEFD 562
Db 735 INGRTIKTMSSSSSSFD 750

RESULT 8
T52633
serine/threonine-specific protein kinase (EC 2.7.1.1-) AKIN11 [validated] - Arabidopsis thaliana
N:Alternate names: SNF1 protein kinase homolog AKIN11
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52633
R:Bhalerao, R.P.; Saichert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid
Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A:Title: Regulatory interaction of PR1 WD protein with Arabidopsis SNF1-like protein ki
A:Reference number: T25116; MUID:99238528; PMID:10220464
A:Accession: T52633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <BHA>
A:Cross-references: UNIPROT:P92958; EMBL:X99279; PIDN:CAA67671.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: AKIN11
C:Function:
A:Description: EC 2.7.1.1-; serine/threonine-specific protein kinase AKIN11 [validated, M
complements SNF1 mutations in yeast
C:Superfamily: AMP-activated protein kinase; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 19.7%; Score 649.5; DB 2; Length 512;
Best Local Similarity 38.6%; Pred. No. 2.2e-19;
Matches 152; Conservative 65; Mismatches 126; Indels 51; Gaps 9;

Qy 57 YEFLETGKGYGVKKARE--SSGLVAIKRKDKDKDEODLLHIREIEMSSLNHPH 115
Db 20 YLCKTIGISFGVKVKAETHVVTGCHVAIKILNRKIKNMEMEKVREIKILRFMHPH 79
Qy 116 IIAIHEVFENSKIVIVMEYASRGDLYDIYISERPLSERDARHFFRQIVSALHYCHQNGI 175
Db 80 IIRQYEVITTSDIYVMEYVYKSGELFDYIVKGRLOEDEARNFQQLISGVEYCHRMV 139
Qy 176 VHRDLKLENTLLDANGNIKADFGSLNLYHKGKFLQTFGSPLYASPEIVNGKPYGVPEV 235
Db 140 VHRDLKLENTLLDANGNIKADFGSLNLYHKGKFLQTFGSPLYASPEIVNGKPYGVPEV 199
Qy 236 DSWSLGVLVLYLVHGTMPFGQDHTLVKQISNGAYREPPK-PSDACGLIRWLLMNPTR 294
Db 200 DVNSCGVILVALLCGTLPFDDENTPNFKIKGGIYILPSHLSSEARDLIPMLIVDPVK 259
Qy 295 RATLEDVASHVWVWVNGYTTGVGEQALREGGHPGDFGRASMDWLRSSRPLLENGAKV 354
Db 260 RITIPERQHRWF-----QTHLPYLAIVSPDPTVEQAKI 294
Qy 355 CSFFKQHVPGGGSVPGLEHROHSUK--KSRKENDMAQNLOQDPAEDTSSRPGKSSLPK 412
Db 295 NEETVQSVN-----MGFDRNQVLESRLNRQND-----ATVTYILLDDNRFRVPS 340
Qy 413 GILKK--KSSTSSGVEQEDPQELRPVDPDTPQPV 444
Db 341 GYLSEFQETDSDG---SNPMR-----TPEAGASPV 368

RESULT 9

A26030
serine/threonine-specific protein kinase (EC 2.7.1.1-) SNF1 - yeast (Saccharomyces cerevi
N:Alternate names: protein YDR477w
C:Species: Saccharomyces cerevisiae
C:Date: 20-Aug-1987 #sequence_revision 20-Aug-1987 #text_change 09-Jul-2004
C:Accession: A26030; S69644
R:Celenza, J.L.; Carlson, M.
Science 233, 1175-1180, 1986
A:Title: A yeast gene that is essential for release from glucose repression encodes a p
A:Reference number: A26030; MUID:86289463; PMID:3526554
A:Accession: A26030
A:Molecule type: DNA
A:Residues: 1-633 <CEL>
A:Cross-references: UNIPROT:P06782; EMBL:M13971; NID:gi72629; PIDN:AAA35058.1; PID:gi726
R:Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
A:Reference number: S69554
A:Accession: S69644
A:Molecule type: DNA
A:Residues: 1-633 <DIE>
A:Cross-references: EMBL:U33050; NID:g927726; PIDN:AAB64904.1; PID:g927732; GSPDB:GN0000
C:Genetics:
A:Gene: SGD:SNF1; MIPS:YDR477w
A:Cross-references: SGD:S0002885; MIPS:YDR477w
A:Map position: 4R
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: required for expression of glucose-repressed genes in response to glucose depriv
C:Superfamily: AMP-activated protein kinase; protein kinase homolog
C:Keywords: ATP; autophosphorylation; magnesium; nucleus; phosphoprotein; phosphotransfe
E:53-306/Domain: protein kinase homolog <KIN>
E:61-69/Region: protein kinase ATP-binding motif
F:84,103,177,179/Active site: Lys, Glu, Asp, Lys #status predicted
F:182,186/Binding site: magnesium (Asn, Asp) #status predicted
F:210/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predicte

Query Match 19.7%; Score 648.5; DB 1; Length 633;
Best Local Similarity 33.1%; Pred. No. 2.9e-19;
Matches 161; Conservative 79; Mismatches 133; Indels 113; Gaps 14;

Qy 47 HHKHNLRH-----RYEFLTLGKTYGVKKKA-RESSGRLV 82
Db 22 HHHHHHHHGGGNSLNNPKSSLDAGHIGNYQIVKTLGEGSGFKVLAHTTTCQKV 81
Qy 83 AIKSIKDKIKDEODLL-HIRREIEMSSLNHPHIIAHEVFENSKIVIVMEYASRGDL 141
Db 82 ALKIINK-KVLAKSDMQGRIEREISYLRLRHPHIIKLYDVIKSKDEIIMVIEYAG-NEL 139
Qy 142 YDIYSERPLSERDARHFFRQIVSALHYCHONGIVHRDLKLENTLLDANGNIKADFGLS 201
Db 140 FDIYVQDKMSGEARFFQQLISAVEYCHRRKILVHRDLKPENLLDEHLNVKIDAFGLS 199
Qy 202 NLXHKGKFLQTFGSPLYASPEIVNGKPYGVPEVDSWSLGLVLYLVHGTMPFGQDHTK 261
Db 200 NIWTDGNTLTCGSPNYAAPEVISGKLYAGPEVDVWSCGVILVLMCRLLPFDESPV 259
Qy 262 LVQISNGAYREPPKPS-DACGLIRWLLMNPTRATLEDVASHVWVWVNGYTTGVGEQEA 320
Db 260 LFKNISNGYVTLPKFLSPGAAGLIKRLMLIVNPLNRIISHEIMQD----- 303
Qy 321 LREGHPSGDFGRASMDWLRSSRPLLENGAKVCSFFKQHVPGGGSVPGLEHROHSUK 380
Db 304 -----DW-----FKVDLP-----EYLLPP 317
Qy 381 SRKENDMAQNLOQDPAEDTSSRPGKSSLPKGLIKKSSSTSSGVEQEDPQELRPVDP 440
Db 318 DLKPHPEENENDSKDGS---PONDEIDNNLVNLSSTMGVEKDEIYESLESSEDT 374
Qy 441 --GQPVDAVSL-PRKILKKSQRRESGYSSPEPSGELLSDASDVFGSDP-----VEQ 493
Db 375 AFNEIRDAYMLIKENKSLIKDMKANKS-----VSDLDTLFSLQSPPTFQQQS 421

QY 494 KSPQAS 499
Db 422 KSHQKS 427

RESULT 10

JC7500
qik protein - chicken
N;Alternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
R;Xia, Y.; Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncogene.
A;Reference number: JC7500
A;Contents: Embryo fibroblasts
A;Accession: JC7500
A;Molecule type: mRNA
A;Residues: 1-798 <XIA>
A;Cross-references: UNIPROT:Q91A86; GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases,
A;Gene: qik
C;Keywords: protein kinase

Query Match 19.7%; Score 648; DB 2; Length 798;
Best Local Similarity 29.4%; Pred. No. 3.8e-19;
Matches 195; Conservative 94; Mismatches 223; Indels 152; Gaps 17;
QY 11 SQAPSALASASARPLADGLIKSPKPLMKQAVRHHKHLRHYEFLETLGKGYGK 70
Db 5 SEDASVPAPSAQAQPRPLRVGF-----YDIERTLGKGNFAV 39
QY 71 VKKARESSRL-VAIKSRDKIKDEQDLHIREIEIMSSLNHPHIIAHEVFENSKI 129
Db 40 VKLARHRTVQVAIKIDKTRL-DPSNLEKIEVQIMKLNHPHIIKLVQVMEKDM 98
QY 130 VIVMEYASRGDLVDYISRPRLSRDARHFRQIVSALHYCHQNGIVHRDLKLENILDA 189
Db 99 YIVTEFAKNGEMFHDLTNSHGLSESEARKKFWILSAVEYCHSHIHRDLKLENILDA 158
QY 190 NGNIKIADFGSLNLYHKGFQTCGSPLYASPELVNGKPVGVGEVDSWSLGLLYLVH 249
Db 159 NNNIKLADFGFNGFYKSGEPLSTWCGSPPYAAPEVTEGKEVTEGPHLDLWSLGVVYLVC 218
QY 250 GTMPFDGQDHTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTTRATLEDVASHWVN 308
Db 219 GSLPFDGPNLTLRQRLVLEGRFIPYFWSDECETLIRMLVVDPTKRITISQIKQKWM- 277
QY 309 WGYTTGVGEALREGHPGSDGFRASWADWLRRSRPL-----LENGAKVCFFQKHPDGG 365
Db 278 -----QADPSLRQQQSLSFMSQNYNSNLGDYNEQVLGI 310
QY 366 GSTVGLERQSHLKK-----SRKENDMAQLQDPAEDTSSRPKSSL 408
Db 311 MQLT-LGIDQRTVESLQNSVNHFAIYVLLERLKEYRSQLSRPAATGQQRPSSEI 369
QY 409 ---KLPGILKKKSSSTGEVQEDQELRPV-----PDTPGQPV-----PAVSLPLR 452
Db 370 SNAEMPQDLSLTLRSLILYQQPSLIQPSLQAECDMNNPLQPVFFVPDNPNGLFR 429
QY 453 KGILKKQRSGSYSSPEPESGELLASDVFSVGDPEQKSPOASGLLHRKGLKLN 512
Db 430 NRSISPSLLETTI---SEVRQEKLED---EIKAYDHPIRIPS-----N 469
QY 513 GKFSSTALEGTPSTFGSLDOLASHPAARPSRPGSAVSEDSILSSSEFDQ----- 563
Db 470 TSSRHLLAEVTHFYQHAPPCIVISSAS-----PTEGTSSSCLTSSNDSVALSSCIA 525
QY 564 -----LDLPERLPETPLRGCVSDNL-----RGLQPPSEGLKR 597

Db 526 GQVMTGSPATARTWTSFAFLASQSDAPVLQVQGWGASLLPVSFQEGRRASDTSLTGLKA 585
QY 598 WMQE 601
Db 586 FRQQ 589

RESULT 11

T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N;Alternate names: SNF1-related protein kinase
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17020
A;Accession: T10449
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>

Query Match 19.5%; Score 641; DB 2; Length 504;
Best Local Similarity 50.4%; Pred. No. 4.7e-19;
Matches 127; Conservative 47; Mismatches 76; Indels 2; Gaps 2;
QY 57 YEFLETLGKTYGKVKKARES-SGRLVATKSIKDKIKDQDLHIREIEIMSSLNHPH 115
Db 8 YKLGKTLGIGSGFKVIAEHALTGKVAIKILNRRKIKNDMEKVRREIKIURLFWHPH 67
QY 116 IIAIHEVFENSSKIVIMVEYASRGDLVDYISRPRLSRDARHFRQIVSALHYCHQNGI 175
Db 68 IIRLYEVIETPSDIYVMEYVKSGLDFDIYVEKGRLEQDEARNFFQIISGVEYCHRMV 127
QY 176 VHRDLKLENILLDANGNIKIADFGSLNLYHKGFQTCGSPLYASPEIYVNGPYGPEV 235
Db 128 VHRDLKLENILLDSKCNVKIADFGSLNIMRDGHFLKTCGSPNYAAPEVSGKLYAGPEV 187
QY 236 DWSLGLVLLYLHVGTMPPDQDHKTIVKQISNGAYREPPK-PSDACGLIRWLLMVNPT 294
Db 188 DVWSCGVILYALLCGLTLPFDENIPNLFKKIGGIYTLPSHLSSGARELIPSLVVDPMK 247
QY 295 RATLEDVASHHW 306
Db 248 RITPEIRQHPW 259

RESULT 12

JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g166600
R;Thummler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g
A;Reference number: S58256

A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: UNIPROT:Q40544; GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 19.2%; Score 631; DB 1; Length 511;
Best Local Similarity 49.6%; Pred. No. 1.2e-18;
Matches 125, Conservative 48; Mismatches 77; Indels 2; Gaps 2;

QY 57 YEFLETIGKYGVKKVKAES-SGRLLVAIKIRDKIKDEODLLHIRRIETMSSLNHPH 115
Db :
19 YKLGTGIGSGFGVKIAEHLTGHKVAVKILNRRIKNMEMEEKVRREIKILRFMPHP 78
QY 116 IIAIHEVFENSSKIVIMVEYASRGDLYISERPLSRDARHFPRQIVSALHYCHONGI 175
Db :
79 IIRLYEVETPSDIYVMVEYKSGELFDYIEKGRLQDEARKFFQQIISSGVEYCHRMV 138
QY 176 VHRDLKENILLDANGNIKIADFGLSNLYHGKGFQTFCGSPLYASPEIWNKPYVGPEV 235
Db :
139 VHRDLKENILLDSKNWVKIADFGLSNMRDGHFKLTCGSPNYAAPEVISGKLYAGPEV 198
QY 236 DWSLGVLLYLIVHGTMPDFQDDHKTLYKQISNGAYRPPPKPS-DACGLIRMLLMVNPT 294
Db :
199 DVNSCGVILYALLCGTLTPFDDENIPNLFPKKIKGMISLPShLSAGARDLI PRMLIVDPMK 258
QY 295 RATLEDVASHWW 306
Db :
259 RMTIPEIRMHPW 270

RESULT 14
S51025
[hydroxymethylglutaryl-CoA reductase (NADPH2)] kinase (EC 2.7.1.109) - human
N;Alternate names: AMPK
N;Contains: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl-CoA r
C;Species: Homo sapiens (man)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51025; I38503
R;Beri, R.K.; Marley, A.B.; See, C.G.; Sopwith, W.F.; Aguan, K.; Carling, D.; Scott, J.;
FEBS Lett. 356, 117-121, 1994
A;Title: Molecular cloning, expression and chromosomal localisation of human AMP-activat
A;Reference number: S51025; MUID:95080410; PMID:7988703
A;Accession: S51025
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-552 <BER>
A;Cross-references: UNIPROT:P54646
R;Aguan, K.; Scott, J.; See, C.G.; Sarkar, N.H.
Gene 149, 345-350, 1994
A;Title: Characterization and chromosomal localization of the human homologue of a rat A
A;Reference number: I38503; MUID:95047501; PMID:7959015
A;Accession: I38503
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-179, T*, 181-270, 'G', 272-402, 'RQ', 405-552 <RES>
A;Cross-references: EMBL:U06454; NID:g758366; PIDN:AAA64745.1; PID:g758367
C;Genetics:
A;Gene: GDB:PRKAA2; PRKAA; AMPK; hAMPK
A;Cross-references: GDB:451905; OMIM:600497
A;Map position: lp31-lp31
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Note: in vivo substrates include hydroxymethylglutaryl-CoA reductase (NADPH) and acety

C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;14-268/Domain: protein kinase homology <KIN>
F;22-30/Region: protein kinase ATP-binding motif
F;45,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted
F;144,148/Binding site: magnesium (Asn, Asp) #status predicted

```
Query Match      19.1%; Score 630.5; DB 1; Length 552;
Best Local Similarity 31.5%; Pred. No. 1.3e-18;
Matches 176; Conservative 91; Mismatches 199; Indels 93; Gaps 17;

Qy 45 KRHHKHNLRHRYEFLTGLTGYGVK-KARESSGRLLVAIKSRKDKIKDEQDQLLHRR 103
Db 5 QKHGRVKIGH-VYLGDTLGVGTGKVGKIGEHQLTGHKVAVKILNRQKIRSLDVVGKIKR 63

Qy 104 EIEIMSSLNHPHIIAIEHVFENSSKIVIMVEYASRGDLYDIYSRPRLSERDARHFRQI 163
Db 64 EIQNLKLFRRPHIILKLYQVISTPTDFVMVEYVSGGELFDYICKHGRVEMEARRLFQOI 123

Qy 164 VSALHYCHONGIVHRDLKLENILLDANGNIKIADFGLSNLVHKGFLOTFCGSPLYASPE 223
Db 124 LSAVDYCHRMVVRDLKPNVLDLDAWNKIAIDFGLSNMDSGEFLRTSCGSPNYAAPE 183

Qy 224 IVNGKPYVGPVDSWSLGLVLLYILVHGTMPDPGDHKTIVKQISNGAYREPPKPS-DACG 282
Db 184 VISGRLYAGPEVDIWSGVLVYALLCGTLFPDDEHVPTLFKKIRGGVFIPEYLNRSVAT 243

Qy 283 LIRWLLMVPNTRATLEDVASHWVNW-----GYTTGVGEQEARLE----- 323
Db 244 LLMHMLQVDPKLRATIKDIREHEWFKQDLPYSLPEDPSYDANVIDDEAVKEVERPECT 303

Qy 324 -----GHPGSGDFGRASMDLRRSSRPLENGAKVCSFFKQHPVGGSTV----- 369
Db 304 ESEVWNSLYSGDPQ---DQLAVAVHLIDNRINWQASE---FYLASSPPSGSFMDDSAM 357

Qy 370 ---PGL-----ERHSL-----KSKRKENDMAQNLQGDPAEDTSSRPKSKSLKLPKGIKXK 418
Db 358 HIPGLKPHPERMPPLIADSPKARCLDAL-----NTTKPKSLAVKAKWHLGIR 407

Qy 419 SSTSSGSEVEDPQLRPVPTPGQPVPAVSLLPK-----GILKSKRQR-----ESGYISS 469
Db 408 SQSKPYDIMAIEVRYAMKQLDFEWKVNAYHLRVRKKNPVGTGNYVKMSLQLYLVNRSYLL 467

Qy 470 PEPSESGELLDASDFVSGDPVEOKSPQASGLLHRRKILKNGKFGRTALE----- 521
Db 468 DFKSIDDEVEQR-----SGSSTPQSCSAAG--LHRP-----RSSPSTTAESHSLSGSL 516

Qy 522 --GTPPTFGSLDQLASSH 538
Db 517 TGSLTGSLSSVSPRLGSH 535
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RESULT 15

S72513
FOG2 protein - yeast (*Kluyveromyces marxianus* var. *lactis*)
C;Species: *Kluyveromyces marxianus* var. *lactis*, Candida sp. *phaerica*
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S72513
R;Goffiani, P.; Picarelli, A.; Donnini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
Curr. Genet. 29, 316-326, 1996
A;Title: FOG1 and FOG2 genes, required for the transcriptional activation of glucose-rep
A;Reference number: S72513; MUID:96171514; PMID:8598052
A;Accession: S72513
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-602 <GOF>
A;Cross-references: UNIPROT:P87209
A;Note: the source is designated as *Kluyveromyces lactis*
C;Genetics:
A;Gene: FOG2
C;Function:
A;Description: probably involved in the regulation of glucose-repressible gene expressio
C;Superfamily: AMP-activated protein kinase; protein kinase homology

F;33-286/Domain: protein kinase homology <KIN>

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Query Match      19.1%; Score 627.5; DB 2; Length 602;
Best Local Similarity 35.6%; Pred. No. 1.9e-18;
Matches 155; Conservative 68; Mismatches 125; Indels 87; Gaps 14;

Qy 47 HHHKHNLRH-----RYEFLTGLTGYGVKVKARE-SSGRLLVAIKSRKDKIKDQDL 98
Db 18 HHORQLTNHAQGHGHIQYIKITLGEFGKVLAVHIISTGQVKALKIINK-KVLAKSDM 76

Qy 99 L-HIRREIETMSSLNHPHIIAIEHVFENSSKIVIMVEYASRGDLYDIYSRPRLSERDAR 157
Db 77 QGRIEREISVRLRLRHPHIIKLYDVITKSQDEIIMVIEYAG-NELFDYIVQDKMPEQEAR 135

Qy 158 HFRQIVSALHYCHONGIVHRDLKLENILLDANGNIKIADFGLSNLVHKGFLOTFCGSP 217
Db 136 RFFQQTIIISAVDYCHRHKIVHRDLKPNVLDLDAWNKIAIDFGLSNIMTGNFLKTSQSP 195

Qy 218 LYASPEIVNGKPYVGPVDSWSLGLVLLYILVHGTMPDPGDHKTIVKQISNGAYREPPK 277
Db 196 NYAAPEVISGKLYAGPEVDVWSSGVLYVWLCRLPPDDESIPLVFNKINSNGVYTIENFL 255

Qy 278 SD-ACGLIRWLLMVPNTRATLEDVASHWVNWNYTTGVGEQEARLEGGHPSGDFGRASM 336
Db 256 SQGAASLIKQMLIVNPNRITVHEIMQDEWF-----KVDL 290

Qy 337 ADMLRSSRPLENGAKVCSFFKQHPVGGSTVP-----G 371
Db 291 PDYLVPAESTHQENS-----ESKTEDGGSPVPLELIDSLVQTLNMTGYDVDEIYEA 343

Qy 372 LERQH---SLKSKR-----KE-----NDMAONLQGDPAEDT---SSRPG--KSSLKLPKG 413
Db 344 LESEDEHPSLNEIRDAYQLIKENRNINLINDIKVKKQSNLDLDTLSQSPTFEQSLHAPPG 403

Qy 414 ILKKKSTSSGSEVQE 428
Db 404 SKNRHSHRHSKRTOQ 418
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Search completed: January 22, 2005, 06:43:51
Job time : 42.5452 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2005, 06:43:09 ; Search time 146.329 Seconds
(without alignments)
1557.950 Million cell updates/sec

Title: US-09-980-464-11

Perfect score: 3293

Sequence: 1 MESVALLQRPQAPSASALA.....DCQEVTAAYRQALGICKLS 631

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3293	100.0	631	14	US-10-355-975-11
2	3186	96.8	640	16	US-10-322-281-23
3	3068	93.2	630	16	US-10-343-514-41
4	2824	85.8	628	9	US-09-963-159-2
5	2824	85.8	628	15	US-10-423-543-44
6	2824	85.8	628	17	US-10-370-715B-640
7	2824	85.8	672	17	US-10-618-941-77
8	2720	82.6	594	15	US-10-311-034-12
9	2712	82.4	616	16	US-10-322-281-26
10	1781	54.1	406	16	US-10-363-829-404
11	1781	54.1	406	16	US-10-363-829-504
12	1699	51.6	661	9	US-09-780-949-2
13	1699	51.6	661	9	US-09-780-949-6

14	1699.5	51.6	661	14	US-10-354-358-82	Sequence 82, Appl
15	1699.5	51.6	661	17	US-10-723-860-2553	Sequence 2553, Ap
16	1325	40.2	251	16	US-10-343-514-103	Sequence 103, App
17	1301.5	39.5	530	9	US-09-836-392-20	Sequence 20, Appl
18	1296	39.4	251	16	US-10-343-514-50	Sequence 50, Appl
19	1276	38.7	251	16	US-10-343-514-101	Sequence 101, App
20	1111.5	33.8	252	16	US-10-343-514-102	Sequence 102, App
21	785.5	23.9	246	10	US-09-898-837A-29	Sequence 29, Appl
22	748	22.7	703	15	US-10-016-248-70	Sequence 70, Appl
23	748	22.7	752	9	US-09-835-081-2	Sequence 2, Appli
24	748	22.7	752	15	US-10-258-106-16	Sequence 16, Appl
25	748	22.7	752	15	US-10-276-645-7	Sequence 7, Appli
26	748	22.7	825	15	US-10-425-114-54516	Sequence 54516, A
27	744	22.6	639	15	US-10-016-248-71	Sequence 71, Appl
28	744	22.6	639	15	US-10-016-248-72	Sequence 72, Appl
29	744	22.6	688	15	US-10-276-645-8	Sequence 8, Appli
30	744	22.6	752	17	US-10-618-941-79	Sequence 79, Appl
31	743.5	22.6	769	15	US-10-363-616-403	Sequence 403, App
32	739	22.4	639	15	US-10-016-248-73	Sequence 73, Appl
33	739	22.4	688	14	US-10-161-565-28	Sequence 28, Appl
34	739	22.4	688	14	US-10-161-565-29	Sequence 29, Appl
35	735	22.4	724	15	US-10-276-645-5	Sequence 5, Appli
36	732.5	22.2	660	15	US-10-276-645-6	Sequence 6, Appli
37	703.5	21.4	729	14	US-10-142-356-11	Sequence 11, Appl
38	703.5	21.4	729	14	US-10-195-101-33	Sequence 33, Appl
39	703.5	21.4	729	14	US-10-161-565-26	Sequence 26, Appl
40	701	21.3	140	16	US-10-343-514-47	Sequence 47, Appl
41	701	21.3	744	9	US-09-835-081-4	Sequence 4, Appli
42	700.5	21.3	1038	15	US-10-424-599-274878	Sequence 274878, A
43	698.5	21.2	634	15	US-10-425-114-70100	Sequence 70100, A
44	698.5	21.2	744	9	US-09-919-585-3	Sequence 3, Appli
45	698	21.2	698	15	US-10-016-248-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-10-355-975-11
; Sequence 11, Application US/10355975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT FILING DATE: 2003-01-30
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/579,664B
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975-11

Query Match 100.0%; Score 3293; DB 14; Length 631;
Best Local Similarity 100.0%; Pred No. 1.4e-206;
Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy . . . 1 MESVALLQRPQAPSASALASARPLADGLIKSPKPLMKQAVKRRHHKHLRHYEFL 60

Db . . . 1 MESVALLQRPQAPSASALASARPLADGLIKSPKPLMKQAVKRRHHKHLRHYEFL 60

Qy . . . 61 ETLLGKGTGYGVKKARESSGRLVAIKRKDKIKDEQDLLHRRREIETIMSSLNPHITAIH 120

Db . . . 61 ETLLGKGTGYGVKKARESSGRLVAIKRKDKIKDEQDLLHRRREIETIMSSLNPHITAIH 120

Qy 121 EVFSSKIVIMVYASRGDLYDISERPLSERDARHFFRQIVSALHYCHONGIVHRDL 180
Db 121 EVFSSKIVIMVYASRGDLYDISERPLSERDARHFFRQIVSALHYCHONGIVHRDL 180
Qy 181 KLENILLDANGNIKIADFGLSNLHYHKGKFLQTFGSGPLYASPEIVNGKPYVGPVDSWSL 240
Db 181 KLENILLDANGNIKIADFGLSNLHYHKGKFLQTFGSGPLYASPEIVNGKPYVGPVDSWSL 240
Qy 241 GVLILYLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 300
Db 241 GVLILYLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 300
Qy 301 VASHWVNWGYTTGVGEQALREGGHPGSDPGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Db 301 VASHWVNWGYTTGVGEQALREGGHPGSDPGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Qy 361 HVPGGSTVPGLEQHSLLKSRKENDMAQNLQGDPAEDTSRRPKGSKSLKLPKGLKKSS 420
Db 361 HVPGGSTVPGLEQHSLLKSRKENDMAQNLQGDPAEDTSRRPKGSKSLKLPKGLKKSS 420
Qy 421 TSSEVOEDPOELRPVDPDPGQPVAVSLLPRKGLKKSRQESGYSSPEPSEGLLD 480
Db 421 TSSEVOEDPOELRPVDPDPGQPVAVSLLPRKGLKKSRQESGYSSPEPSEGLLD 480
Qy 481 ASDVFVSGDPVEQKSPQASGLLLHRRKGLKNGKFSRTALEGTPSTFGSLDOLASSHPA 540
Db 481 ASDVFVSGDPVEQKSPQASGLLLHRRKGLKNGKFSRTALEGTPSTFGSLDOLASSHPA 540
Qy 541 ARPSRPGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLRGLQEPPEGLKRWQ 600
Db 541 ARPSRPGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLRGLQEPPEGLKRWQ 600
Qy 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631
Db 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631

RESULT 2

US-10-322-281-23
; Sequence 23, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-23

Query Match 96.8%; Score 3186; DB 16; Length 640;
Best Local Similarity 98.3%; Pred. No. 1.4e-199;
Matches 620; Conservative 0; Mismatches 1; Indels 10; Gaps 5;

Qy 1 MESVALLQRPSPASALASESARPLADGLIKSPKLMKKQAVKRHHKHNLRHYEFL 60
Db 20 MESV--LQRPSPASAS--ASESARPLADGLIKSPKLMKKQAVKRHHKHNLRHYEFL 75
Qy 61 ETLGKGTGKVKKARESSGRVVAIKSRDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
Db 76 ETLGKGTGKVKKARESSGRVVAIKSRDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 135
Qy 121 EVFSSKIVIMVYASRGDLYDISERPLSERDARHFFRQIVSALHYCHONGIVHRDL 180
Db 136 EVFSSKIVIMVYASRGDLYDIS--PRLS--DARHFFRQIVSALHYCHONGIVHRDL 191
Qy 181 KLENILLDANGNIKIADFGLSNLHYHKGKFLQTFGSGPLYASPEIVNGKPYVGPVDSWSL 240

Db 192 KLENILLDANGNIKIADFGLSNLHYHKGKFLQTFGSGPLY--DEIVNGKPYVGPVDSWSL 249
Qy 241 GVLILYLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 300
Db 250 GVLILYLVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTTRATLED 309
Qy 301 VASHWVNWGYTTGVGEQALREGGHPGSDPGRASMDWLRSSRPLLENGAKVCSFFKQ 360
Db 310 VASHWVNWGYTTGVGEQALREGGHPGSDPGRASMDWLRSSRPLLENGAKVCSFFKQ 369
Qy 361 HVPGGSTVPGLEQHSLLKSRKENDMAQNLQGDPAEDTSRRPKGSKSLKLPKGLKKSS 420
Db 370 HVPGGSTVPGLEQHSLLKSRKENDMAQNLQGDPAEDTSRRPKGSKSLKLPKGLKKSS 429
Qy 421 TSSEVOEDPOELRPVDPDPGQPVAVSLLPRKGLKKSRQESGYSSPEPSEGLLD 480
Db 430 TSSEVOEDPOELRPVDPDPGQPVAVSLLPRKGLKKSRQESGYSSPEPSEGLLD 489
Qy 481 ASDVFVSGDPVEQKSPQASGLLLHRRKGLKNGKFSRTALEGTPSTFGSLDOLASSHPA 540
Db 490 ASDVFVSGDPVEQKSPQASGLLLHRRKGLKNGKFSRTALEGTPSTFGSLDOLASSHPA 549
Qy 541 ARPSRPGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLRGLQEPPEGLKRWQ 600
Db 550 ARPSRPGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLRGLQEPPEGLKRWQ 609
Qy 601 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 631
Db 610 ESLGDSFSLTDCQEVTAAYRQALGICSKLS 640

RESULT 3

US-10-343-514-41
; Sequence 41, Application US/10343514
; Publication No. US20040132025A1
; GENERAL INFORMATION:

; APPLICANT: DRUCKER, Daniel J.
; APPLICANT: ROSEN, Cheryl E.
; APPLICANT: LEFEBVRE, Diana L.
; TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
; FILE REFERENCE: DPA-DRUC2/PCT
; CURRENT APPLICATION NUMBER: US/10/343,514
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: PCT/CA01/01109
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,650
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/274,613
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: CA 2,340,780
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 630
; TYPE: PRT
; ORGANISM: RAT
US-10-343-514-41

Query Match 93.2%; Score 3068.5; DB 16; Length 630;
Best Local Similarity 94.0%; Pred. No. 6.4e-192;
Matches 593; Conservative 12; Mismatches 25; Indels 1; Gaps 1;

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Qy 61 ETLGKGTGKVKKARESSGRVVAIKSRDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
Db 61 ETLGKGTGKVKKARESSGRVVAIKSRDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
Qy 121 EVFSSKIVIMVYASRGDLYDISERPLSERDARHFFRQIVSALHYCHONGIVHRDL 180

Db 121 EVFENSKIIVMEYASRGDLYISERPRNERDARHFRQIYSAHYCHONGIYVHRDL 180
Qy 181 KLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLYASPEIYVNGKPYVGPVDSWSL 240
Db 181 KLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLYASPEIYVNGKPYVGPVDSWSL 240
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Db 241 GVLLYILVHGTMPDGDHKTIVKQISNGAYRPPKPSDACGLIRWLLMNPTRATLED 300
Qy 301 VASHWVNWGYTTGCGEQEALREGGHPGDSGRASMDLRRSRPILLENGAKVCSFPKQ 360
Db 301 VASHWVNWGYTTGCGEQEALREGGHPGDSGRASMDLRRSRPILLENGAKVCSFPKQ 360
Qy 361 HVPGGGTVPLGRQHSLSKSRKENDMAQNLQGDPAEDTSSRPCKSKSLPKGLKXKSS 420
Db 361 HVPGGGTVPLGRQHSLSKSRKENDMAQNLQGDPAEDTSSRPCKSKSLPKGLKXKSS 420
Qy 421 TSSEVOEDQELRPVDPDTPGQVPAVSLPRKGLKXKSRQESGYSSPEPESGELL 480
Db 421 TSSEVOEDQELRPVDPDTPGQVPAVSLPRKGLKXKSRQESGYSSPEPESGELL 480
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Db 481 ASDVFGSDPVEQKSPQASGLLHRRKGLKXKSRQESGYSSPEPESGELL 540
Qy 541 ARPSRPGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQPPSEGLKRWQ 600
Db 541 ARPSRPGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQPPSEGLKRWQ 600
Qy 601 ESLGDSRFSLTDCQEVTAAYRQALGICSKLS 631
Db 601 ESLGDSRFSLTDCQEVTAAYRQALGICSKLS 630

RESULT 4

US-09-963-159-2
; Sequence 2, Application US/09963159
; Patent No. US20020077312A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR
; FILE REFERENCE: 10147-50U1
; CURRENT APPLICATION NUMBER: US/09/963,159
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-159-2

Query Match 85.8%; Score 2824.5; DB 9; Length 628;
Best Local Similarity 85.7%; Pred. No. 5.4e-176;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;
Qy 1 MESVALLQRFPSQAPSASALASESARPLADGLIKSPKPKMKKQAVKRRHHKHLRHYEFL 60
Db 1 MESLVFARRSGPTFS----AAELARPLAEGLIKSPKPKMKKQAVKRRHHKHLRHYEFL 56
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Db 57 ETLGKGYGVKKVARESSGRVLAIKSRKDKIQDEQLLHRIEIMSSLNPHIATIH 116
Qy 121 EVFENSKIIVMEYASRGDLYISERPRNERDARHFRQIYSAHYCHONGIYVHRDL 180
Db 117 EVFENSKIIVMEYASRGDLYISERPRNERDARHFRQIYSAHYCHONGIYVHRDL 176

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Db 177 KLENILLDANGNIKIADFGLSNLYHKGFQTFGCSPLYASPEIYVNGKPYVGPVDSWSL 236
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Db 237 GVLLYILVHGTMPDGDHKTIVKQISNGAYRPPKPSDACGLIRWLLMNPTRATLED 296
Qy 301 VASHWVNWGYTTGCGEQEALREGGHPGDSGRASMDLRRSRPILLENGAKVCSFPKQ 360
Db 297 VASHWVNWGYTTGCGEQEALREGGHPGDSGRASMDLRRSRPILLENGAKVCSFPKQ 356
Qy 361 HVPGGGTVPLGRQHSLSKSRKENDMAQNLQGDPAEDTSSRPCKSKSLPKGLKXKSS 420
Db 357 HAPGGGTTPLGRQHSLSKSRKENDMAQNLQGDPAEDTSSRPCKSKSLPKGLKXKSS 416
Qy 421 TSSEVOEDQELRPVDPDTPGQVPAVSLPRKGLKXKSRQESGYSSPEPESGELL 480
Db 417 ASAGVQEDQELRPVDPDTPGQVPAVSLPRKGLKXKSRQESGYSSPEPESGELL 473
Qy 481 ASDVFGSDPVEQKSPQASGLLHRRKGLKXKSRQESGYSSPEPESGELL 540
Db 474 AGDVFGSDPVEQKSPQASGLLHRRKGLKXKSRQESGYSSPEPESGELL 533
Qy 541 ARPSRPGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQPPSEGLKRWQ 596
Db 534 ARASRPGAVSEDSILSESFDQDLPERLPETPLRCVSDNLRGLQPPSEGLKRWQ 593
Qy 597 RHWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 594 RWRQDLGDSFSLTDCQEVTAAYRQALGICSKLS 628

RESULT 5

US-10-423-543-44
; Sequence 44, Application US/10423543
; Publication No. US2004005835A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Libermann, Rosana K.
; APPLICANT: Hunter, John J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Chun, Miyoung
; APPLICANT: Williamson, Mark J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 21910, 56634, 55053, 2504, 15977,
; TITLE OF INVENTION: 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638,
; TITLE OF INVENTION: 18610, 33217, 21967, h1983, m1983, 38555 OR 593 MOLECULES
; FILE REFERENCE: MPI03-023OMNIM
; CURRENT APPLICATION NUMBER: US/10/423,543
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 10/278,036
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 09/711,216
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/205,447
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 10/012,055
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,325
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 10/003,690
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/248,893
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 09/797,039

; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 10/217,168
; PRIOR FILING DATE: 2002-08-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-423-543-44

Query Match 85.8%; Score 2824.5; DB 15; Length 628;
Best Local Similarity 85.7%; Pred. No. 5.4e-176;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;
Qy 1 MESVALLQRPSPASALASESARPLADGLIKSPKPLMKKQAVKRRHHKHNLRHYEFL 60
Db 1 MESLVFARRSGPTFS----AAELARPLAELGLIKSPKPLMKKQAVKRRHHKHNLRHYEFL 56
Qy 61 ETLGKGTGKVKKARESSGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
Db 57 ETLGKGTGKVKKARESSGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 116
Qy 121 EVFENSISKIVIMYASRGDLVDYISERPLSRDARHFRQIVSALHYCHONGIVHRDL 180
Db 117 EVFENSISKIVIMYASRGDLVDYISERQQLSREARHFRQIVSALHYCHONRVHRDL 176
Qy 181 KLENILLDANGNIKIADFGLSNLYHGKFLQTCGSPLYASPELVNGKPYVGPVEDWSWL 240
Db 177 KLENILLDANGNIKIADFGLSNLYHGKFLQTCGSPLYASPELVNGKPYTGPVEDWSWL 236
Qy 241 GVLLYILVHGTMPFDGDKHTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRATLED 300
Db 237 GVLLYILVHGTMPFDGDKHTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRATLED 296
Qy 301 VASHWWNWGTYTGVGQEARLREGHSPGDPGRASMDWLRSSRPILLENGAKVCSFFKQ 360
Db 297 VASHWWNWGTYATRVGEQAPHEGHPGSDSARASMDWLRSSRPILLENGAKVCSFFKQ 356
Qy 361 HVPGGSTVPCLEHQSLKSKRKENDMAQNLQGPDAEDTSRPPCKSSILKPKGLKKKVS 420
Db 357 HAPGGGTTTGLERQSLKSKRKENDMAQSLHSDTADDTAHRPCKSNLKLKPKGLKKKVS 416
Qy 421 TSSEGEQEDPQLRPVDPDPGQPVPAVSLPRKGLKSKRQRESGYSSPEPSESGLLD 480
Db 417 ASAEVQEDPPELSPASPQQAAP---LLPKGILKKPRQRESGYSSPEPSESGLLD 473
Qy 481 ASDVFSVSGDPVEQKSPQASGLLLHRKGLKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Db 474 AGDVFSVSGDPKEQKPPQASGLLLHRKGLKNGKFSQTALEAAPTTFGSLDELAPRPL 533
Qy 541 ARPSRPSGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLRGLEQPPSEG---LK 596
Db 534 ARASRPSGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLTGLEPPEPSEGCLR 593
Qy 597 RWMQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 594 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 628

RESULT 6
US-10-370-715B-640
; Sequence 640, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET

; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 640
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-640

Query Match 85.8%; Score 2824.5; DB 17; Length 628;
Best Local Similarity 85.7%; Pred. No. 5.4e-176;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;
Qy 1 MESVALLQRPSPASALASESARPLADGLIKSPKPLMKKQAVKRRHHKHNLRHYEFL 60
Db 1 MESLVFARRSGPTFS----AAELARPLAELGLIKSPKPLMKKQAVKRRHHKHNLRHYEFL 56
Qy 61 ETLGKGTGKVKKARESSGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 120
Db 57 ETLGKGTGKVKKARESSGRLVAIKSRKDKIKDEQDLHRRREIEMSSLNHPHIIAIIH 116
Qy 121 EVFENSISKIVIMYASRGDLVDYISERPLSRDARHFRQIVSALHYCHONGIVHRDL 180
Db 117 EVFENSISKIVIMYASRGDLVDYISERQQLSREARHFRQIVSALHYCHONRVHRDL 176
Qy 181 KLENILLDANGNIKIADFGLSNLYHGKFLQTCGSPLYASPELVNGKPYVGPVEDWSWL 240
Db 177 KLENILLDANGNIKIADFGLSNLYHGKFLQTCGSPLYASPELVNGKPYTGPVEDWSWL 236
Qy 241 GVLLYILVHGTMPFDGDKHTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRATLED 300
Db 237 GVLLYILVHGTMPFDGDKHTLVKQISNGAYREPPKPSDACGLIRWLLMVPTRATLED 296
Qy 301 VASHWWNWGTYTGVGQEARLREGHSPGDPGRASMDWLRSSRPILLENGAKVCSFFKQ 360
Db 297 VASHWWNWGTYATRVGEQAPHEGHPGSDSARASMDWLRSSRPILLENGAKVCSFFKQ 356
Qy 361 HVPGGSTVPCLEHQSLKSKRKENDMAQNLQGPDAEDTSRPPCKSSILKPKGLKKKVS 420
Db 357 HAPGGGTTTGLERQSLKSKRKENDMAQSLHSDTADDTAHRPCKSNLKLKPKGLKKKVS 416
Qy 421 TSSEGEQEDPQLRPVDPDPGQPVPAVSLPRKGLKSKRQRESGYSSPEPSESGLLD 480
Db 417 ASAEVQEDPPELSPASPQQAAP---LLPKGILKKPRQRESGYSSPEPSESGLLD 473
Qy 481 ASDVFSVSGDPVEQKSPQASGLLLHRKGLKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Db 474 AGDVFSVSGDPKEQKPPQASGLLLHRKGLKNGKFSQTALEAAPTTFGSLDELAPRPL 533
Qy 541 ARPSRPSGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLRGLEQPPSEG---LK 596
Db 534 ARASRPSGAVSEDSILSESFDQLDLPERLPETPLRGCVSDNLTGLEPPEPSEGCLR 593
Qy 597 RWMQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 594 RWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 628

RESULT 7
US-10-618-941-77
; Sequence 77, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN

; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-77

Query Match 85.8%; Score 2824.5; DB 17; Length 672;
Best Local Similarity 85.7%; Pred. No. 5.9e-176;
Matches 544; Conservative 26; Mismatches 54; Indels 11; Gaps 3;

Qy 1 MESVALIQRPSQAPSASALASESARPLADGLIKSPKPLMKQAVKRHHKHLRHYEFL 60
Db 45 MESLVFARRSGTPS---AAELARPLAELGKSPKPLMKQAVKRHHKHLRHYEFL 100

Qy 61 ETLGKGTGKVKKARESGRLVAIKSRKDKIKDEODLLHRRREIEMSSLNHPHIIAH 120
Db 101 ETLGKGTGKVKKARESGRLVAIKSRKDKIKDEODLLHRRREIEMSSLNHPHIIAH 160

Qy 121 EVFENSSKIVIMEYASRGDLVDYISERPLSRDARHFRQIVSALHYCHONGIVHRDL 180
Db 161 EVFENSSKIVIMEYASRGDLVDYISERQQUSEARHFRQIVSALHYCHONRVHRDL 220

Qy 181 KLENILLDANGNIKIADFGLSNLHYKGFLOTQCGSPLYASPEIVNGKPYVGPVDSWSL 240
Db 221 KLENILLDANGNIKIADFGLSNLHYKGFLOTQCGSPLYASPEIVNGKPYVGPVDSWSL 280

Qy 241 GVLLYILVHGTMPDQDHKTLVQISNGAYREPPKSDACGLIRWLLMNPTRATLED 300
Db 281 GVLLYILVHGTMPDQDHKTLVQISNGAYREPPKSDACGLIRWLLMNPTRATLED 340

Qy 301 VASHWWNWGTYTGVGOEALREGHPGSDGDFGRASMDWLRSSRPILLENGAKVCSFFKQ 360
Db 341 VASHWWNWGTYTGVGOEALREGHPGSDGDFGRASMDWLRSSRPILLENGAKVCSFFKQ 400

Qy 361 HVPGGSTVTPGLERQHSIKSRKENDMAQNLQGDPAEDTSRPGKSSIKLPKILKKSS 420
Db 401 HAPGGSTVTPGLERQHSIKSRKENDMAQNLQGDPAEDTSRPGKSSIKLPKILKKSS 460

Qy 421 TSSEVEDQPELAPVDPDTPQVPVAVSLLPKILKKRQRESGYSSPEPSSEGLLD 480
Db 461 ASAEVQEDPPPELSPFIPASPCQAAP--LLPKGILKKRQRESGYSSPEPSSEGLLD 517

Qy 481 ASDVFSVSDPVEOKSPQASGLLHRRKGLILKNGKFSRTALEGTTPTFGSLDQLASSHPA 540
Db 518 AGDVFSVSDPVEOKSPQASGLLHRRKGLILKNGKFSRTALEGTTPTFGSLDQLASSHPA 577

Qy 541 ARPSRPGVSEDSILSESDQDLDELPERLPETPLRGCVSDNLRGLEQPPSEG---LK 596
Db 578 ARASRPGVSEDSILSESDQDLDELPERLPETPLRGCVSDNLRGLEQPPSEG---LK 637

Qy 597 RWMQESLGDSCFSLTDCQEVTAARQALGICSKLS 631
Db 638 RWRQDPLGDSFSLTDCQEVTAARQALGICSKLS 672

RESULT 8

US-10-311-034-12
; Sequence 12, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Javalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAPALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.
; APPLICANT: KHAH, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GREYER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
; 60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0-0
25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CD1
US-10-311-034-12

Query Match 82.6%; Score 2720.5; DB 15; Length 594;
Best Local Similarity 87.3%; Pred. No. 3.1e-169;
Matches 521; Conservative 22; Mismatches 47; Indels 7; Gaps 2;

Qy 39 MKQAVRHHKHLRHYEFLETGKGTGKVKKARESGRLVAIKSRKDKIKDEODL 98
Db 1 MKQAVRHHKHLRHYEFLETGKGTGKVKKARESGRLVAIKSRKDKIKDEODL 60

Qy 99 LHIRREIEMSSLNHPHIIAHEVFENSSKIVIMEYASRGDLVDYISERPLSRDARH 158
Db 61 MHIRREIEMSSLNHPHIIAHEVFENSSKIVIMEYASRGDLVDYISERQQLSREARH 120

Qy 159 FFRQIVSALHYCHONGIVHRDLKLENILLDANGNIKIADFGLSNLHYKGFLOTFCGSPL 218
Db 121 FFRQIVSALHYCHONGIVHRDLKLENILLDANGNIKIADFGLSNLHYKGFLOTFCGSPL 180

Qy 219 YASPEIVNGKPYVGPVDSWSLGVLLYILVHGTMPDQDHKTLVQISNGAYREPPKPS 278
Db 181 YASPEIVNGKPYVGPVDSWSLGVLLYILVHGTMPDQDHKTLVQISNGAYREPPKPS 240

Qy 279 DACGLIRWLLMNPTRATLEDVASHWWNVNGYTTGVGOEALREGHPGSDGFCRASMD 338
Db 241 DACGLIRWLLMNPTRATLEDVASHWWNVNGYTTGVGOEALREGHPGSDGFCRASMD 300

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Qy 339 WLRSSRLLENGAKVCSFFKQHPGCGSTVPGLEHSHLKKSKENDMAONLQDPAED 398
Db 301 WLRSSRLLENGAKVCSFFKQHPGCGSTVPGLEHSHLKKSKENDMAQSHSDTADD 360
Qy 399 TSSRPGSSSLKPKGILKKKSTSSGEVQEDPQELRPVDPFGQPVPAVSLLPKRGILKK 458
Db 361 TAHRPGKSNLKPGLKKVKSASAGVQEDPPELSPASPQGAAP---LLPKGILKK 417
Qy 459 SRORESGYSSPEPSESGELLADSDVFSVGPVQKQPQASGLLHRRKILKNGKFSRT 518
Db 418 PRORESGYSSPEPSESGELLADSDVFSVGPVQKQPQASGLLHRRKILKNGKFSQT 477
Qy 519 ALEGTSTFGSLDQASHHPAARPSRSGAVSDESISSSFQDLDPERLPETPLRG 578
Db 478 ALELAAPTTFGSLDELAPPRLARASRPSGAVSDESISSSFQDLDPERLPETPLRG 537
Qy 579 VSDNLRGLEQPPSEG---LKRWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 538 VSDNLTGLEPPSEGCGSCLRRWRQDPLGDSFSLTDCQEVTAAYRQALRVCSKLT 594

RESULT 9
US-10-322-281-26
; Sequence 26, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-26

Query Match 82.4%; Score 2712.5; DB 16; Length 616;
Best Local Similarity 84.3%; Pred. No. 1.1e-168;
Matches 535; Conservative 25; Mismatches 52; Indels 23; Gaps 9;

Qy 1 MESVALLQRPQASASALASESRAPLADGLIKSPKLMKKQAVKRRHHKINLRHYEFL 60
Db 1 MESLVFARRSGPTFS---AAELARPLAEGSLIKSPKLMKKQAVKRRHHKINLRHYEFL 56
Qy 61 ETLGKTYGVKKARESGRLVAIKSRKDKIKDEQDLHTRREIEIMSSLNHPHIIAIIH 120
Db 57 ETLGKTYGVKKARESGRLVAIKSRKDKIKDEQDLHTRREIEIMSSLNHPHIIAIIH 116
Qy 121 EVFENSKIVMYSAGRDLYDYISERPLSRDARHFRQIVSALHYCHQNGIVHRDL 180
Db 117 EVFENSKIVMYSAGRDLYDYISQ--QLSE--ARHFRQIVSAYHYCHQNRVHRDL 172
Qy 181 KLENILDANIKIADFGSLNLYHKGFLQTCGSPLYASPEIVNGKPYVGPVDSWSL 240
Db 173 KLENILDANIKIADFGSLNLYHKGFLQTCGSPLY--DEIVNGKPYTGPVDSWSL 230
Qy 241 GVLLIYLVHGTMPDGDHKTLLVQISNGAYREPPKPSDACGLIRWLLMWNPTRRATLED 300
Db 231 GVLLIYLVHGTMPDGDHKTLLVQISNGAYREPPKPSDACGLIRWLLMWNPTRRATLED 290
Qy 301 VASHWVNWGVTGVBQEARREGHPSGDFGRASMDLWLRSSRPLLENGAKVCSFFKQ 360
Db 291 VASHWVNWGVTATRVGEQEAFF--GGHPGDSARASMDLWLRSSRPLLENGAKVCSFFKQ 348
Qy 361 HVPGGSGTVPGLERQHSILKKSKENDMAONLQDPAEDTSSRPGKSSILKPKGILKKKSS 420
Db 349 HAPGGSGTTPGLERQHSILKKSKENDMAQSHSDTADDTAHRPGKSNLKPGLKKKVS 408
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Qy 421 TSSEVQEDPQELRPVDPFGQPVPAVSLLPKRGILKKSKRQRESGYSSPEPSESGELL 480
Db 409 ASAEVQEDPPELSPDPD---GQAAP---LLPKGILKKRQRESGYSSPEPSESGELL 463
Qy 481 ASDVFSVGDPEVQKQPQASGLLHRRKILKNGKFSRTALEGTTPTSTFGSLDQASHHPA 540
Db 464 AGDVFSVGDPEKQKQPQASGLLHRRKILKNGKFSQTALELAAPTTFGSLDELAPRPL 523
Qy 541 ARSRPSGAVSDESISSSFQDLDPERLPETPLRGCVSDNLRGLRQPPSEG---LK 596
Db 524 ARASRPSGAVSDESISSSFQDLDPERLPETPLRGCVSDNLTGLLEPPSEGPGCLR 583
Qy 597 RWOQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 584 RWRQDPLGDSFSLTDCQEVTA--YQALRVCSKLT 616

RESULT 10
US-10-363-829-404
; Sequence 404, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anisea L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiya, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10/363,829
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: PCT/US01/27628
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,610
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/230,597
; PRIOR FILING DATE: 2000-09-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PERL Program
; SEQ ID NO 404
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LG:982800.1.orf1.2000SEP08
US-10-363-829-404
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Query Match 54.1%; Score 1781.5; DB 16; Length 406;
Best Local Similarity 83.6%; Pred. No. 4.1e-108;
Matches 342; Conservative 16; Mismatches 44; Indels 7; Gaps 2;

Qy 227 GKPVGVPEVDSWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRW 286
Db 1 GKPYTGVPEVDSWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRW 60

Qy 287 LLMVNPTRRATLEDVASHWVNMVNYTTGVGQEQALREGHPGSDGRASMAWMLRRSSRP 346
Db 61 LLMVNPTRRATLEDVASHWVNMVNYTTGVGQEQALREGHPGSDGRASMAWMLRRSSRP 120

Qy 347 LLENGAKVCSFFKQHVPGGSGTVPLERQHSLSKSRKENDMAQNLQDPAEDTSSRPCKS 406
Db 121 LLENGAKVCSFFKQHVPGGSGTVPLERQHSLSKSRKENDMAQNLQDPAEDTSSRPCKS 180

Qy 407 SLKLPKGLKSKSTSSEGEVQEDPQELRPVDPDTGQVPAVSLPLPRKGLKSKSRQESGY 466
Db 181 NLKLPKGLKSKSTSSEGEVQEDPQELRPVDPDTGQVPAVSLPLPRKGLKSKSRQESGY 237

Qy 467 YSSPEPSESGELLASHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSDNLRG 586
Db 298 YSSPEPSESGELLASHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSDNLRG 357

Qy 587 LEQPPSESG-----LKRWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 358 LEEPPSESGCLRRWRQDPLGDSCLFSLTDCQEVTAAYRQALRVCSKLT 406

RESULT 11
US-10-363-829-504
; Sequence 504, Application US/10363829
; Publication No. US20040142331A1
; GENERAL INFORMATION:
; APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
; APPLICANT: Alcus, Christina M.; Dufour, Gerard E.;
; APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
; APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
; APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
; APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
; APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
; APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
; APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
; APPLICANT: Gerstin, Jr., Edward H.; Panzer, Scott R.;
; APPLICANT: David, Marie H.; Panzer, Scott R.;
; APPLICANT: Flores, Vincent Z.; Daffo, Abel;
; APPLICANT: Marwaha, Rakesh; Chen, Alice J.;
; APPLICANT: Chang, Simon C.; Au, Alan P.;
; APPLICANT: Inman, Rebekah R.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1183 USN
; CURRENT APPLICATION NUMBER: US/10363829
; CURRENT FILING DATE: 2003-03-05
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/229,751
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,749
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,750
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,747
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/229,748
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,583
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 60/230,517
; PRIOR FILING DATE: 2000-09-06

Query Match 51.6%; Score 1699.5; DB 9; Length 661;
Best Local Similarity 83.6%; Pred. No. 4.1e-108;
Matches 342; Conservative 16; Mismatches 44; Indels 7; Gaps 2;

Qy 227 GKPVGVPEVDSWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRW 286
Db 1 GKPYTGVPEVDSWSLGVLLYLIVHGTMPFDGQDHKTLVKQISNGAYRPPKPSDACGLIRW 60

Qy 287 LLMVNPTRRATLEDVASHWVNMVNYTTGVGQEQALREGHPGSDGRASMAWMLRRSSRP 346
Db 61 LLMVNPTRRATLEDVASHWVNMVNYTTGVGQEQALREGHPGSDGRASMAWMLRRSSRP 120

Qy 347 LLENGAKVCSFFKQHVPGGSGTVPLERQHSLSKSRKENDMAQNLQDPAEDTSSRPCKS 406
Db 121 LLENGAKVCSFFKQHVPGGSGTVPLERQHSLSKSRKENDMAQNLQDPAEDTSSRPCKS 180

Qy 407 SLKLPKGLKSKSTSSEGEVQEDPQELRPVDPDTGQVPAVSLPLPRKGLKSKSRQESGY 466
Db 181 NLKLPKGLKSKSTSSEGEVQEDPQELRPVDPDTGQVPAVSLPLPRKGLKSKSRQESGY 237

Qy 467 YSSPEPSESGELLASHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSDNLRG 586
Db 298 YSSPEPSESGELLASHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSDNLRG 357

Qy 587 LEQPPSESG-----LKRWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
Db 358 LEEPPSESGCLRRWRQDPLGDSCLFSLTDCQEVTAAYRQALRVCSKLT 406

RESULT 12
US-09-780-949-2
; Sequence 2, Application US/09780949
; Patent No. US20020006618A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: Methods for Using 20893, a Human Protein
; TITLE OF INVENTION: Kinase
; FILE REFERENCE: 035800/209015
; CURRENT APPLICATION NUMBER: US/09/780,949
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,690
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 661
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-780-949-2
```

Best Local Similarity 55.5%; Pred. No. 1.7e-102;
Matches 372; Conservative 74; Mismatches 151; Indels 73; Gaps 18;

QY 14 PSASALASESARPLADGLIKSPKPMKKQAVKRRHHKHNLRHRYEFLETGKGYGVKK 73
Db 13 PDLGLGAPGSPREAVAGATAALEP-RKPHGVKRRHHKHNLRHRYELOETLGKGYGVKK 71
QY 74 ARES-SGRVAIKSRKDKIKDEQDLHIREIEMSSLNHPHIIAHEVFENSKIIV 132
Db 72 ATERFSGRVVAIKSRKDKIKDEQDMVHIRREIEMSSLNHPHIIISIVYFENKDKIVII 131
QY 133 MEYASRGDLYIISERPRLSERDARHFRQIVSALHYCHONGIHRDLKLENILLDANGN 192
Db 132 MEYASKGELYDYISERRRLSERETRHFRQIVSAVHYCHONGVVRDLKLENILLDNCN 191
QY 193 IKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVGVPEVDSWSLGLVLLYLVHGT 252
Db 192 IKIADFGLSNLYQDKFLOTFCGSPLYASPEIVNGRPRYRGPVDSWALGVLLYLVYGT 251
QY 253 PFDGQDHTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDAVSHWVNWGYT 312
Db 252 PFDGFDHKNLIRQISSGEYREPTQPSDARGLIRWLLMVNPTRRATIEDIANHWWNWGYK 311
QY 313 TGVEQEALREGGHPGSDGFRASMDWLRSSRPILLENGAKVCSFFKQHVPGGSGTVPGL 372
Db 312 SSVCCDHALHDSPL---LARIIDWHHRSTGLQADTEAKMKGLAK---PTTSEVM--L 362
QY 373 ERQSLKSKKENDMAQNLQDPAEDTSSRPGKSSKLPKGLKSKS-----STSSGEVQ 427
Db 363 ERQSLKSKKENDFAQSGQDAPES-----PSKLSKRPKGLKSKSENSEHRSHTGFIE 418
QY 428 -----EDPQEL-----RPVPTPGQVPVAVS--LLPRKGLKSKRSRSGY 466
Db 419 GVVGPAIPSTFKMQDLCTGTVLLPSSPEAEVPGKSPQKQATMPKKGILKKTQRESGY 478
QY 467 YSSPESESGELLDASDVFSVGDVPEQKSP-----QASGLLLHRKGLKNGKFSRTAL 520
Db 479 YSSPERSESELDSNDVM--GSSIPSPSPDPAVTSLSLSCRRKGLKHSKYAGTM 536
QY 521 EGTTPS-----TFGSLDQ-----LASSHPAARSPRGAVSEDSILSSSEFDDLDLPER 569
Db 537 DPALVSPMPTLESSEPGVPAEGLRSY-----SRPSSVISDDSVLSSDSFDDLDLQEN 591
QY 570 LP-ETPLRGCVSDN-----LRGLEQPPSEGLKRWQESLGDSCFS-LTDCQEVTAAYR 621
Db 592 RPQRIRSCVSAENFLQIQDFEGLQNRPRPQYLKRYNRNLADSSFLSLTMDMDVTVQYK 651
QY 622 QALGICSKLS 631
Db 652 QALEICSKLN 661

RESULT 13

US-09-780-949-6
; Sequence 6, Application US/09780949
; Patent No. US20020006618A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: Methods for Using 20893, a Human Protein
; FILE REFERENCE: 035800/209015
; CURRENT APPLICATION NUMBER: US/09/780,949
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: US 60/181,690
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 661
; TYPE: PRT
; ORGANISM: H. sapiens

US-09-780-949-6

Query Match 51.6%; Score 1699.5; DB 9; Length 661;
Best Local Similarity 55.5%; Pred. No. 1.7e-102;
Matches 372; Conservative 74; Mismatches 151; Indels 73; Gaps 18;

QY 14 PSASALASESARPLADGLIKSPKPMKKQAVKRRHHKHNLRHRYEFLETGKGYGVKK 73
Db 13 PDLGLGAPGSPREAVAGATAALEP-RKPHGVKRRHHKHNLRHRYELOETLGKGYGVKK 71
QY 74 ARES-SGRVAIKSRKDKIKDEQDLHIREIEMSSLNHPHIIAHEVFENSKIIV 132
Db 72 ATERFSGRVVAIKSRKDKIKDEQDMVHIRREIEMSSLNHPHIIISIVYFENKDKIVII 131
QY 133 MEYASRGDLYIISERPRLSERDARHFRQIVSALHYCHONGIHRDLKLENILLDANGN 192
Db 132 MEYASKGELYDYISERRRLSERETRHFRQIVSAVHYCHONGVVRDLKLENILLDNCN 191
QY 193 IKIADFGLSNLYHKGFLOTFCGSPLYASPEIVNGKPYVGVPEVDSWSLGLVLLYLVHGT 252
Db 192 IKIADFGLSNLYQDKFLOTFCGSPLYASPEIVNGRPRYRGPVDSWALGVLLYLVYGT 251
QY 253 PFDGQDHTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDAVSHWVNWGYT 312
Db 252 PFDGFDHKNLIRQISSGEYREPTQPSDARGLIRWLLMVNPTRRATIEDIANHWWNWGYK 311
QY 313 TGVEQEALREGGHPGSDGFRASMDWLRSSRPILLENGAKVCSFFKQHVPGGSGTVPGL 372
Db 312 SSVCCDHALHDSPL---LARIIDWHHRSTGLQADTEAKMKGLAK---PTTSEVM--L 362
QY 373 ERQSLKSKKENDMAQNLQDPAEDTSSRPGKSSKLPKGLKSKS-----STSSGEVQ 427
Db 363 ERQSLKSKKENDFAQSGQDAPES-----PSKLSKRPKGLKSKSENSEHRSHTGFIE 418
QY 428 -----EDPQEL-----RPVPTPGQVPVAVS--LLPRKGLKSKRSRSGY 466
Db 419 GVVGPAIPSTFKMQDLCTGTVLLPSSPEAEVPGKSPQKQATMPKKGILKKTQRESGY 478
QY 467 YSSPESESGELLDASDVFSVGDVPEQKSP-----QASGLLLHRKGLKNGKFSRTAL 520
Db 479 YSSPERSESELDSNDVM--GSSIPSPSPDPAVTSLSLSCRRKGLKHSKYAGTM 536
QY 521 EGTTPS-----TFGSLDQ-----LASSHPAARSPRGAVSEDSILSSSEFDDLDLPER 569
Db 537 DPALVSPMPTLESSEPGVPAEGLRSY-----SRPSSVISDDSVLSSDSFDDLDLQEN 591
QY 570 LP-ETPLRGCVSDN-----LRGLEQPPSEGLKRWQESLGDSCFS-LTDCQEVTAAYR 621
Db 592 RPQRIRSCVSAENFLQIQDFEGLQNRPRPQYLKRYNRNLADSSFLSLTMDMDVTVQYK 651
QY 622 QALGICSKLS 631
Db 652 QALEICSKLN 661

RESULT 14

US-10-354-358-82
; Sequence 82, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 7522, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,

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; TITLE OF INVENTION: 8990, 2100, 92888, 64598, 10480, 20893, 32330, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 56428 MOLECULES
; FILE REFERENCE: MPI02-020P1ENOMNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-354-358-82

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Query Match	51.8%	Score 1699.5	DB 14	Length 661
Best Local Similarity	55.5%	Pred. No. 1.7e+102		
Matches	372	Conservative 74	Mismatches 151	Indels 73
				Gaps 18
QY	14	PSASALASASARPLADGLIKSPKPLMKQAVKQHHKHNLRHRYEFLTLGKTYGKVKK	73	
DB	13	PDGLGAGSPREAVAGATAALEP-RKPHGVKQHHKHNLKHRYEQLTLGKTYGKVKR	71	
QY	74	ARES-SGRIVAIKSIKDKIKBDQDLHLHRRRETEIMSSLNHPHIIAIEHFVFNSSKIVIV	132	
DB	72	ATERFSGRVAIKSIKDKIKBDQDMHHIRRETEIMSSLNHPHIIISIEVFENDKKIVII	131	
QY	133	MEYASRGDIYDYSERPLSERDARHFFROIVSALHYCHONGIVHVRDLKLENILLDANGN	192	
DB	132	MEYASKGELYDYSERRRLSERETRIHFFROIVSAPHYCHNGVVRDLKLENILLDDNCN	191	
QY	193	IKIADFGLSNLVHKHGFLOTFCGSPLYASPEIYNGRPYGVPEVDSWLSGLLYLVHGTW	252	
DB	192	IKIADFGLSNLVQDKFLOTFCGSPLYASPEIYNGRPYGVPEVDSWALGVLLVTVYGTW	251	
QY	253	PDGQDHKTLVKIQSINGATREPPKPSDACGLIHWLWVNPTRATIEDVASHWWVNGYTT	312	
DB	252	PDGDFDHKNLIRIISGSEYREPTQPSDARGILSWMLMNPDRRATTIEDIANHWWVNGYK	311	
QY	313	TGVGEQEARREGHPSGDFGRASWADWLRRSPILLENGAKVCSFPKHQVPGGGSVPGL	372	
DB	312	SSVCDCCDALHDSSEPL----LARIIDWHHRSTGLQADTEAKMKGLAK----PTTSEVM--L	362	
QY	373	ERQHSLSKKRKENDMAQNLOQDPAEDTSRPGKSSLLPKGIILKKKS-----STSSGEVQ	427	
DB	363	ERQRSLSKKKENDPQSGQDAVPES-----PSKLSKSRPKGIILKKRSNSHRSHSTGFIE	418	
QY	428	-----EDPQEL-----RPVPDPTGPQVPAPVS-LLPKRGILKKSRQRESGY	466	
DB	419	GVVGPALPSTFKMEQDLCRTGVLLPSSPEAEVPGKLSPKQSATMPKGIILKTKQRESGY	478	
QY	467	YSSPEPSESGELDASDVVFVSGDPVEQKSP-----QASGLLHHRKGIILKNGKFSRTAL	520	

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Db      479  YSSPERSSESLDSNDVM--GSSISPSPPDPDPARTVSHSLSCRRKGILKHSKYSAGTM 536
QY      521  EGTFTFS-----TFGSLDQ-----LASSHPAARPSRGAVSDESDTSSSFQDLDLPER 569
Db      537  DPALVSPMPFTLESLSPPGVPAGLSRSY-----SRPSSVISDDSVLSSDSFDLLDLQEN 591
QY      570  LP-ETPLRGCVSDVN-----LRGLRQPPSEGLKRWQESLGDSCFS-LTDCQEVTAAYR 621
Db      592  RPARQRIRSCVSAENFLIQDFEGLQNRPRPQYLKRYNRRLADSSFSLLTDDMDVTVQVK 651
QY      622  QALGICSKLS 631
Db      652  QALEICSKLN 661

RESULT 15
US-10-723-860-2553
; Sequence 2553, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Composition
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2553
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2553

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Query Match	51.6%	Score	1699.5	DB	17	Length	661
Best Local Similarity	55.5%	Pred.	No. 1.7e-102				
Matches	372	Conservative	74	Mismatches	151	Indels	73
							Gaps
QY	14	PSALAS	SESARPLADGLIKSPKPLMKQAVRHHHKNLRHYEFLETLGKGTGYKKVK	73			
DB	13	PDLGLGAPGSPREAVAGATAALEP	-RPHGVKRRHHHKNLRHYELQETLGGTGYKKVKR	71			
QY	74	ARES	-SGRLVAIKSRKDKIKDQDULLHTRRETEIMSSLNHPHIIAIEHVFENSSKIVT	132			
DB	72	ATERPSGRVAIKSRKDKIKDQDMWHTRRETEIMSSLNHPHIIISIEVFENKDKI	VII	131			
QY	133	MEYASRGDLYDISERPLSERDARHFFRQIVSALHYCHQNGIVHRDLKLEILLDANGN	192				
DB	132	MEYASKGELYDISERRLSERETRHFRRQIVSAVHYCHKNGVHRDLKLEILLDDNCN	191				
QY	193	IKIADPGLSNLYHKGKPLQTFCGSPLYASPEIYNGPYGPEVDSWSGLVLYILVHGTM	252				
DB	192	IKIADPGLSNLYQDKFELQTFCGSPLYASPEIYNGPYRGPEVDSWALGVLYITLYGTM	251				
QY	253	PFQDQDKHTLVKQISGAVREPKPSDACLIRLLVMVNPTRATLEDVASHHWVNWGVT	312				
DB	252	PFDFDHNKLIRQISSGEYREPTQPSDAGLRIRMLVMVNPDRATTIEDANHHWVNWGYK	311				
QY	313	TGVGEQBALRGCHPSGDFGRASGADWLRSSRPLLENGAKVCSFPKQHPVGGG	372				
DB	312	SSVCDALHDSPL---	LARIIDWHHRSTGLQADTEAKKGLAK---	362			
QY	373	ERQHSCLKSRKENDMAQNGDPAEDTSRPGKSSUKLPKGLIKKKS	-----	STSSGEVQ	427		
DB	363	ERQSLKKSKENDFAQSGQDAVPES	----	PSKLSKRPKGILKKRSNSEHRSHSTGTFIE	418		
QY	428	-----	EDQEL-----	RPVDPFGQVPVAVS	-----	LLPRKGILKKRSORESGY	466
DB	419	GVGVPALPSTPFKMQDDLCRTGVLLSPSPAIEVPGLKSPKQSATMPKGLIKKTQORESGY	478				

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Qy 467 YSSPESGELLASDVFSQDPVEQKSP-----QASGLLLHRKGIKUNGKFSRTAL 520
Db 479 YSSPESGELLASDVFSQDPVEQKSP-----QASGLLLHRKGIKUNGKFSRTAL 520
Qy 521 EGTTPS---TFGSLDQ-----LASSHPAARPSRPSGAVSEDSILSSSEFDOLDLPER 569
Db 537 DPALVSPMPTELESUSEPGVPAEGLRSY-----SRPSSVSDSDSVLSSDSFDLLDIQEN 591
Qy 570 LP-ETPLRGCVSDN-----LRGLEQPPSEGLKRWQESLGDSGFS-LTDCQEVTAAYR 621
Db 592 RPARQIRSCVSAENFLQIQDFEGLQNRPRPQYLKRYENRLADSSFSLLTDMDDVTQVYK 651
Qy 622 QALGICSKLS 631
Db 652 QALEICSKLN 661

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Search completed: January 22, 2005, 07:00:33
 Job time : 150.329 secs